



MRC Cognition  
and Brain  
Sciences Unit



UNIVERSITY OF  
CAMBRIDGE

# Functional Magnetic Resonance Imaging



**GitHub** [https://github.com/dcdace/fMRI\\_training](https://github.com/dcdace/fMRI_training)

Dace [datza] Apšvalka

February 2025

# Outline

---

- Introduction
- Experimental design
- Data management
- **Pre-processing**
- Statistical analysis
- Practical demo



# Environment



**Data**  
Organise & Manage

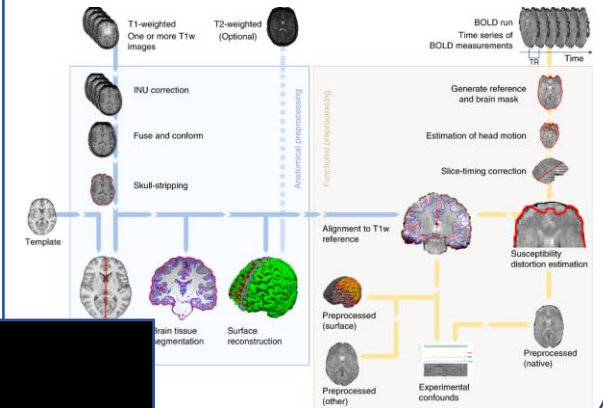
Pre-process

## Collect the data



Why can't we analyse right away?

## Pre-process & Analyse

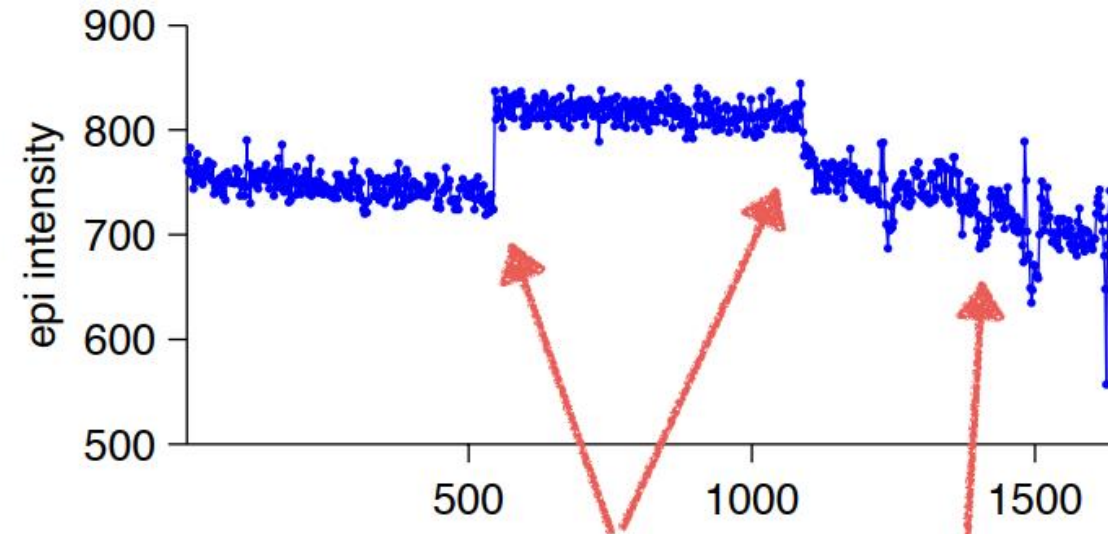


```
dicomdir/  
  1208200617178_22/  
    1208200617178_22_8973.dcm  
    1208200617178_22_8943.dcm  
    1208200617178_22_2973.dcm  
    1208200617178_22_8923.dcm  
    1208200617178_22_4473.dcm  
    1208200617178_22_8783.dcm  
    1208200617178_22_7328.dcm  
    1208200617178_22_9264.dcm  
    1208200617178_22_9967.dcm  
    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/
```

# Raw data in example voxel

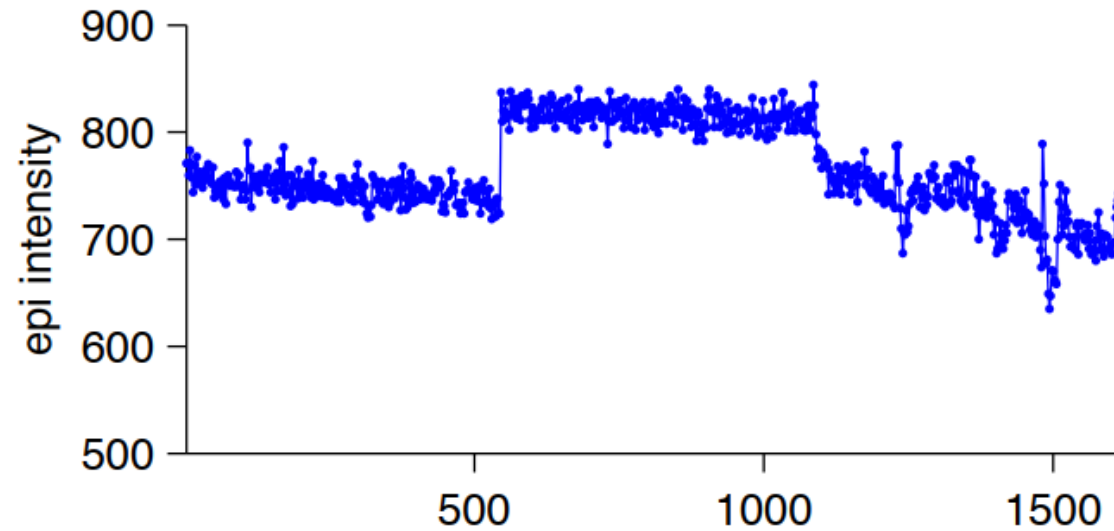


run transitions  
(head movement  
between scans?)

