



MRC Cognition
and Brain
Sciences Unit



UNIVERSITY OF
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fMRI analysis

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Environment



Data
Organise & Manage

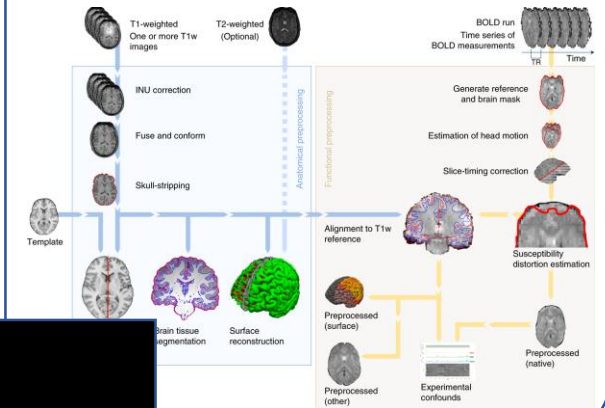
Pre-process

Collect the data

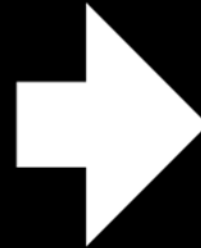


Why can't we analyse right away?

Pre-process & Analyse



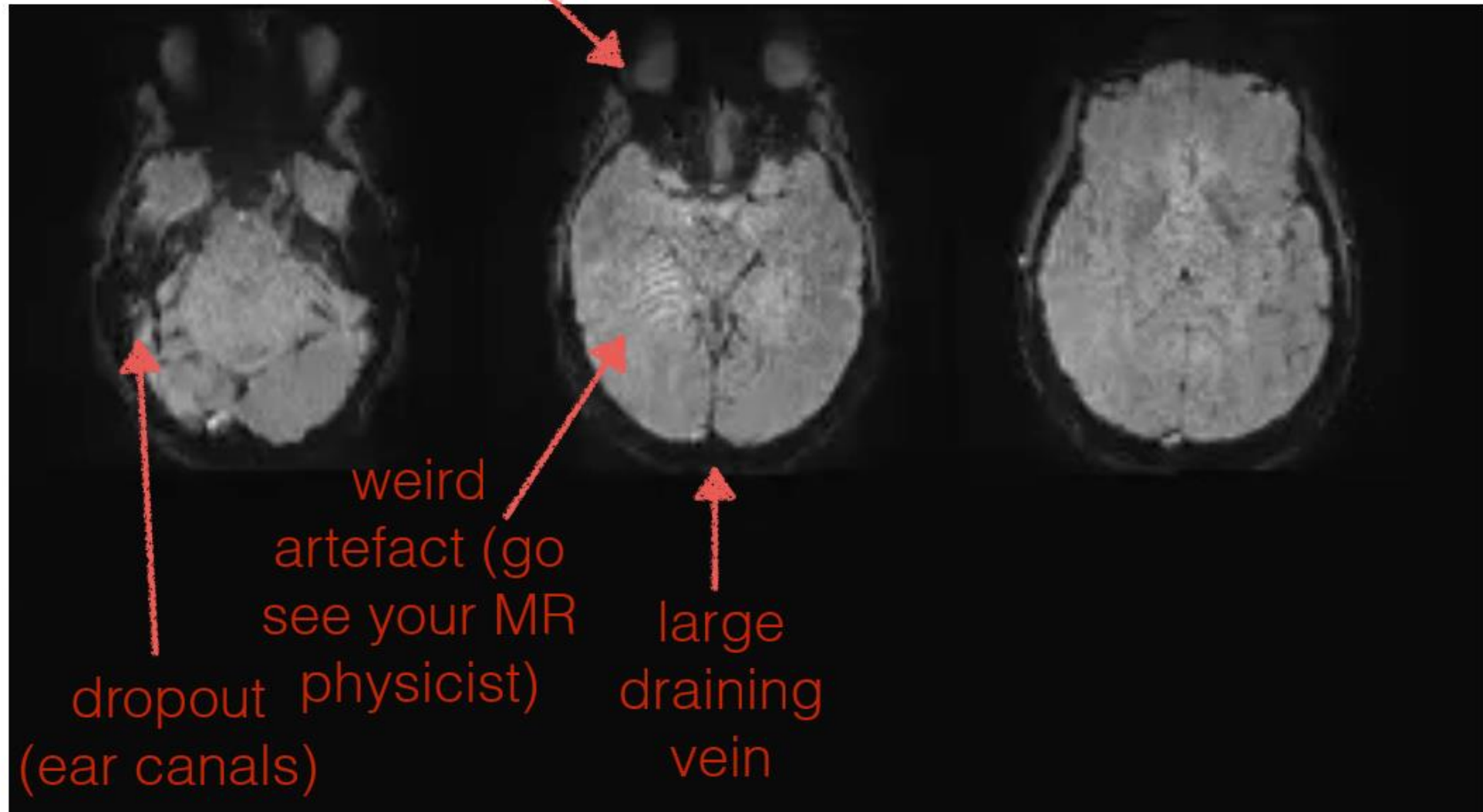
```
dicomdir/  
├── 1208200617178_22/  
│   ├── 1208200617178_22_8973.dcm  
│   ├── 1208200617178_22_8943.dcm  
│   ├── 1208200617178_22_2973.dcm  
│   ├── 1208200617178_22_8923.dcm  
│   ├── 1208200617178_22_4473.dcm  
│   ├── 1208200617178_22_8783.dcm  
│   ├── 1208200617178_22_7328.dcm  
│   ├── 1208200617178_22_9264.dcm  
│   ├── 1208200617178_22_9967.dcm  
│   ├── 1208200617178_22_3894.dcm  
│   └── 1208200617178_22_3899.dcm  
├── 1208200617178_23/  
├── 1208200617178_24/  
└── 1208200617178_25/
```



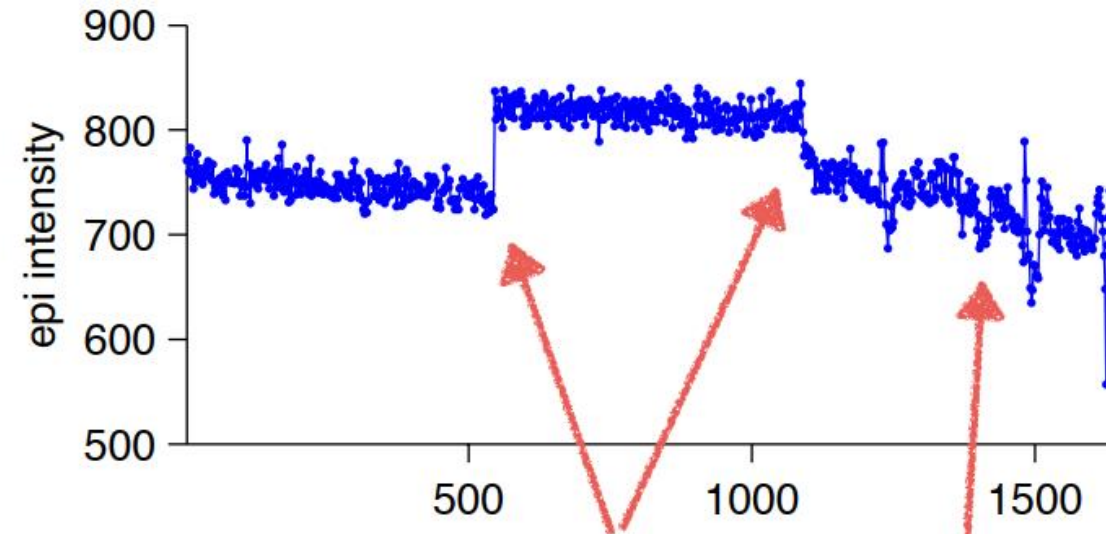
```
my_dataset/  
├── participants.tsv  
├── sub-01/  
│   ├── anat/  
│   │   └── sub-01_T1w.nii.gz  
│   ├── func/  
│   │   ├── sub-01_task-rest_bold.nii.gz  
│   │   ├── sub-01_task-rest_bold.json  
│   │   └── dwi/  
│   │       ├── sub-01_dwi.nii.gz  
│   │       ├── sub-01_dwi.json  
│   │       ├── sub-01_dwi.bval  
│   │       └── sub-01_dwi.bvec  
├── sub-02/  
├── sub-03/  
└── sub-04/
```

Artefacts

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



Raw data in example voxel

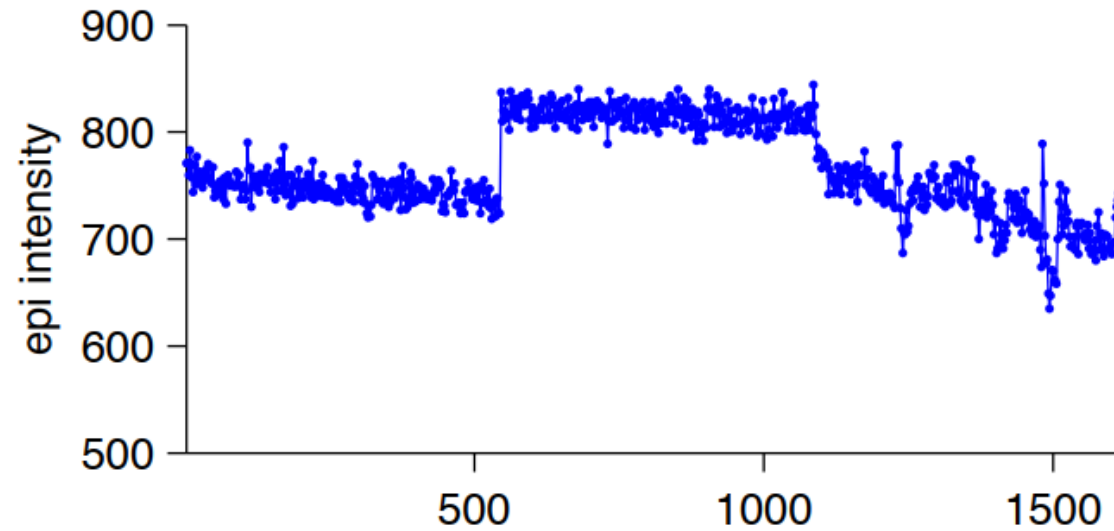


run transitions
(head movement
between scans?)