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

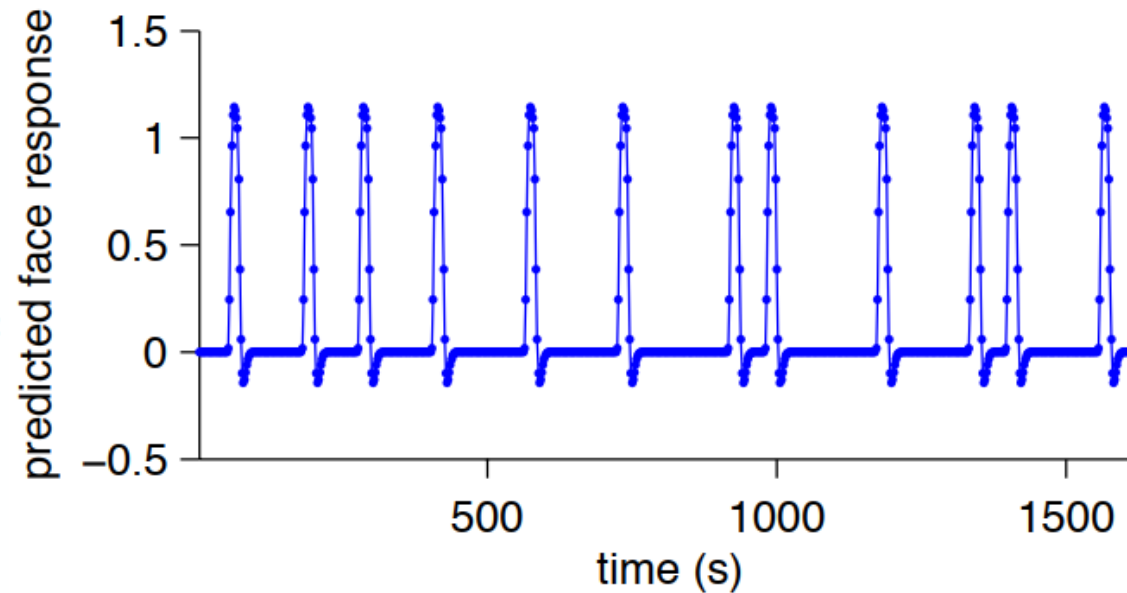
# Raw data in example voxel

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

---

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



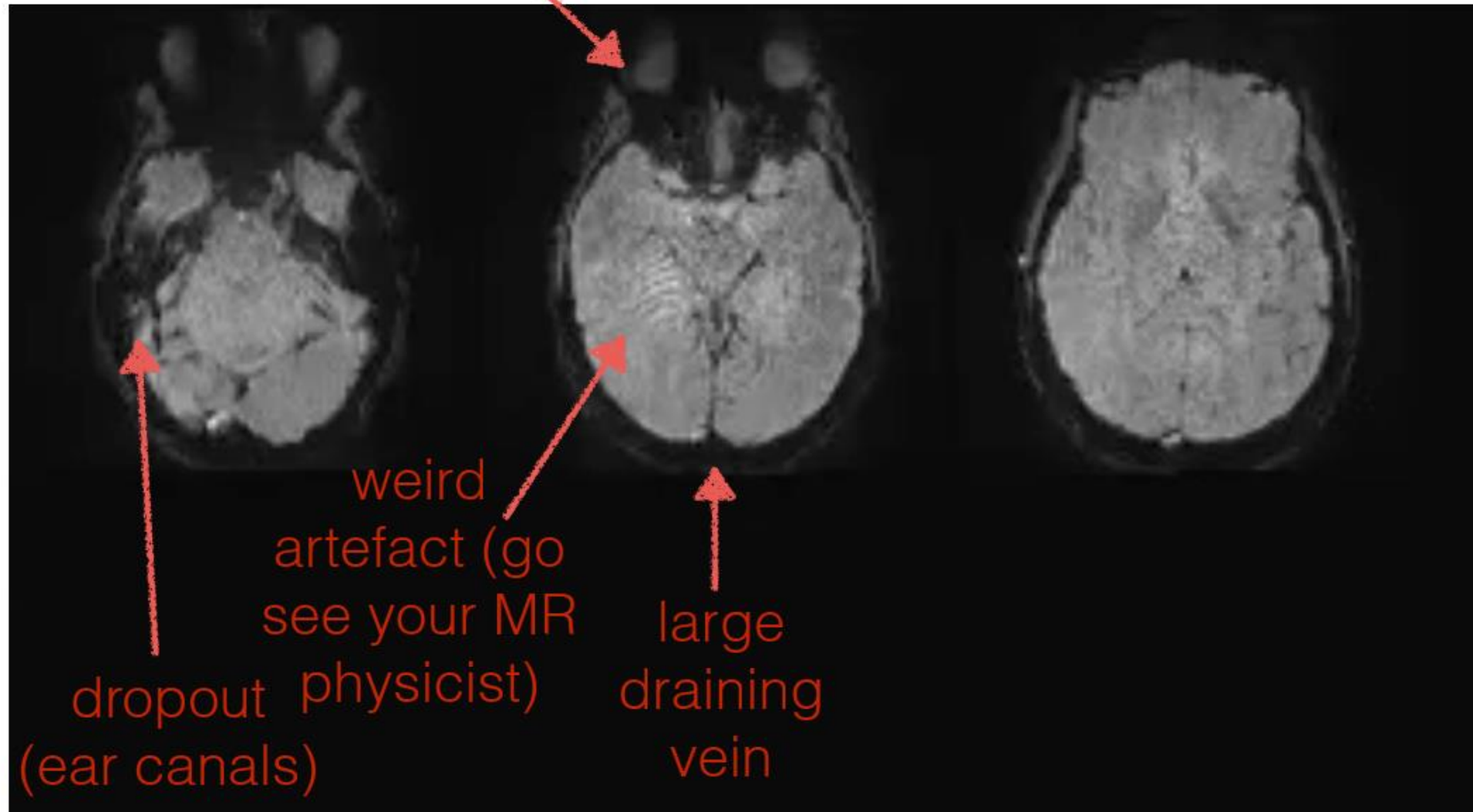
# Problems with fMRI data

---

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

# Artefacts

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

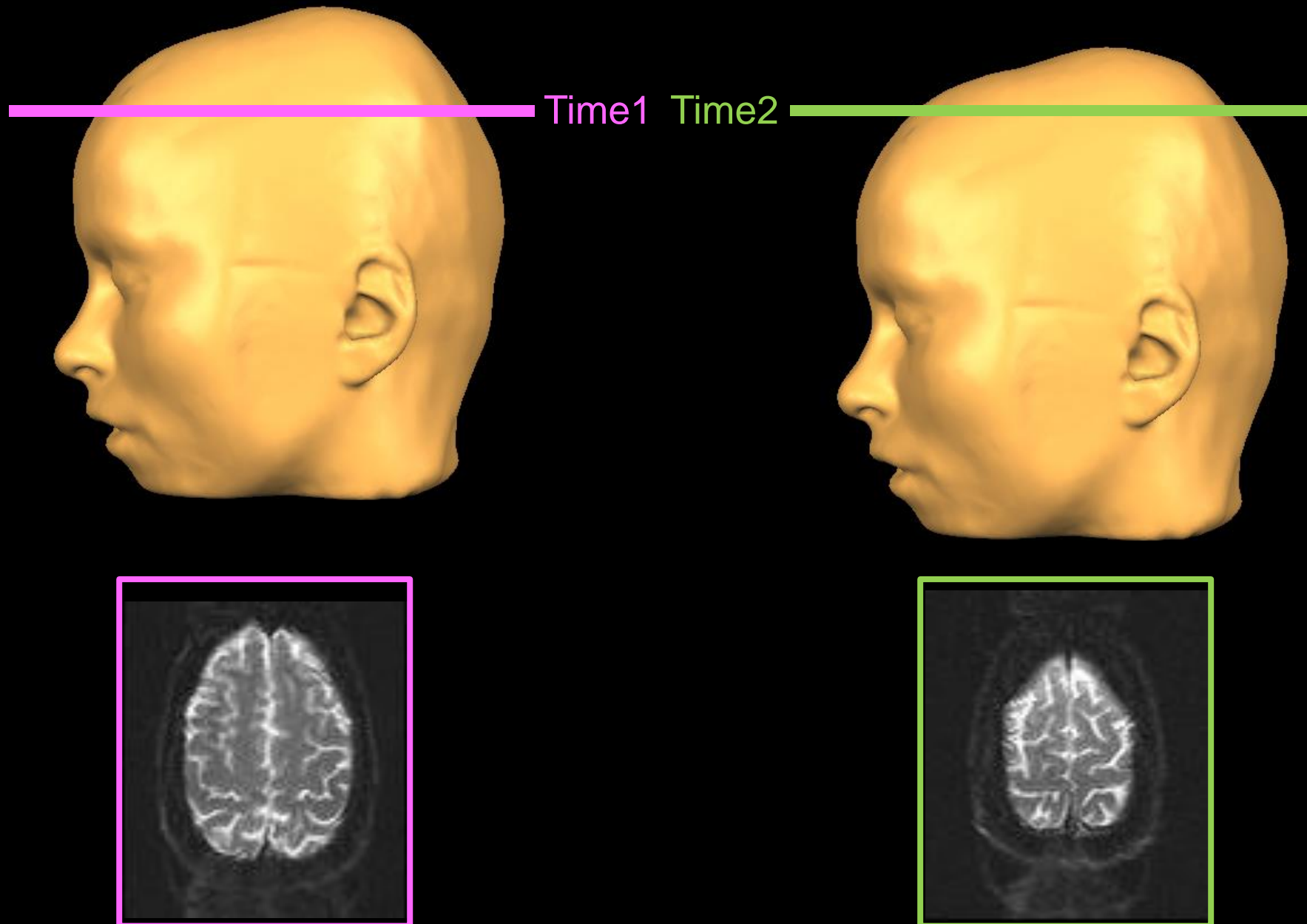


# Problems with fMRI data

---

- Artefacts
- Head motion
- Slice timing
- 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

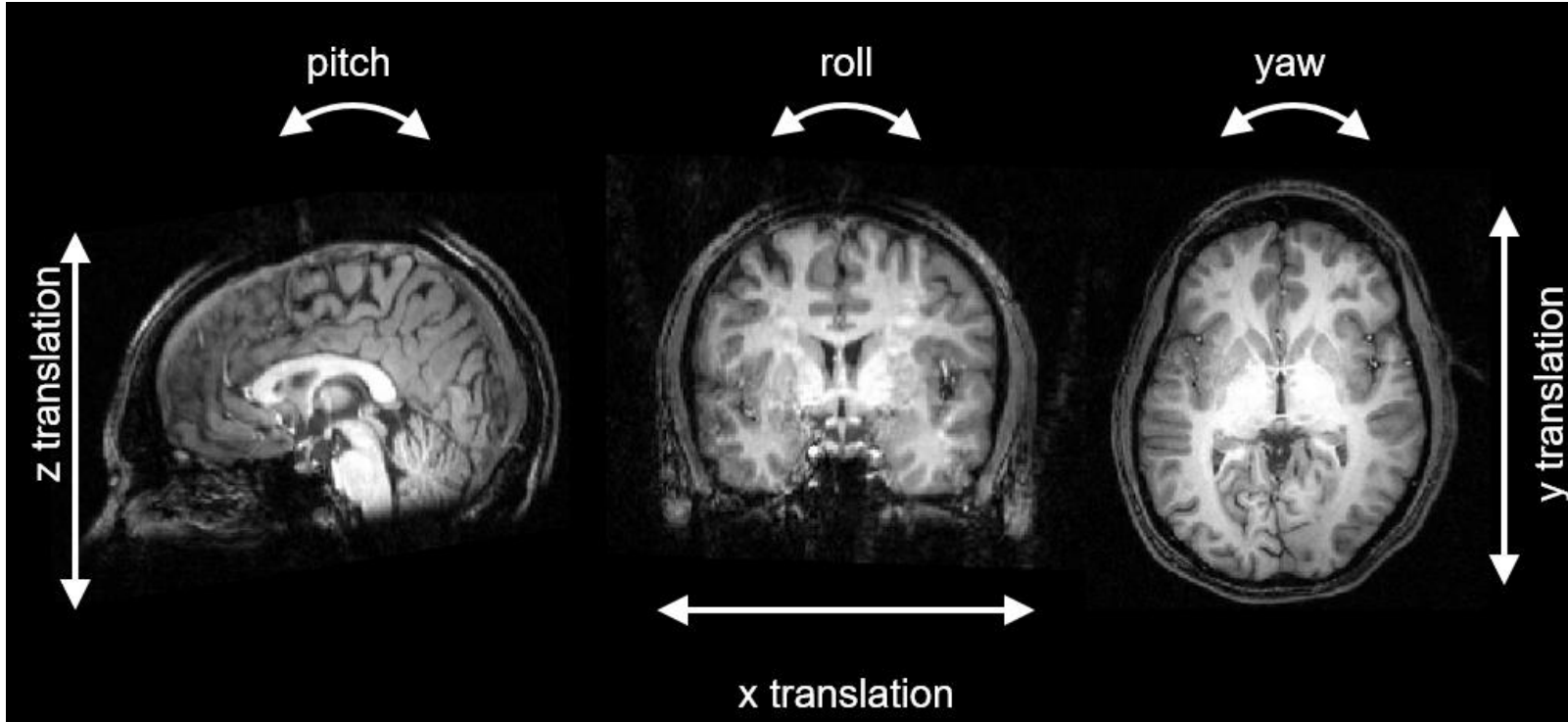


Vacuum pack

Often a bunch of foam padding works as well as anything

# Head motion correction

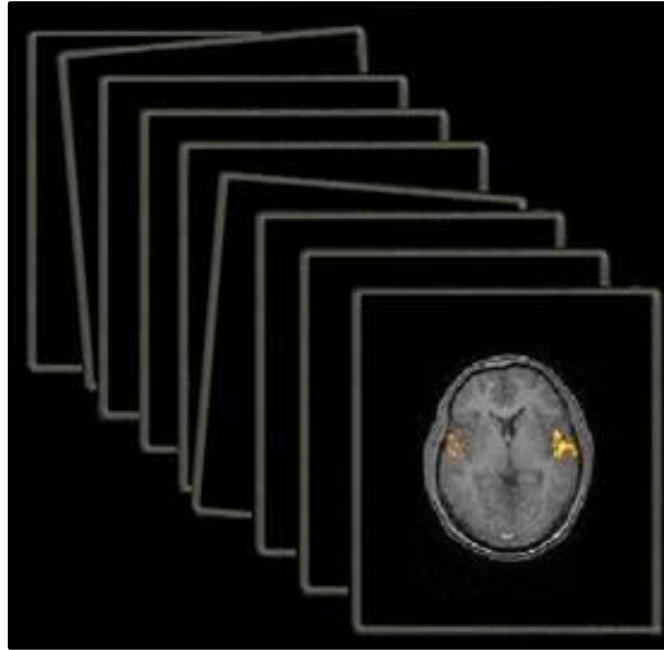
- Spatial realignment



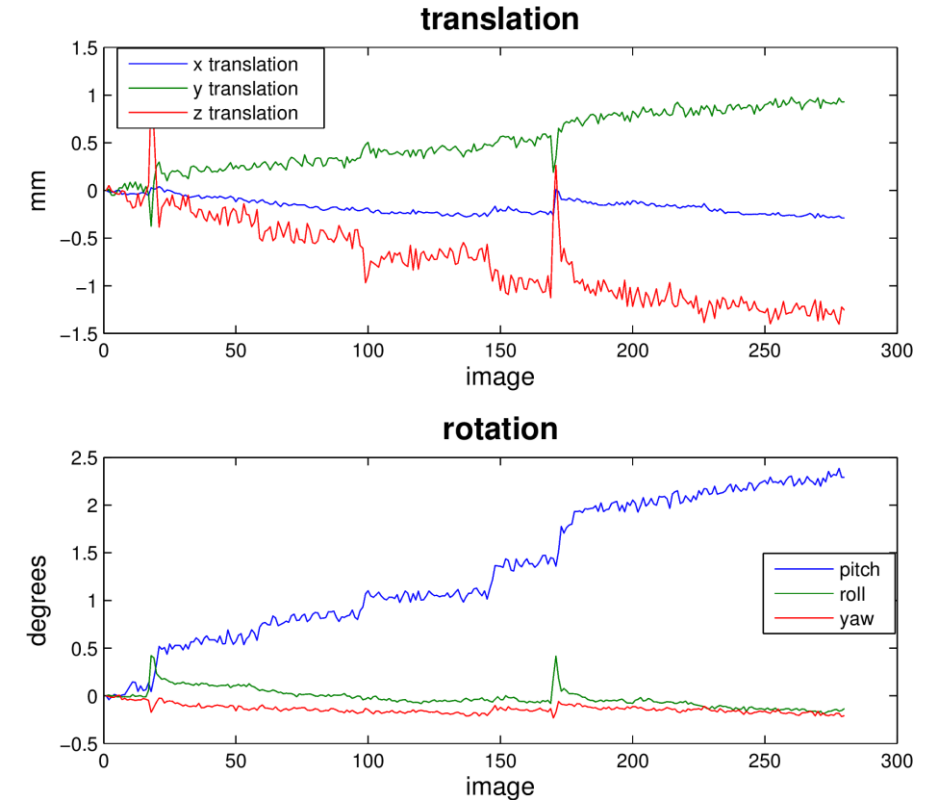
- Most algorithms assume a rigid body (= the brain doesn't deform with movement)
- Align each volume of the brain to a **target volume** using **6 parameters**: 3 translations and 3 rotations
- Target volume: e.g., the mean image of the first run