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

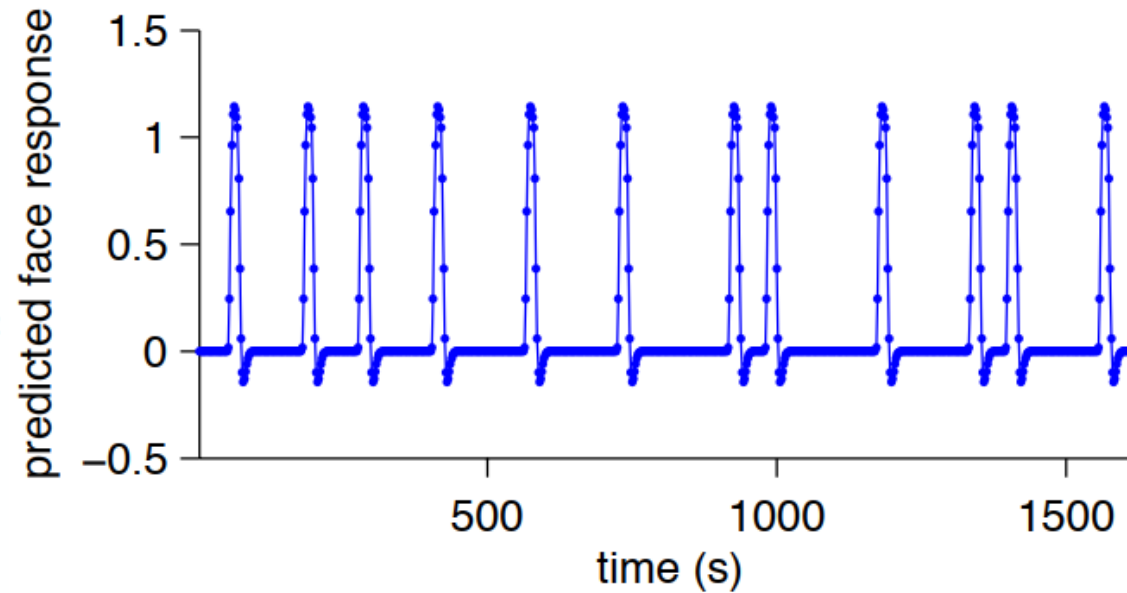
Raw data in example voxel

The (raw) fMRI data



The cognitive model

Not much hope of
this working
without signal
processing





RAW fMRI DATA



CLEANED fMRI DATA

CENTRO DE ESTUDIOS BORJANOS

Problems with fMRI data

- Slice timing
- Head motion
- Brain differences
- Noise
- ... and many others

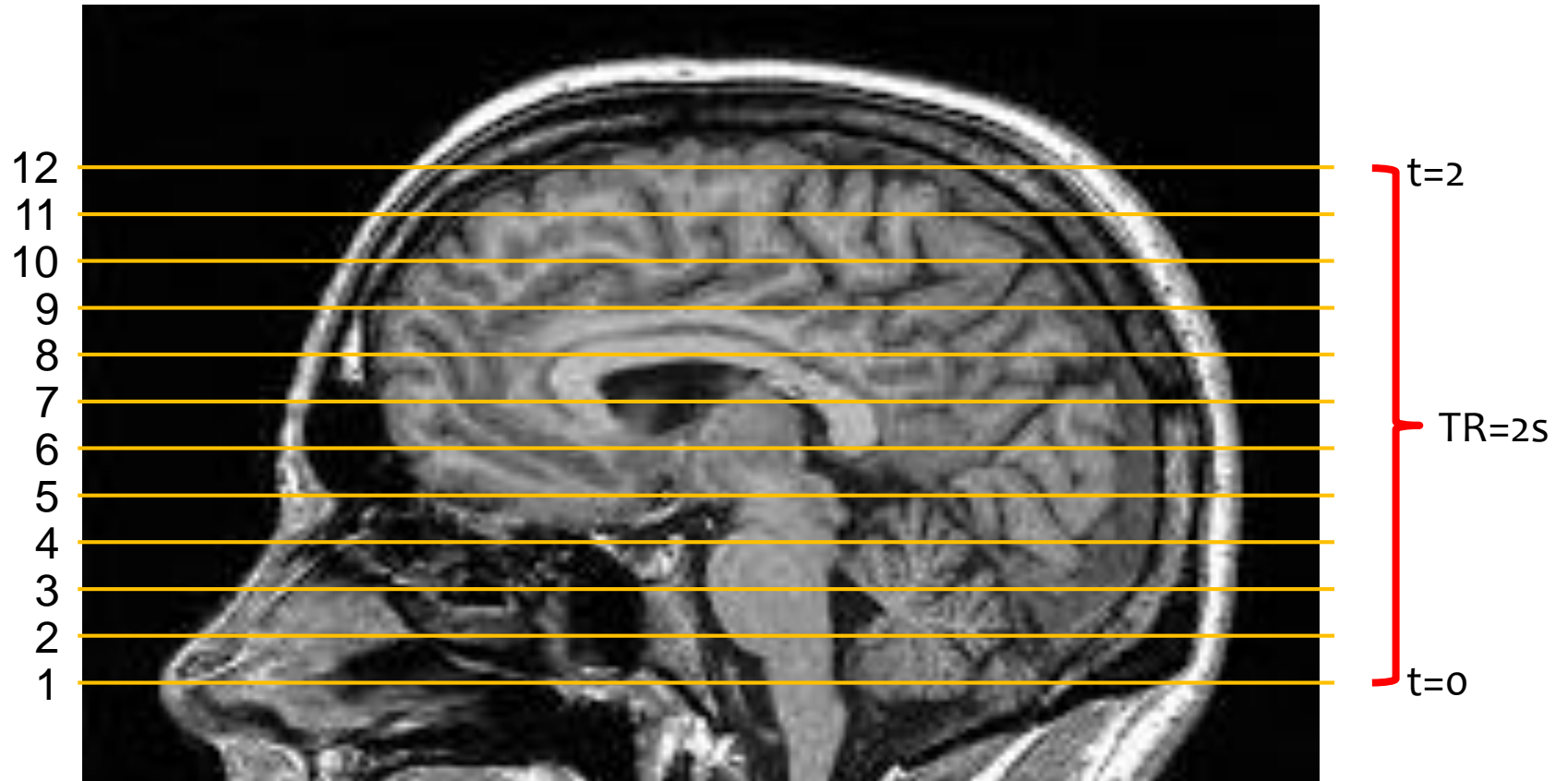
Problems with fMRI data

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- Brain differences
- Noise
- ... and many others

Slice timing

The fMRI data are acquired slice-by-slice – not whole brain all at once!

Order: **Ascending**



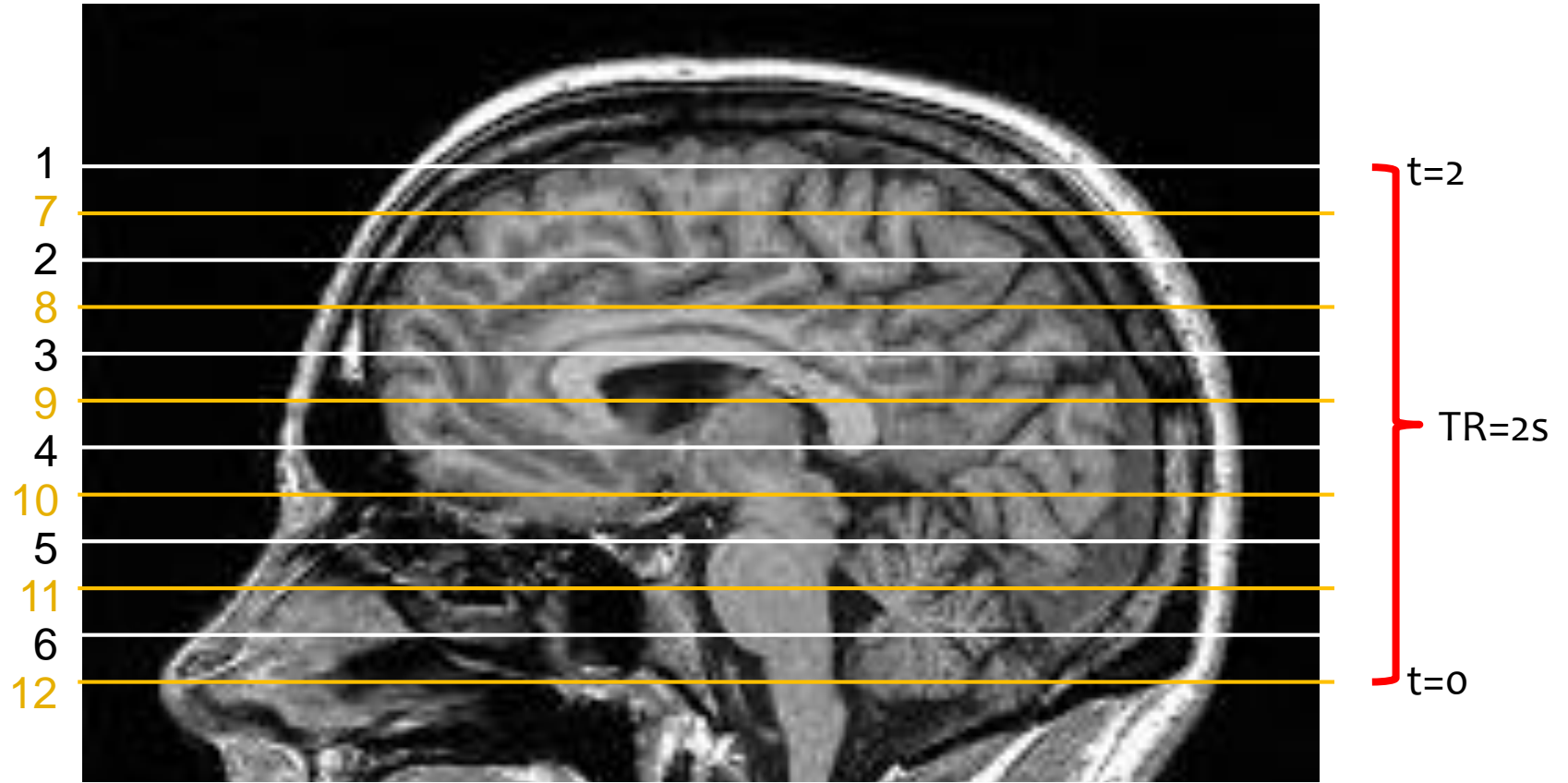
- The first slice is collected almost 2s before the last slice!
- Excitation of one slice may carry over to next slice!
 - Can be solved by **interleaved** acquisition



Slice timing

The fMRI data are acquired slice-by-slice – not whole brain all at once!

Descending-Interleaved

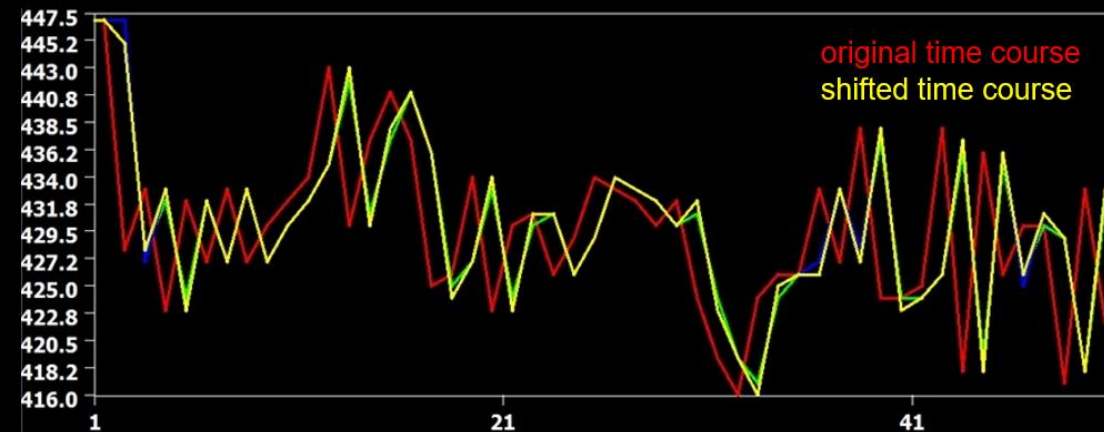
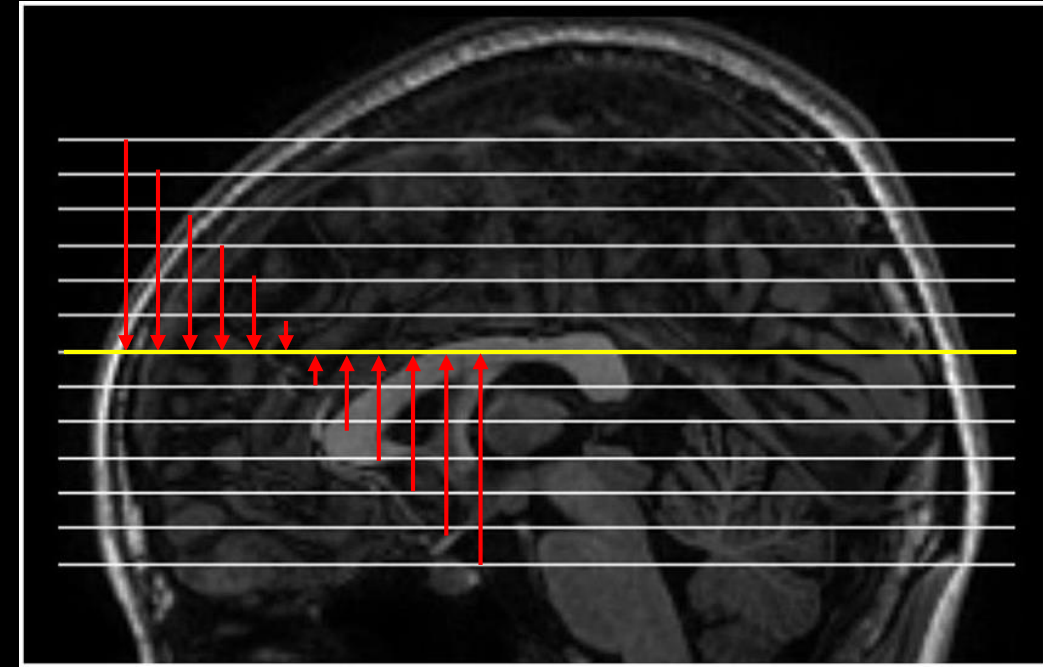


- The first slice is collected almost 2s before the last slice!



Slice time correction

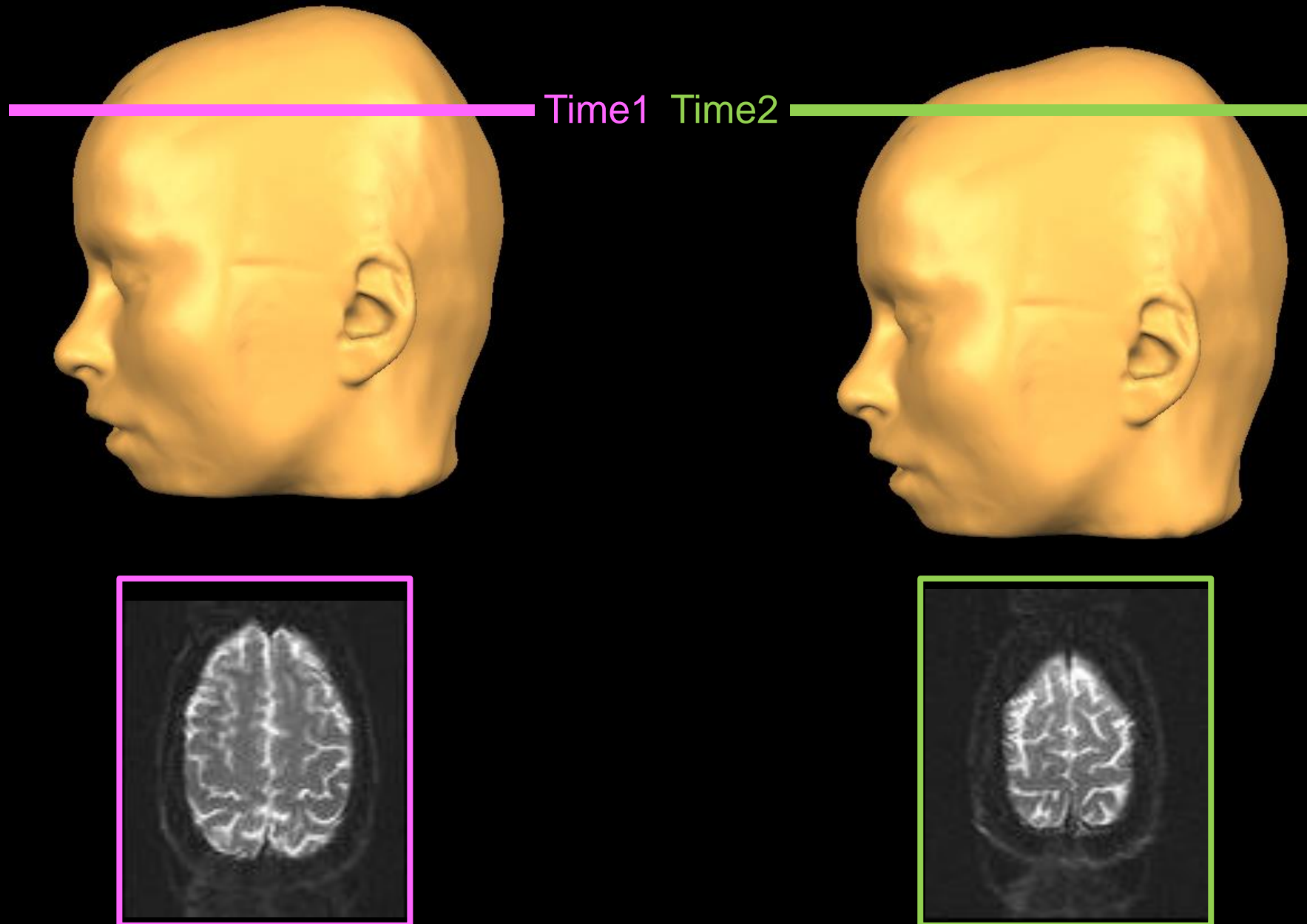
- **Temporal interpolation**
 - Adjusts the timing of a slice collected at the end of the volume so that it is **as if it had been collected simultaneously** with the first slice
- Key parameters
 - **Reference slice**
 - The only slice that is not interpolated
 - Typical choice is to use the middle slice
 - **Slice order**
 - **TR**
- No need to slice time correct if TR is very short (e.g., multi-band: multiple slices at the same time)