# 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



# Problems with fMRI data

---

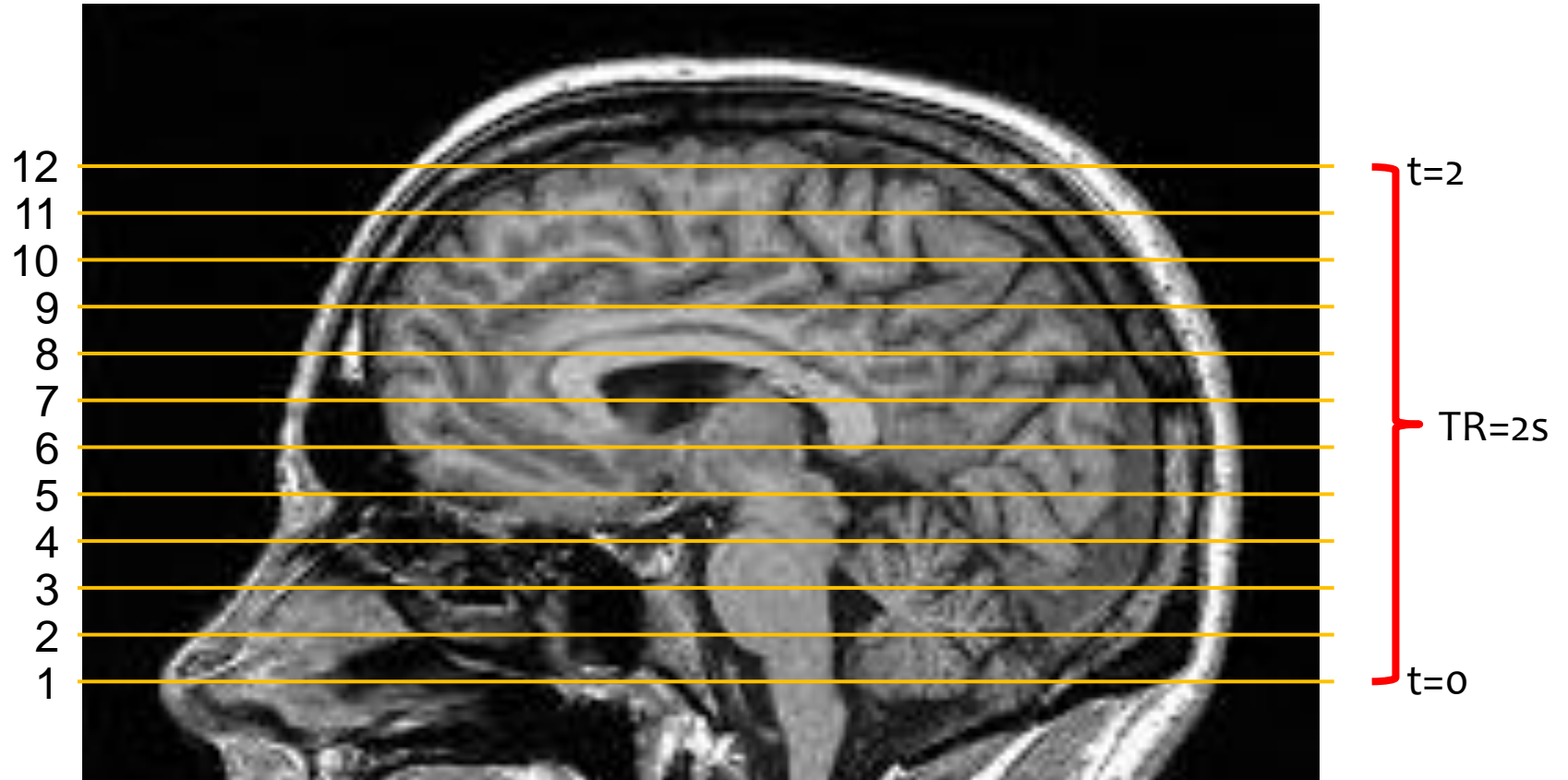
- Artefacts
- Head motion
- Slice timing
- Brain differences
- Noise
- ... and many others



# Slice timing

Typically, the fMRI data are acquired slice-by-slice – not the whole brain all at once

Order: **Ascending**



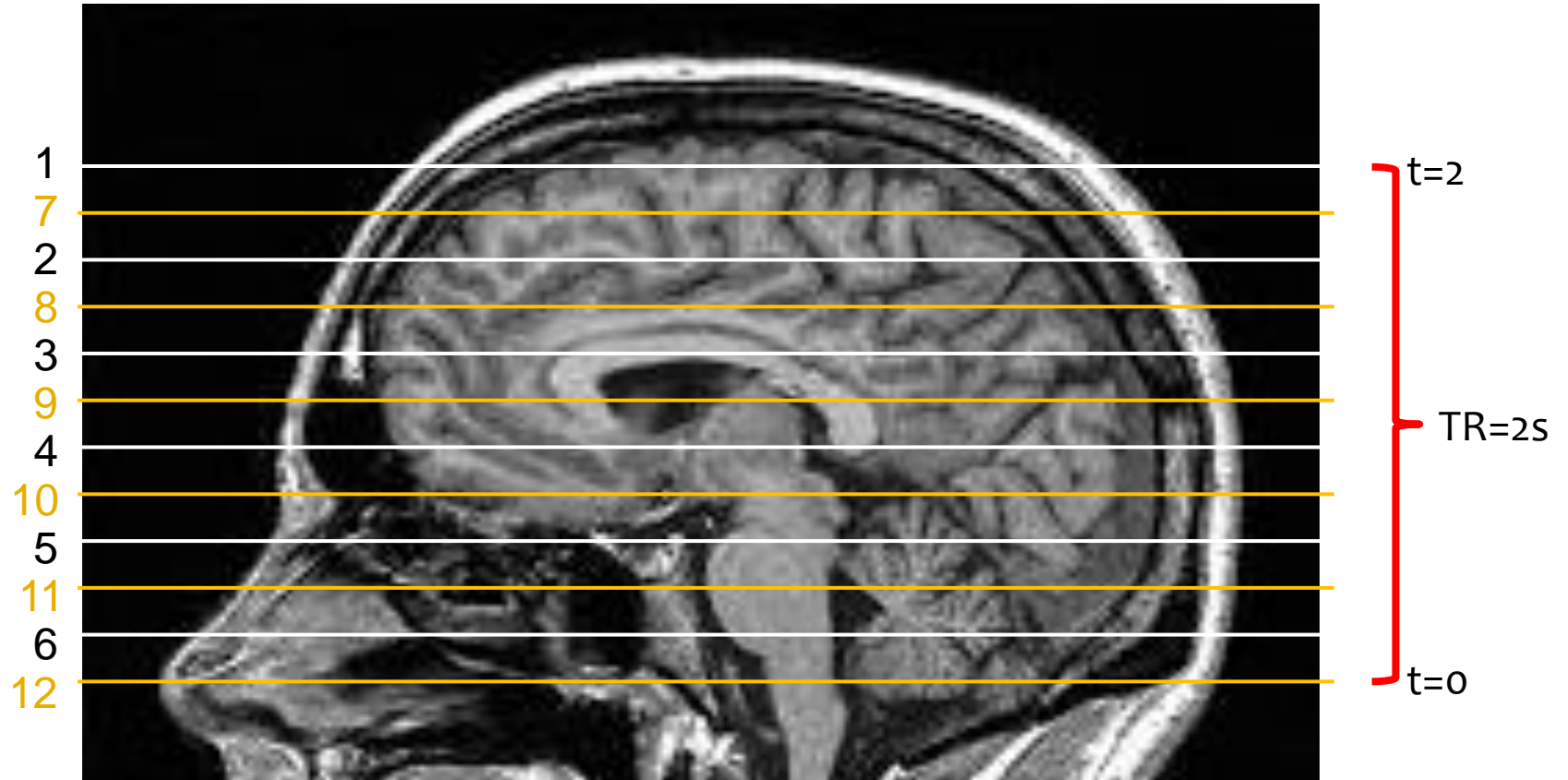
- The first slice is collected almost 2s before the last slice!
- Excitation of one slice may carry over to next slice!
  - Can be solved by **interleaved** acquisition