Problems with fMRI data

- Slice timing
- Head motion
- Brain differences
- Noise
- ... and many others

Head motion



Head motion correction

- Prevention is the best remedy
- Tell your subjects how to be good subjects
- Make sure the subject is comfortable going in
- Discourage any movements that would displace the head between scans



Bite bar



Thermoplastic mask

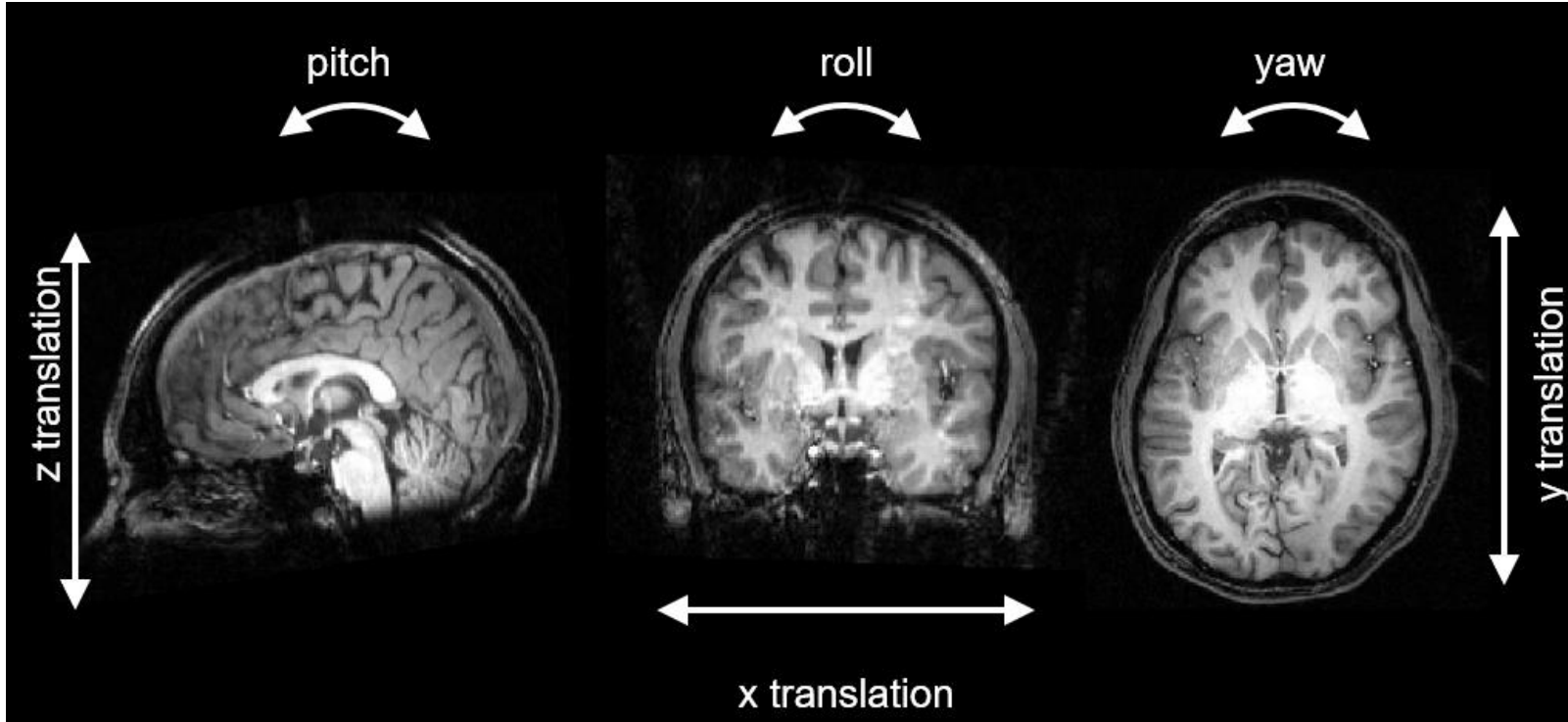


Vacuum pack

Often a bunch of foam padding works as well as anything

Head motion correction

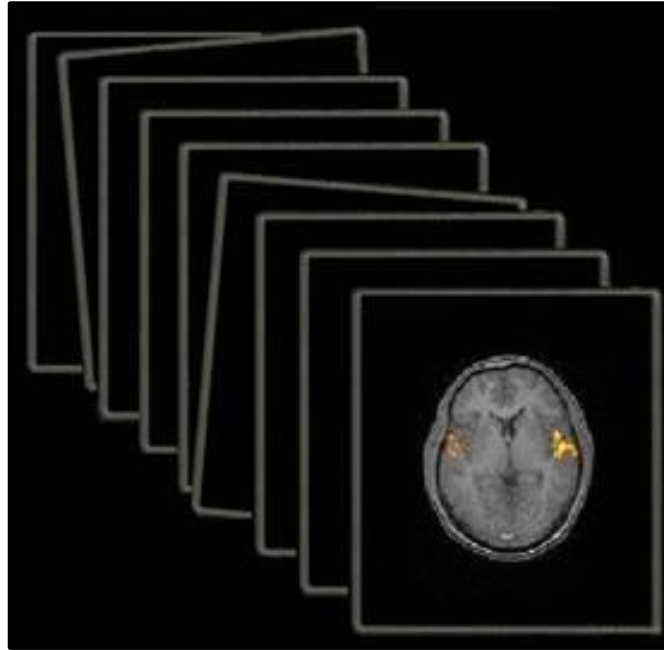
- Spatial realignment



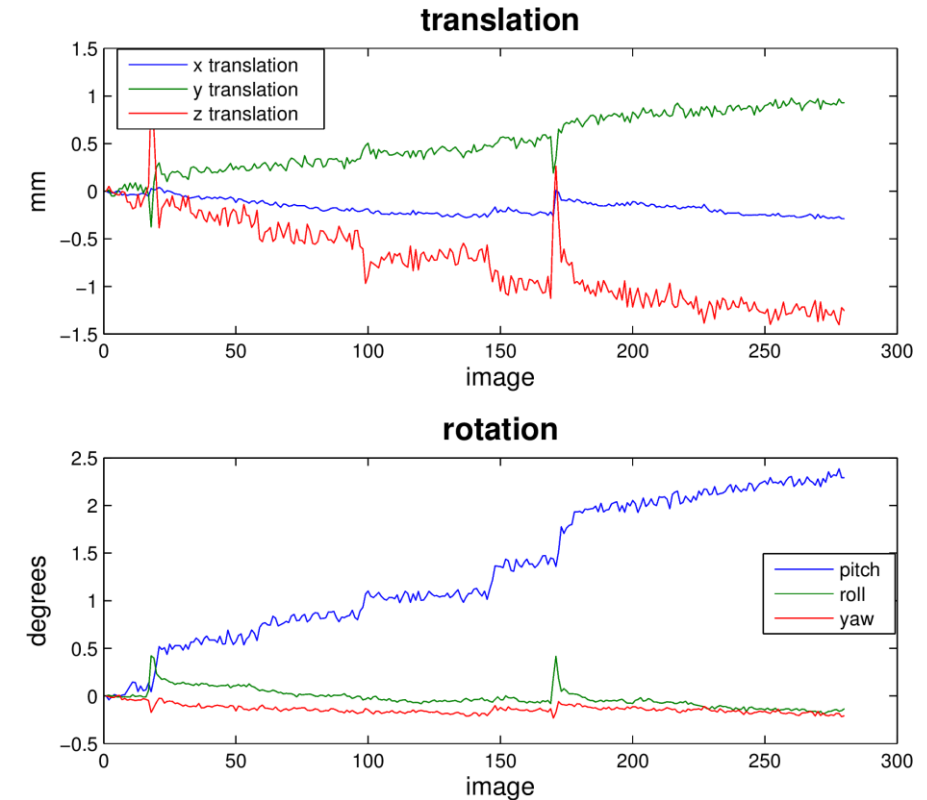
- Most algorithms assume a rigid body (= the brain doesn't deform with movement)
- Align each volume of the brain to a **target volume** using **6 parameters**: 3 translations and 3 rotations
- Target volume: e.g., the mean image of the first run

Head motion correction

- Spatial realignment
 - Not expected to work perfectly, but it helps
 - Be suspicious of data with a lot of head movement!

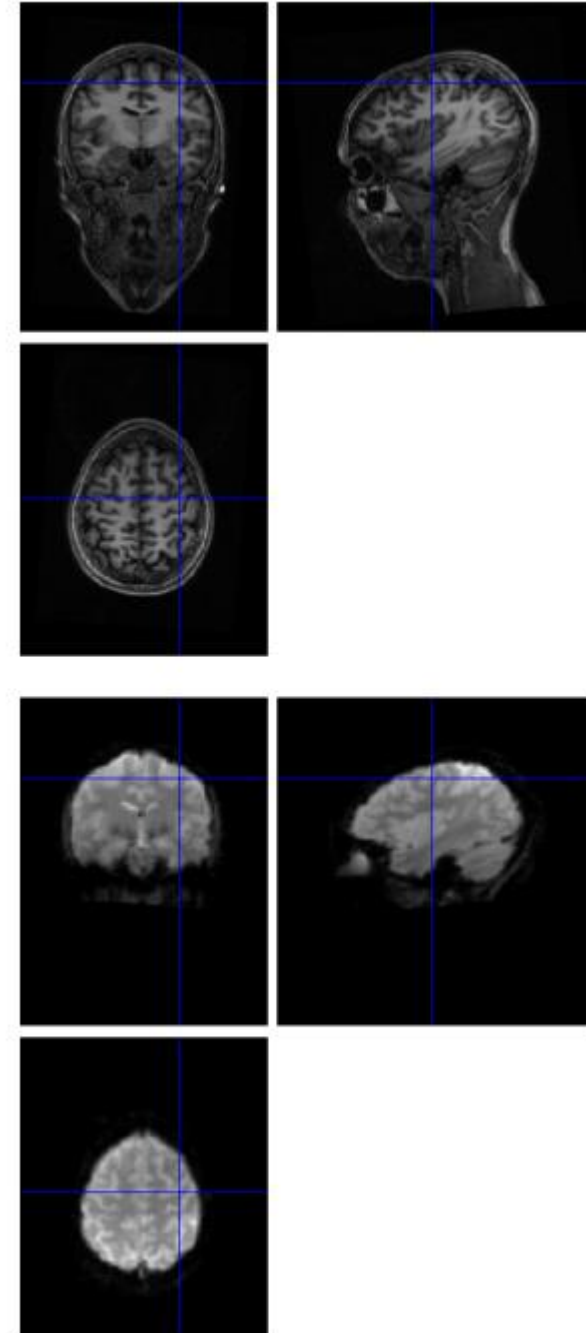


Translation (mm)			Rotation (rad)		
x	y	z	Pitch	Roll	Yaw
0.3417	0.3348	1.8892	0.0182	0.0065	0.001
0.2733	0.418	1.5832	0.0165	0.0063	0.0061
0.8953	0.4925	0.8524	0.0234	0.0123	0.0269
1.8179	1.5353	1.8285	0.0327	0.0222	0.0939
1.0054	0.3014	0.7574	0.0043	0.0197	0.0094
0.737	0.9508	1.0428	0.026	0.0171	0.0164



Coregistration

- Structural – Functional
- Rigid-body align between modalities
- Similar to spatial realignment, but
 - different algorithm to accommodate differences in image contrast
 - transformations are typically only applied to the structural header

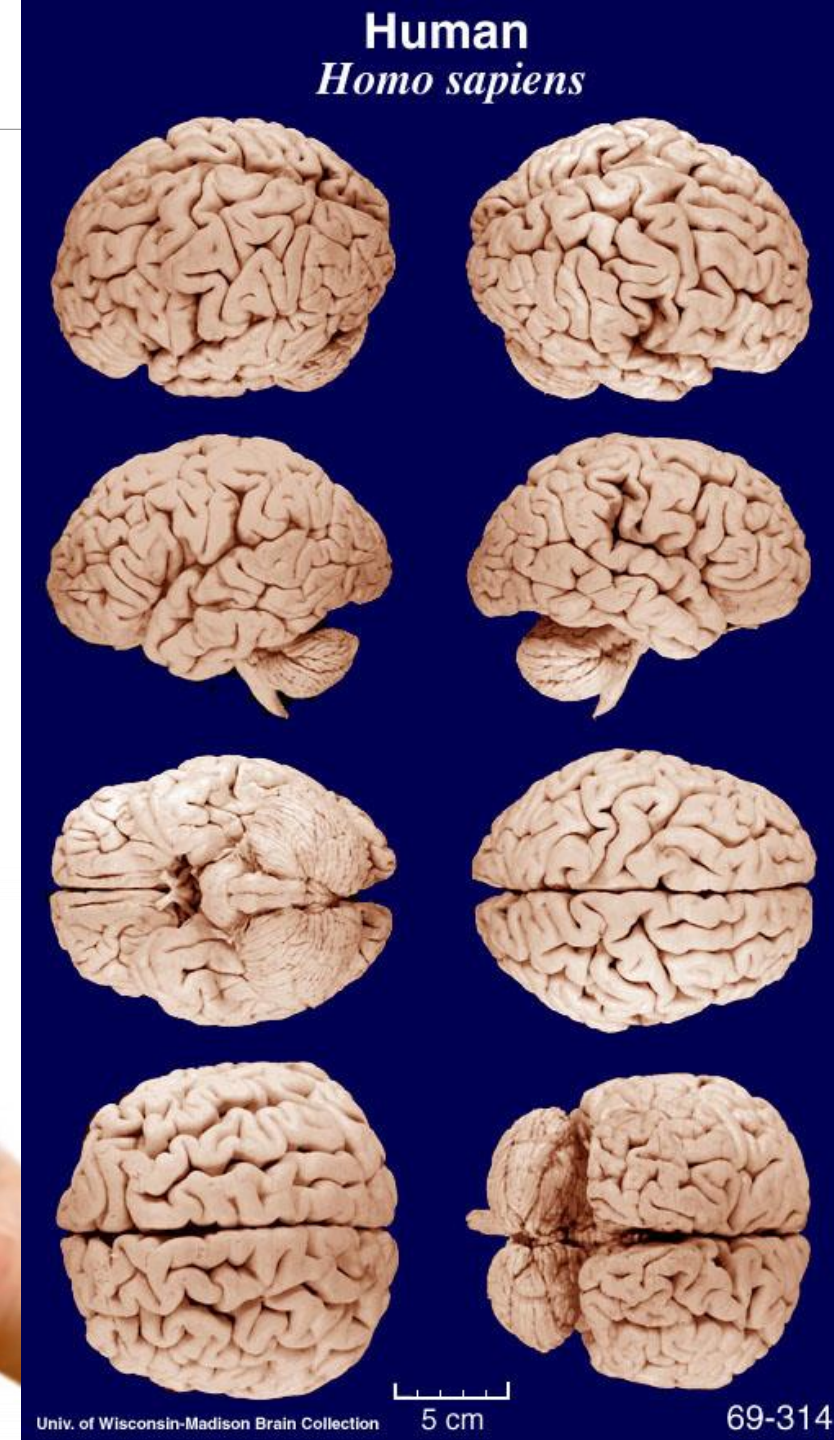


Problems with fMRI data

- Slice timing
- Head motion
- Brain differences
- Noise
- ... and many others

Brain differences – between subjects

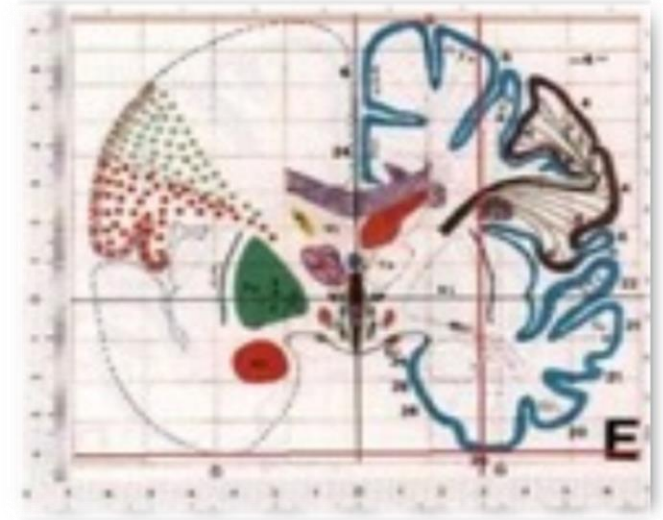
- Brain size can differ (up to 30%)
- Brain shape can differ
- Solution: **normalise to a standard template**
 - stretching, squeezing and warping each brain to the “standard brain”



Standard brain template

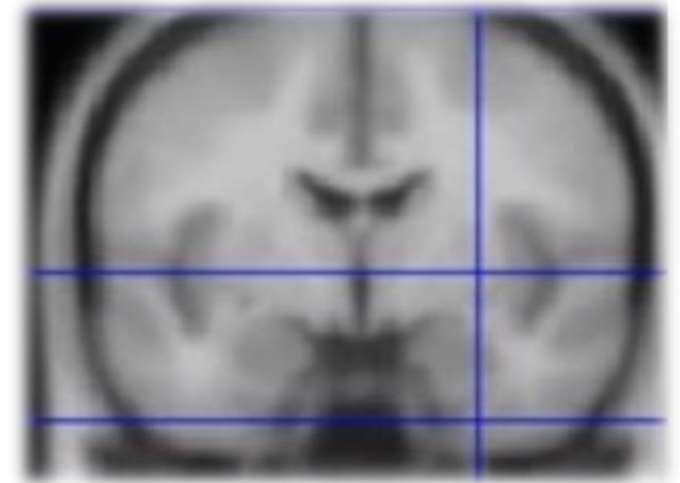
- **Talairach space**

- From atlas of Talairach and Tournoux (1988)
- Based on **single subject (60y, Female, Cadaver)**