# Slice timing

Typically, the fMRI data are acquired slice-by-slice – not the whole brain all at once

**Descending-Interleaved**

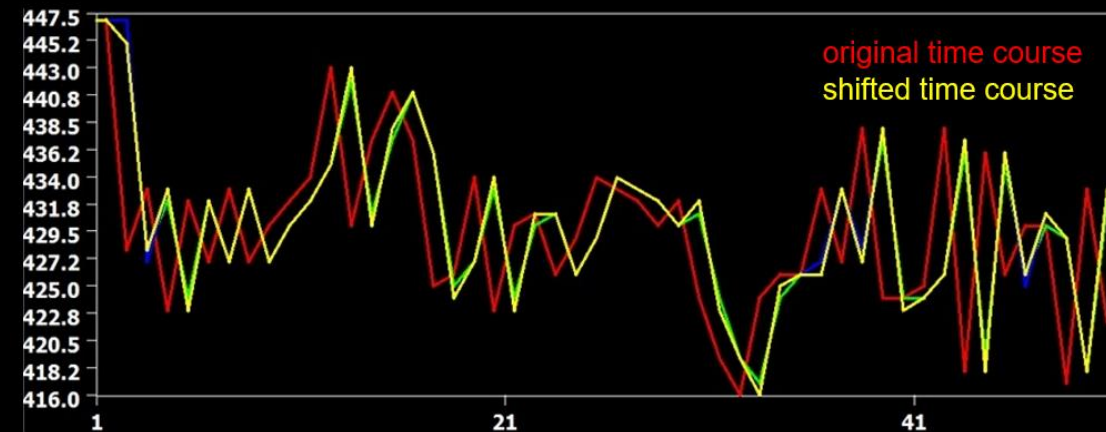
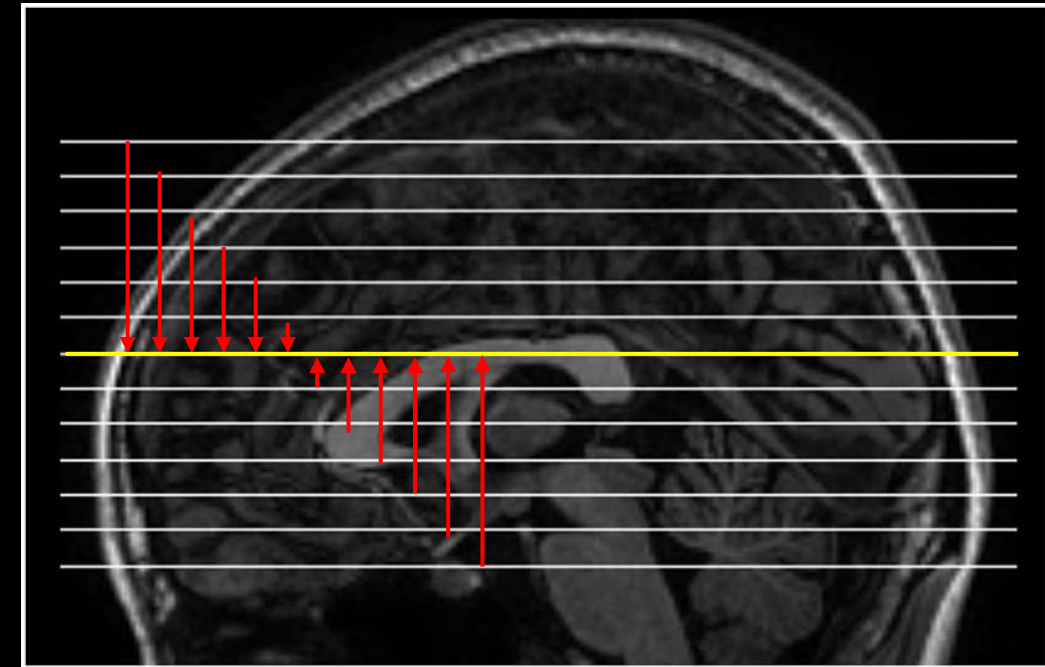


- The first slice is collected almost 2s before the last slice!



# Slice time correction

- **Temporal interpolation**
  - Adjusts the timings of the slices so that it is **as if they had been collected simultaneously**
  - Uses information from nearby time points to **estimate the amplitude of the MR signal** at the onset of each TR
- **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