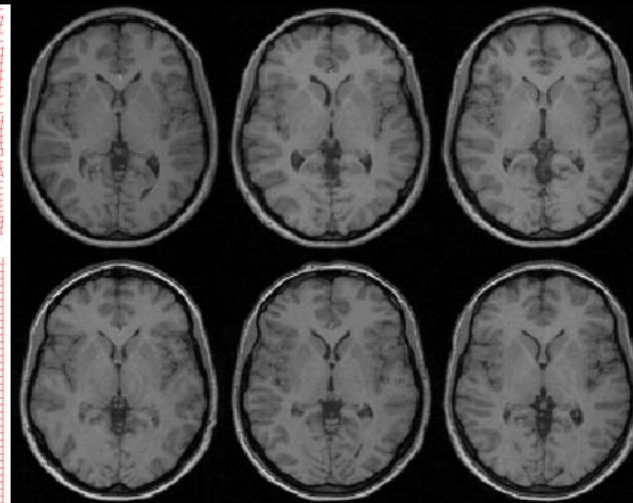
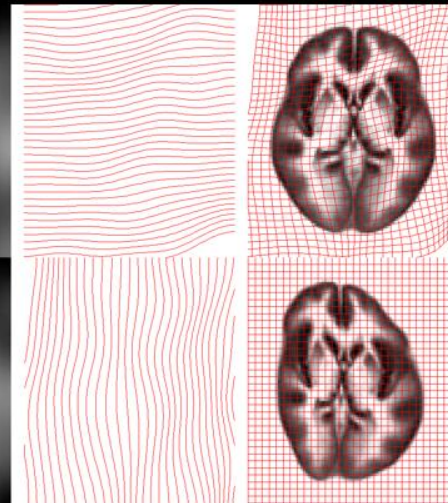
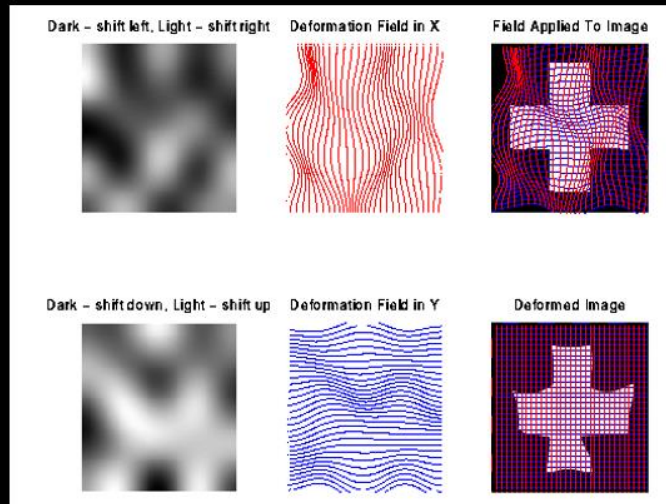
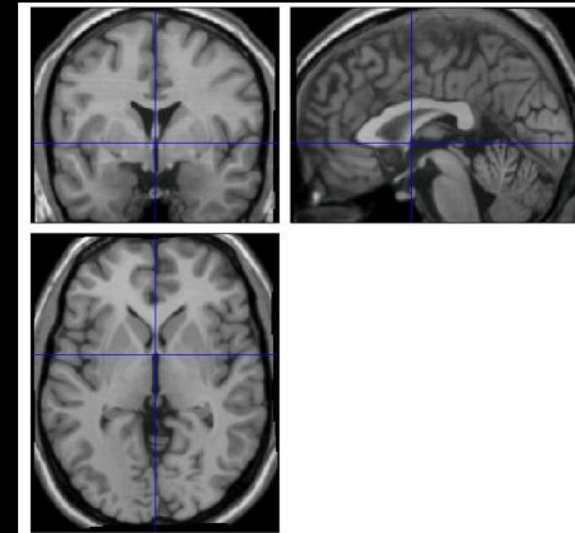
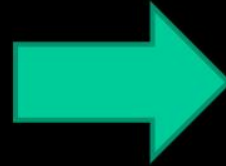
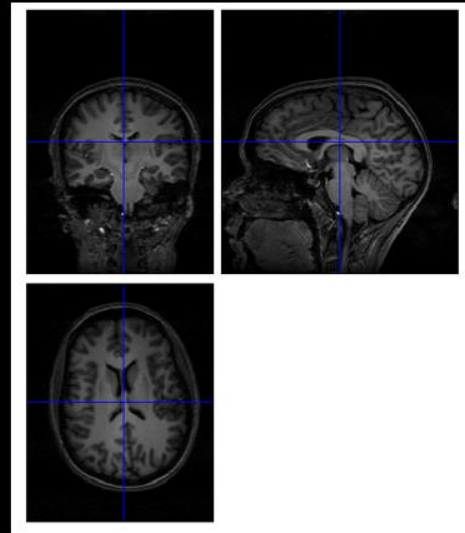


- **MNI – Montreal Neurological Institute**

- Average scan of **152 ‘normal’ right-handed subjects**
- Approximated to Talairach space
- Slightly larger



Normalisation



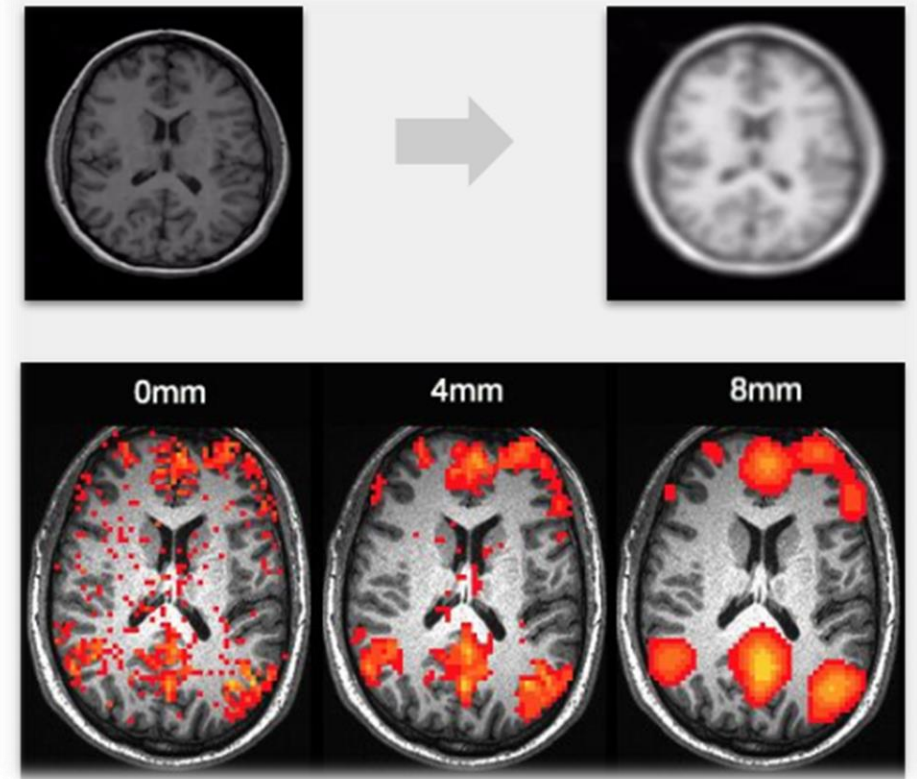
Non-linear spatial transformations



FMRI 4 NEWBIES .COM

Spatial smoothing

- Necessary for validity of multiple corrections within random field theory
- Helps make residual errors in previous spatial pre-processing stages less problematic (e.g., imperfect normalisation, motion correction)
- Can increase signal-to-noise ratio
- But it reduces the image resolution



Problems with fMRI data

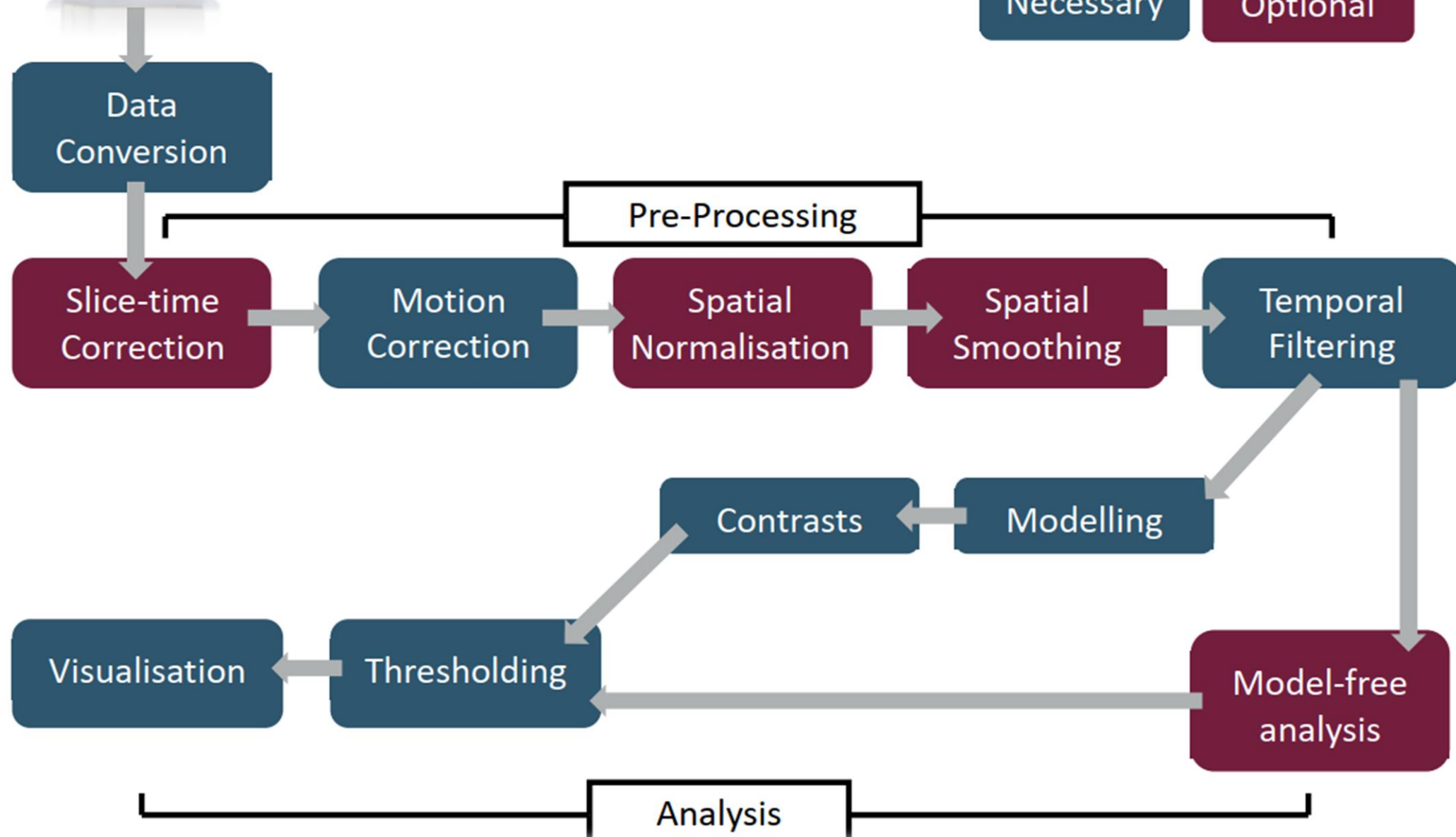
- Slice timing
- Head motion
- Brain differences
- Noise – can be modelled in GLM
- ... and many others



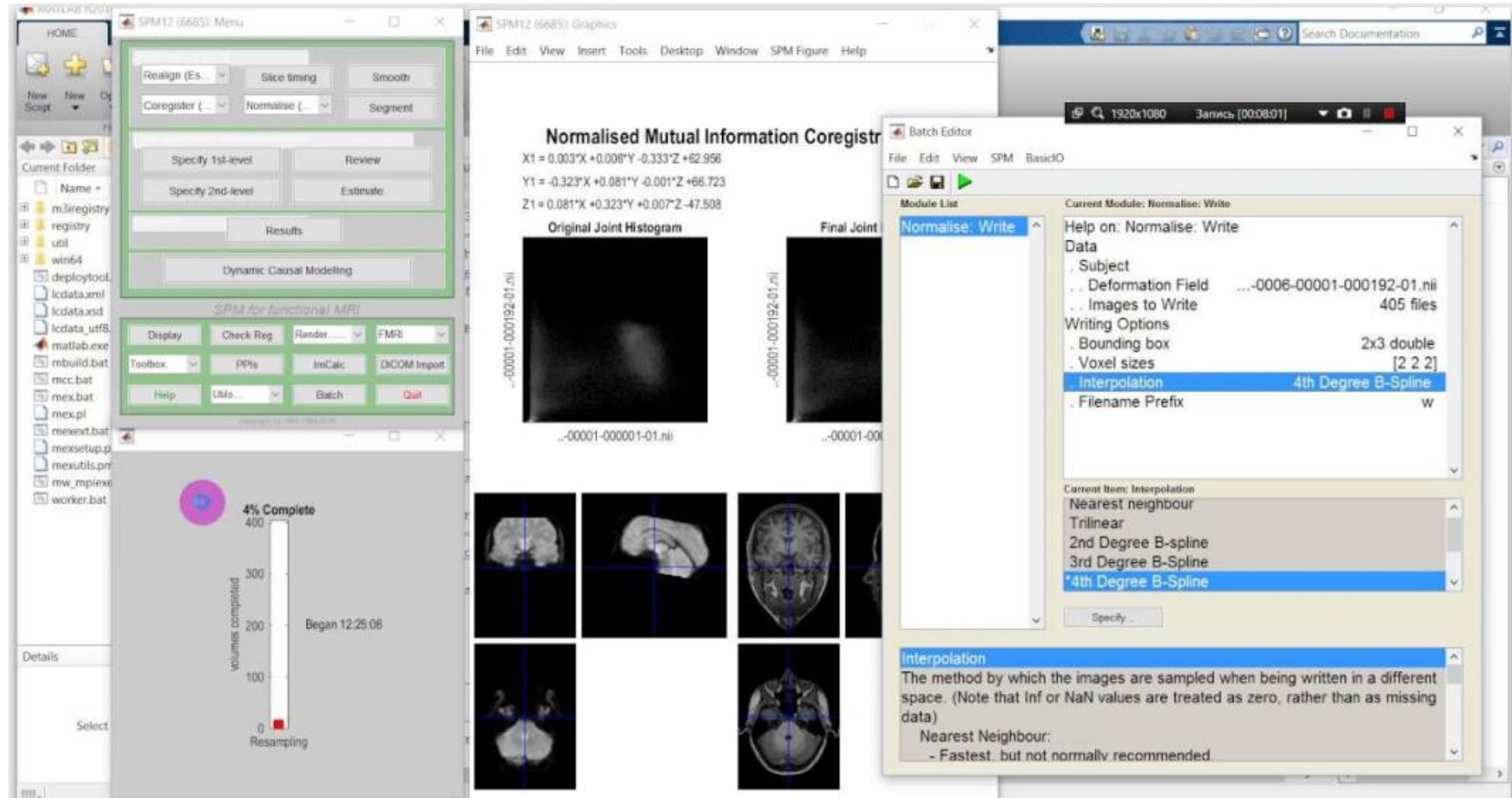
Canonical Analysis Pipeline

Necessary

Optional



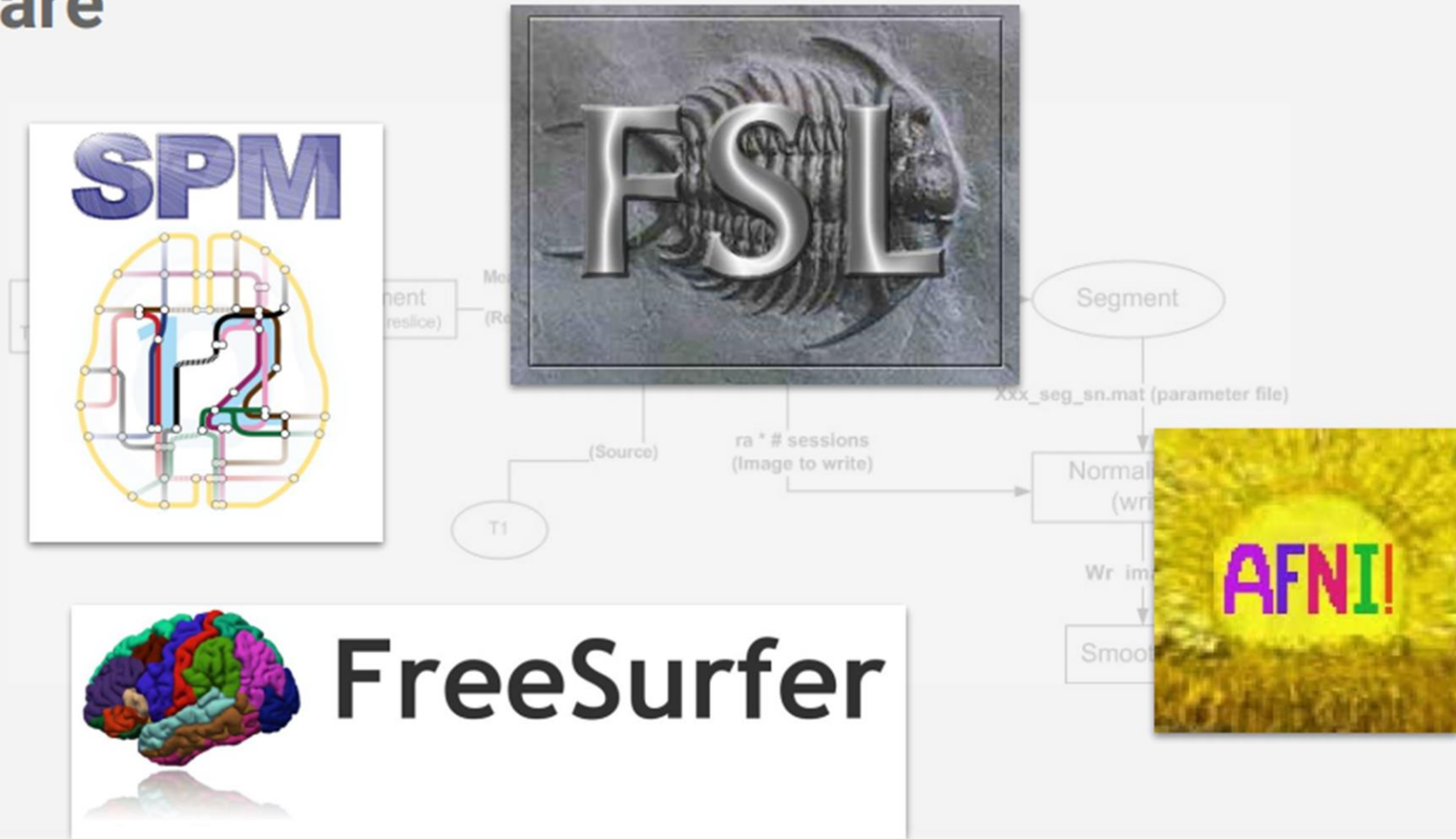
Pre-processing tools



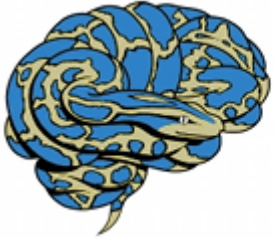
Statistical Parametric Mapping: <https://www.fil.ion.ucl.ac.uk/spm/>