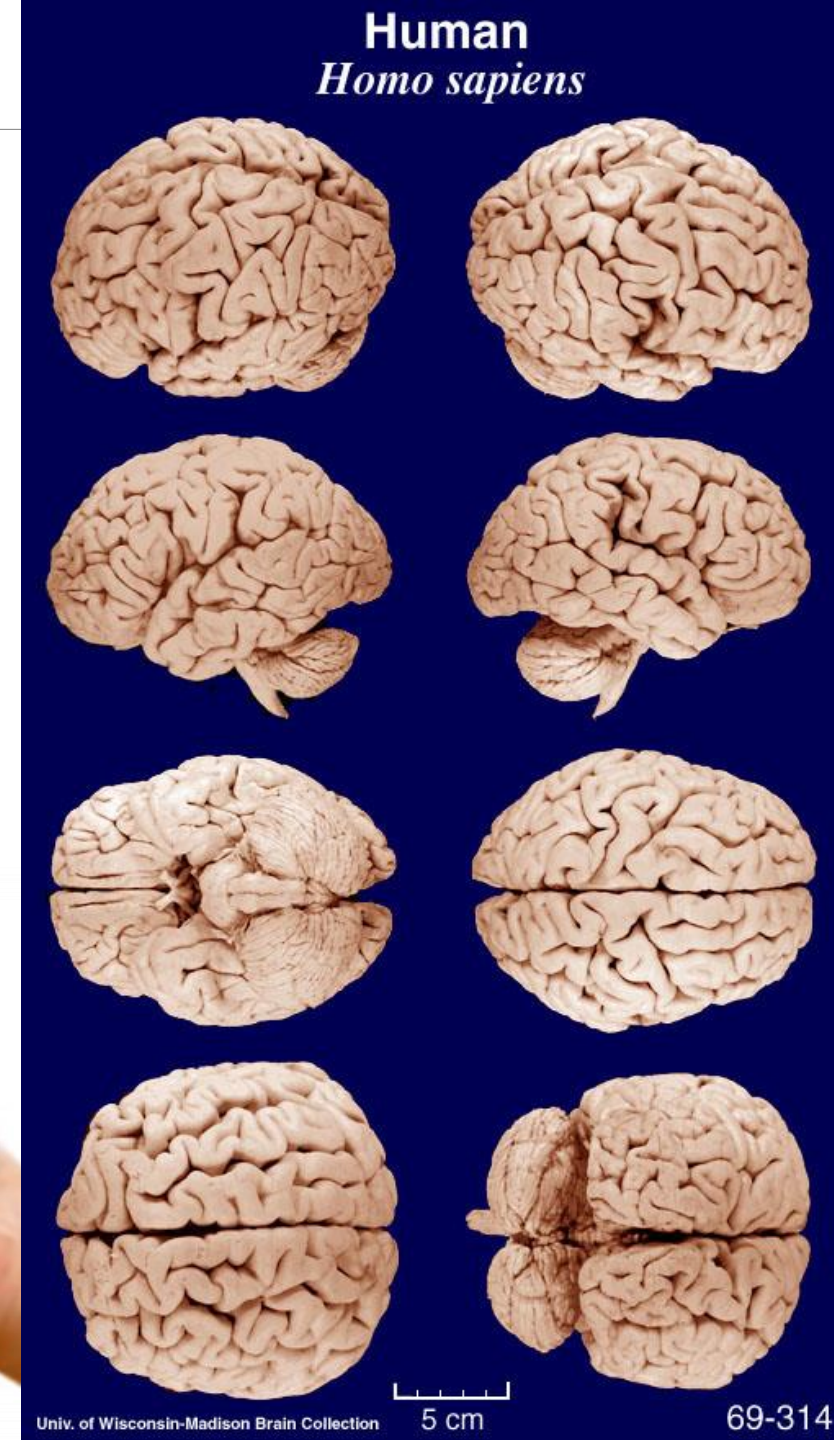
---

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



# Brain differences – between subjects

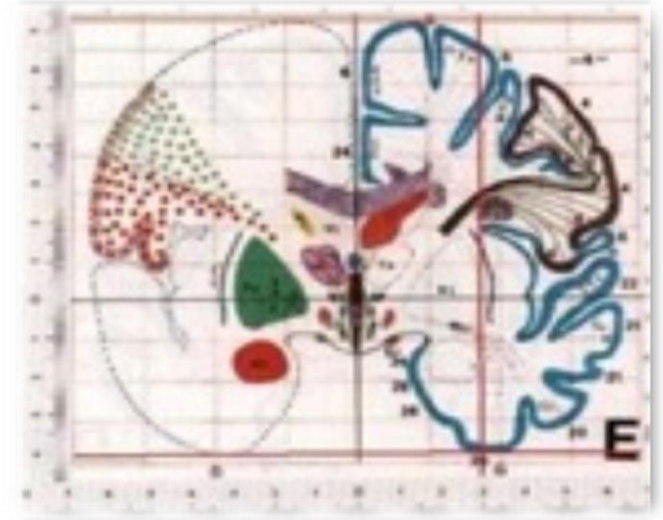
- Brain size can differ (up to 30%)
- Brain shape can differ
- Solution: **normalise to a standard template**
  - stretching, squeezing and warping each brain to the “standard brain”



# Standard brain template

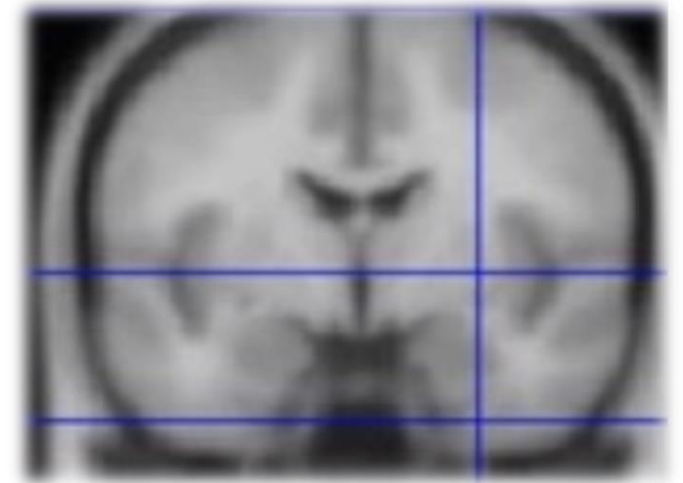
- **Talairach space**

- 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





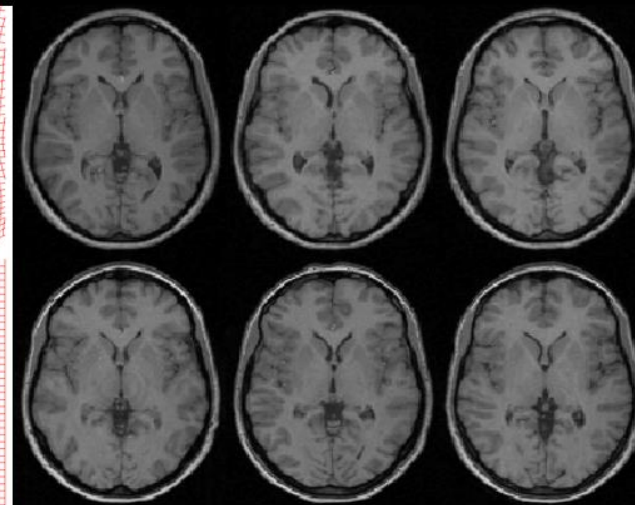
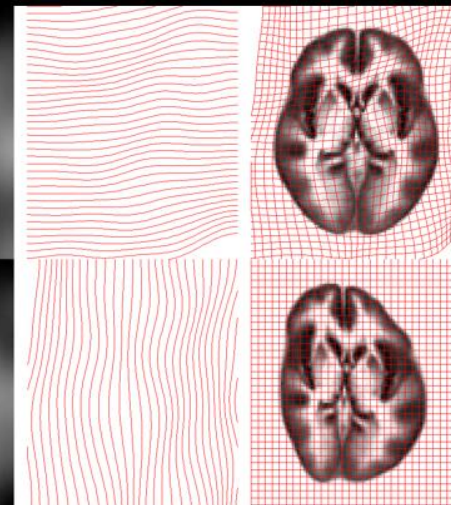
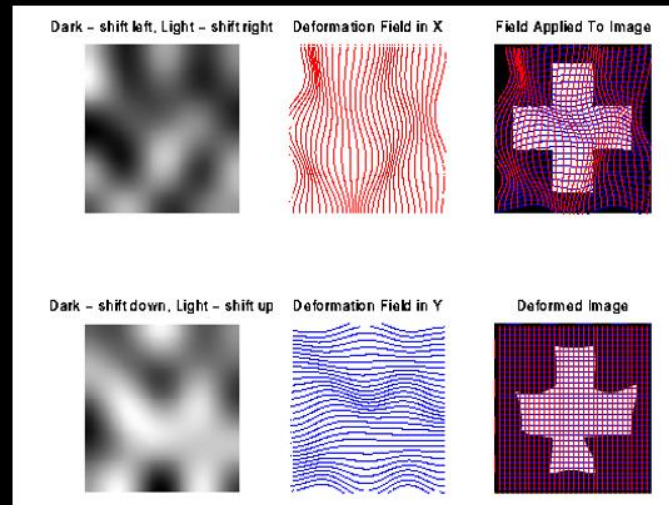
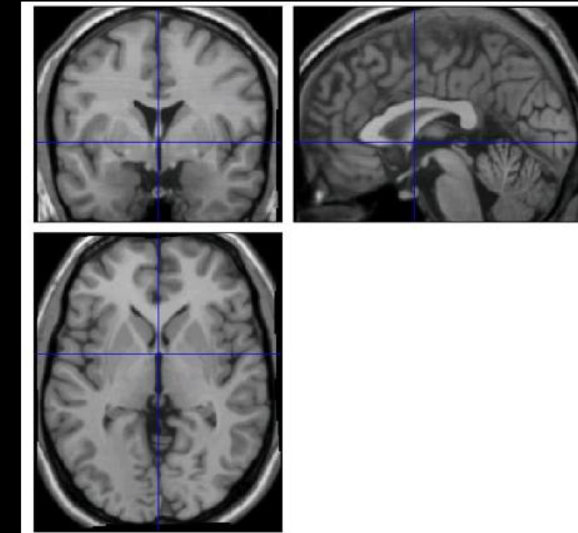
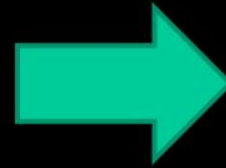
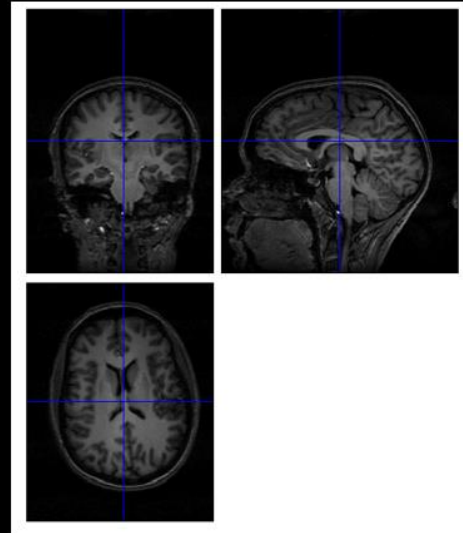
## About the MNI space(s)