Pre-processing tools

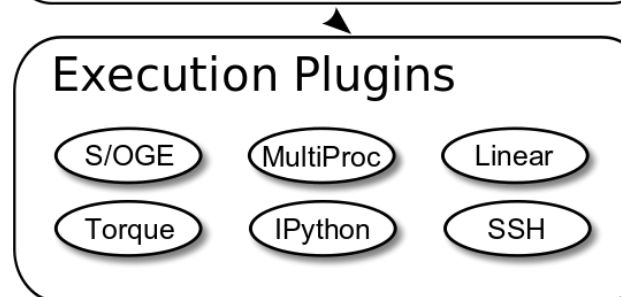
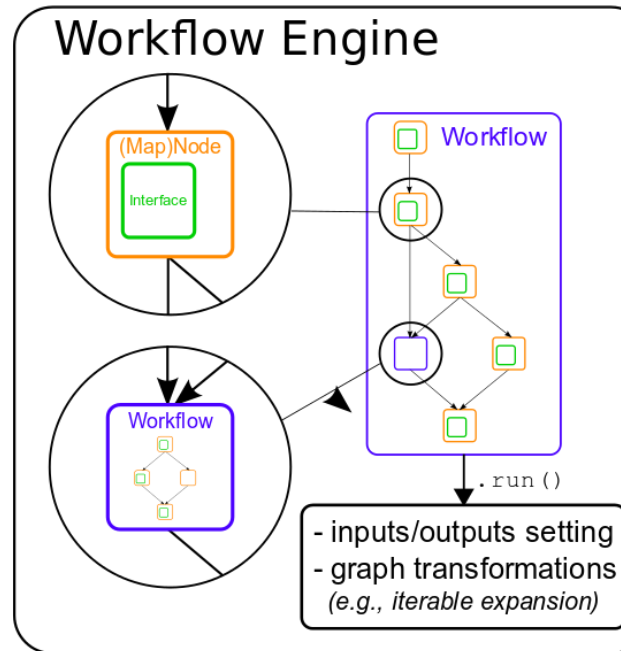
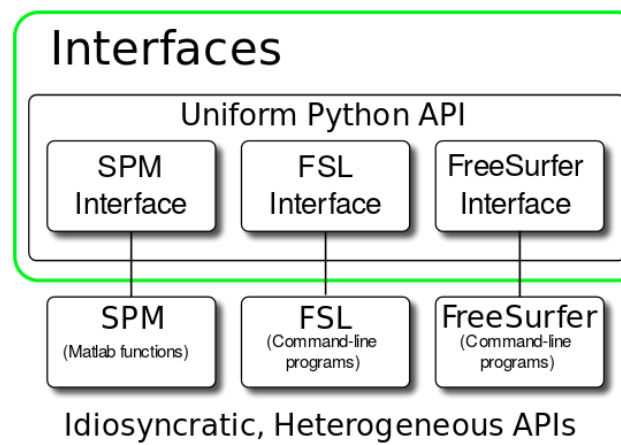
Software



Pre-processing tools



Nipype: Neuroimaging in Python Pipelines and Interfaces

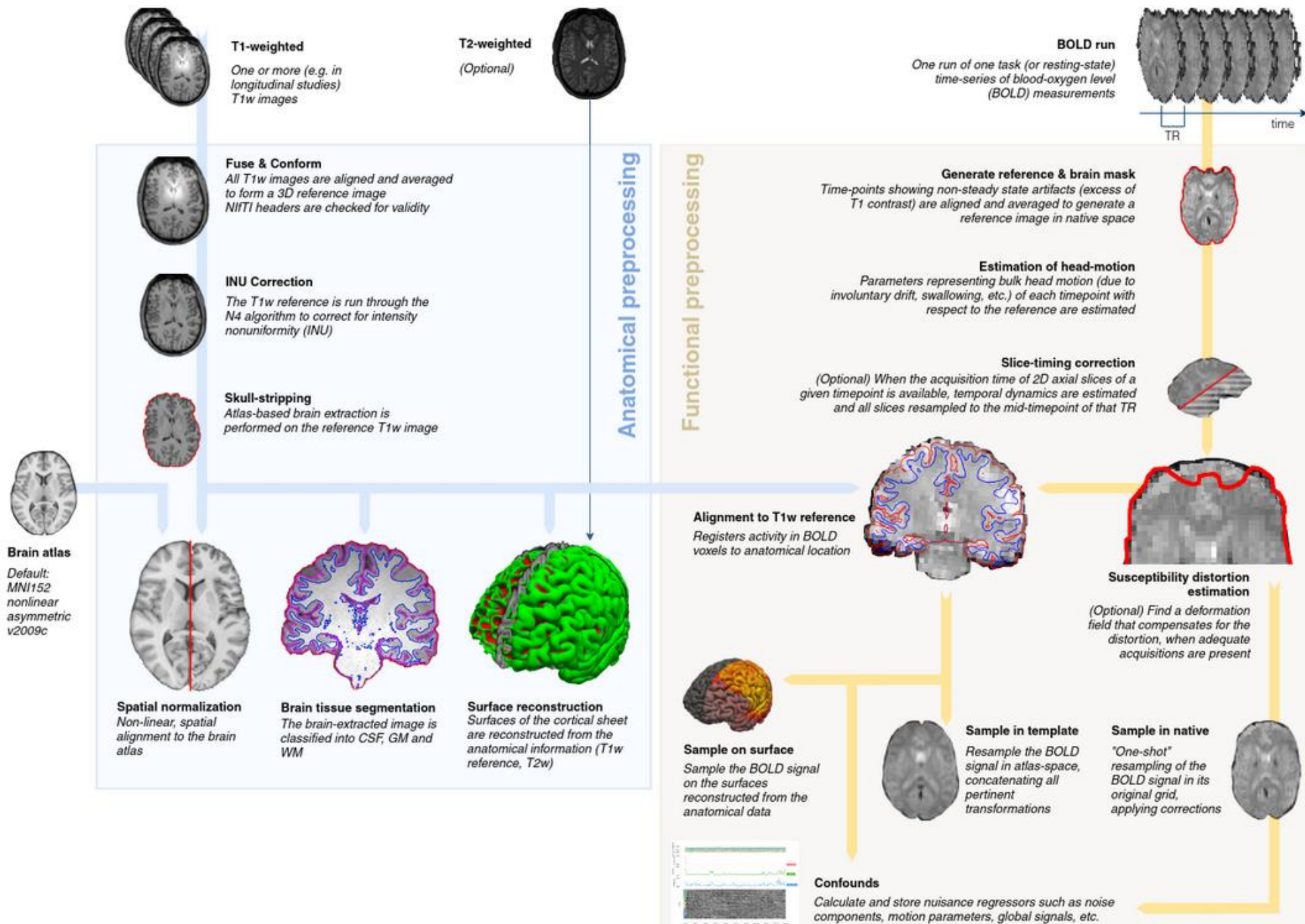


Pre-processing tools

- fMRIPrep <https://fmriprep.org/en/stable/>
 - Fully automated fMRI data pre-processing tool
 - The workflow is based on [Nipype](#) and encompasses a large set of tools from well-known neuroimaging packages, including [FSL](#), [ANTs](#), [FreeSurfer](#), [AFNI](#), and [Nilearn](#). This pipeline was designed to provide the best software implementation for each state of pre-processing, and will be updated as newer and better neuroimaging software becomes available.
 - **Robustness** - The pipeline adapts the pre-processing steps depending on the input dataset and should provide results as good as possible independently of scanner make, scanning parameters or presence of additional correction scans (such as fieldmaps).
 - **Ease of use** - Thanks to dependence on the BIDS standard, manual parameter input is reduced to a minimum, allowing the pipeline to run in an automatic fashion.
 - **“Glass box” philosophy** - Automation should not mean that one should not visually inspect the results or understand the methods. Thus, fMRIPrep provides visual reports for each subject, detailing the accuracy of the most important processing steps. This, combined with the documentation, can help researchers to understand the process and decide which subjects should be kept for the group level analysis.

Pre-processing

- fMRIPrep



Remarks

- Reproducibility requires automation
 - e.g., SPM batch scripts, fmriprep
- Pre-processing errors are often only apparent on plotting the images. Check functional-functional (realign), functional-structural (coregistration), structural-MNI (normalisation)
- Put your data in a standard, sharable format (BIDS) *before* analysing it to
 - save pain later if you want to share data with working analysis code
 - make use of new analysis tools like fmriprep, which requires BIDS-format input