<https://www.lead-dbs.org/about-the-mni-spaces/>

- **MNI305**: 305 normal MRI brains were linearly coregistered (9-param) to 241 brains that had been coregistered (roughly) to the Talairach atlas. This was the first MNI template. It is T1 only.
- **Colin27 original**: Colin Holmes, a lab member of the MNI, was scanned 27 times. This was used as the standard template in SPM96. This template was matched to the MNI305. In the original release, only a T1 template was available.
- **MNI152 linear**: 152 normal images were linearly coregistered (9-param) to the 305 space. This was adopted to define standard anatomy by the International Consortium of Brain Mapping (ICBM) and is used by SPM from version 99 on. Only a T1 template is available.
  - **SPM**: Note that in later iterations, SPM defined its own “space” based on scans acquired within the **IXI dataset**, leveraging on the concept of segmentation-based normalizations (as applied in the **Unified Segmentation**, **DARTEL** and **SHOOT** approaches). This space, **referred to as the IXI549Space** is largely similar to MNI152 and of similar resolution (where it's likely safe to say that differences do not matter as much for most applications). Along the same lines, both spaces are unsuitable for use in DBS imaging, in our opinion. **More info here.**
- **MNI152 NLIN 6th generation**: Here, the 152 brains were nonlinearly registered into 305 space. Again, only a T1 template is available.
  - **FSL**: The FSLR is an adapted version of this space but in its asymmetric flavor (MNI152NLIN6Asym, hence different to the official **one provided here**). The template also provides surface coordinates references. **More info here.**
- **Colin27 hires T1/T2 version (2008)**: The MNI also released a high-resolution version of the Colin27 space.
- **MNI152 NLIN 2009**: Finally, in 2009, the MNI released an updated version after again nonlinearly co-registering the 152 acquisitions. This template exhibits the best resolution and detail to date and is available in T1, T2, PD and T2-relaxometry versions. It has not (yet) been adopted by SPM or FSL though and it's anatomy is slightly different in direct comparison to the 6th generation templates. Moreover, it comes in three versions (two of which are explicitly mentioned here) that each have a symmetric and asymmetric subversion:
  - **MNI152 NLIN 2009a**: Probably the official new template in  $1 \times 1 \times 1$  mm resolution. It comes in T1, T2, PD and T2-relaxometry versions. There is a symmetric and an asymmetric version (latter not featuring T2-relaxometry).
  - **MNI152 NLIN 2009b**: The only of the novel templates available in  $0.5 \times 0.5 \times 0.5$  mm resolution. It is available in a T1, T2 and PD version. Due to the high resolution of this template, **it has been adopted by Lead-DBS as the primary anatomy template**. Lead-DBS uses the asymmetric version of this template.



# Normalisation



Non-linear spatial transformations

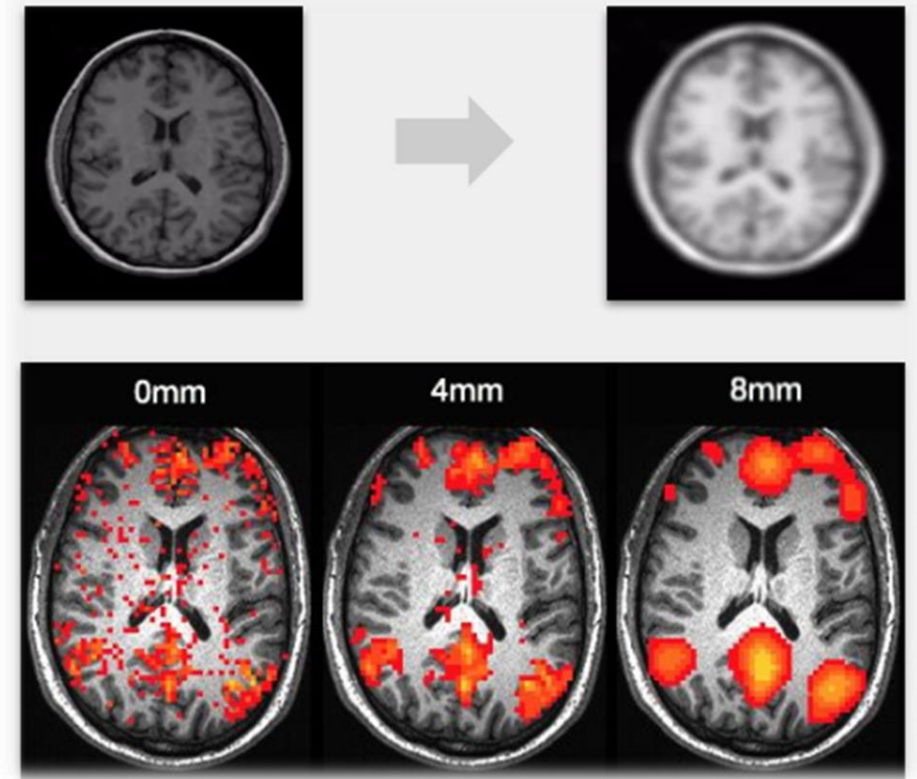


FMRI 4 NEWBIES .COM



# Spatial smoothing

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

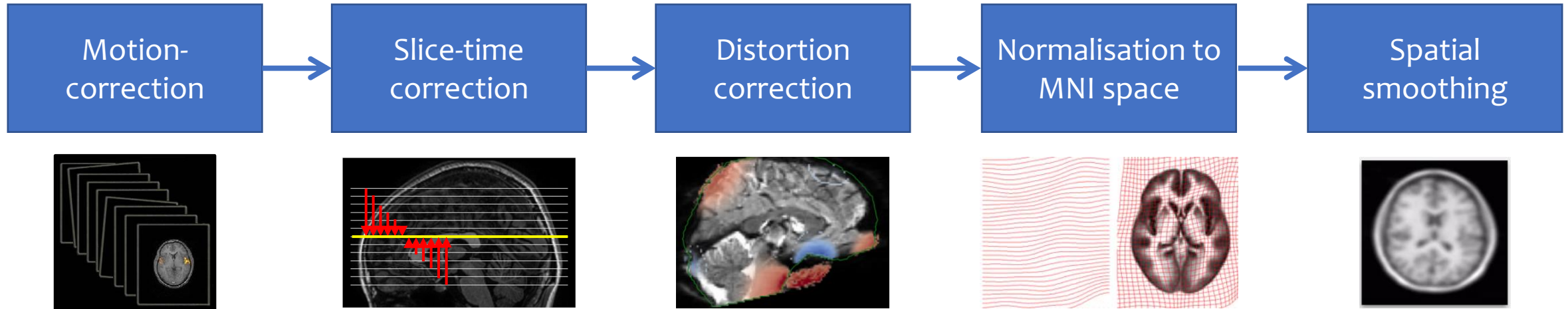


# Problems with fMRI data

---

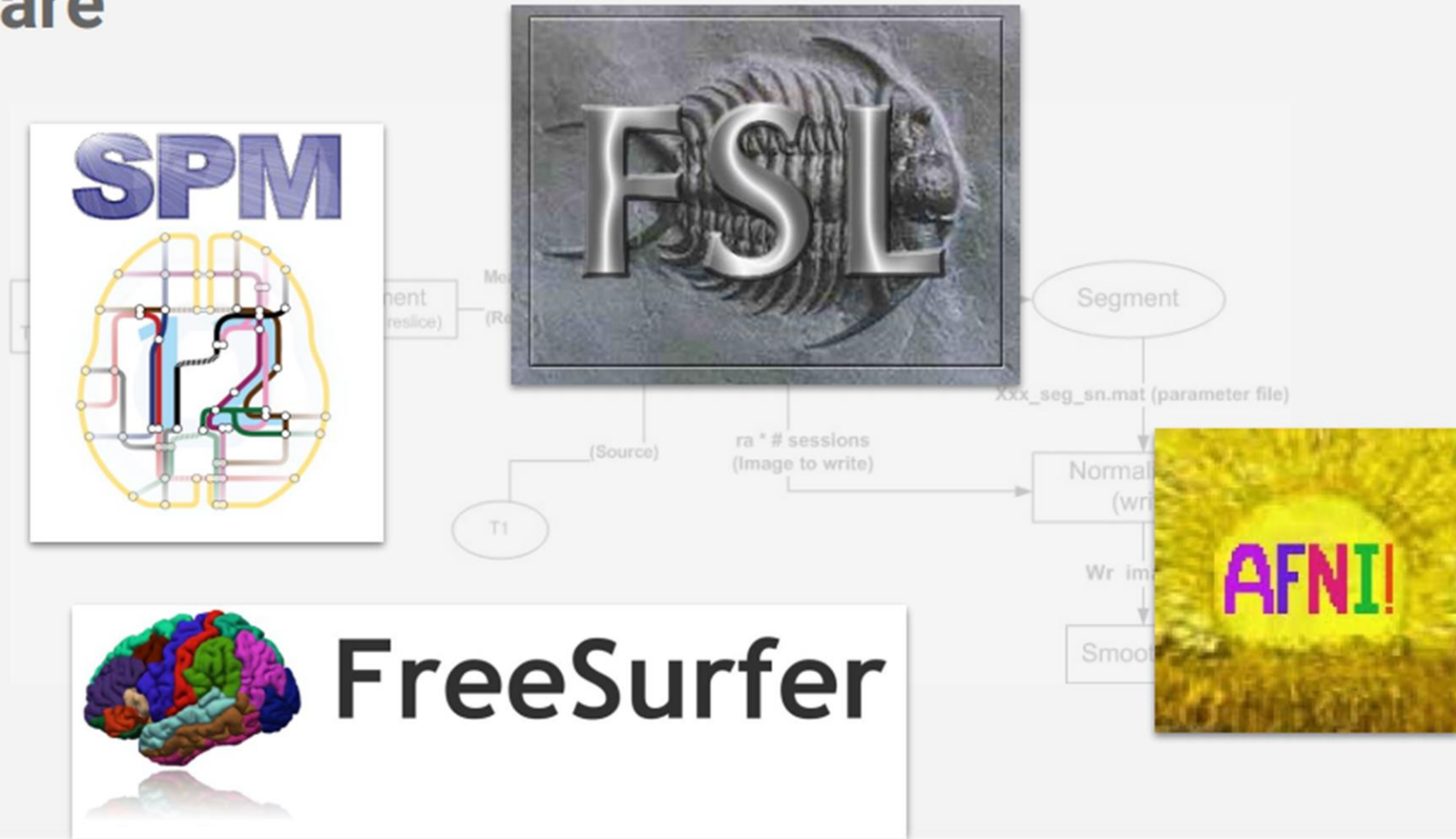
- Artefacts
- Head motion
- Slice timing
- Brain differences
- Noise – can be modelled in GLM
- ... and many others

# Typical pre-processing pipeline



# Pre-processing tools

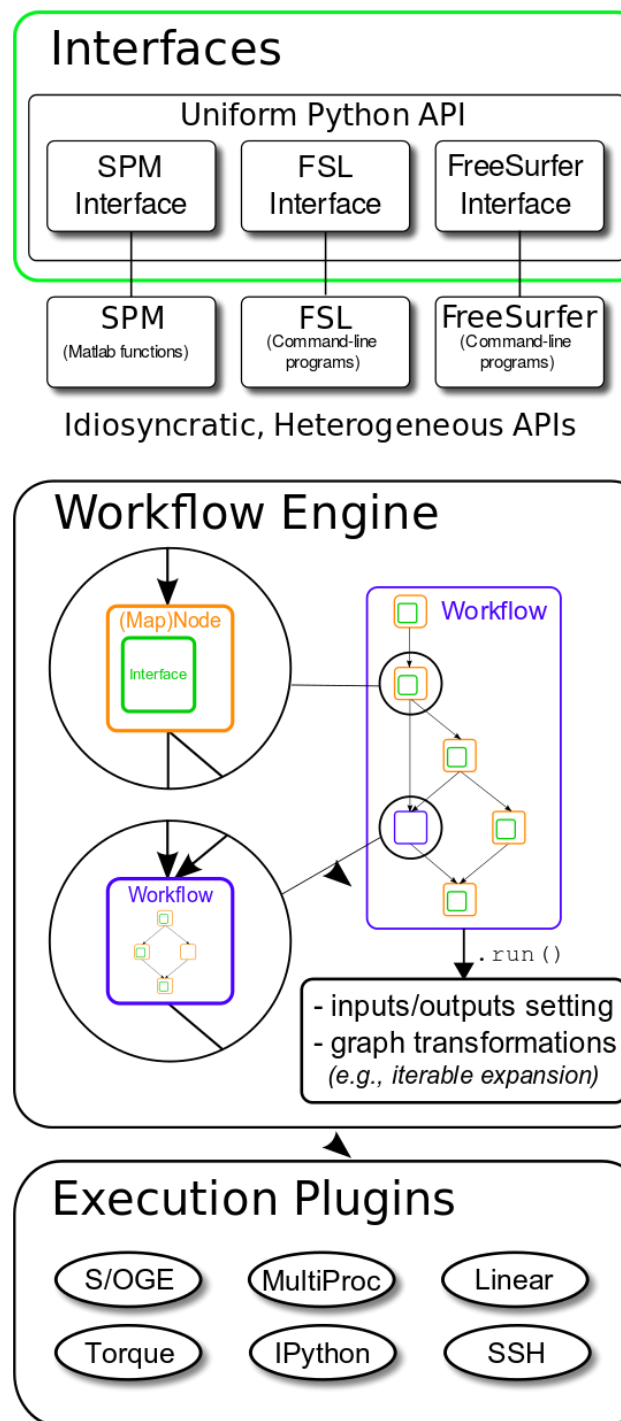
## Software



# Pre-processing tools



## Nipype: Neuroimaging in Python Pipelines and Interfaces



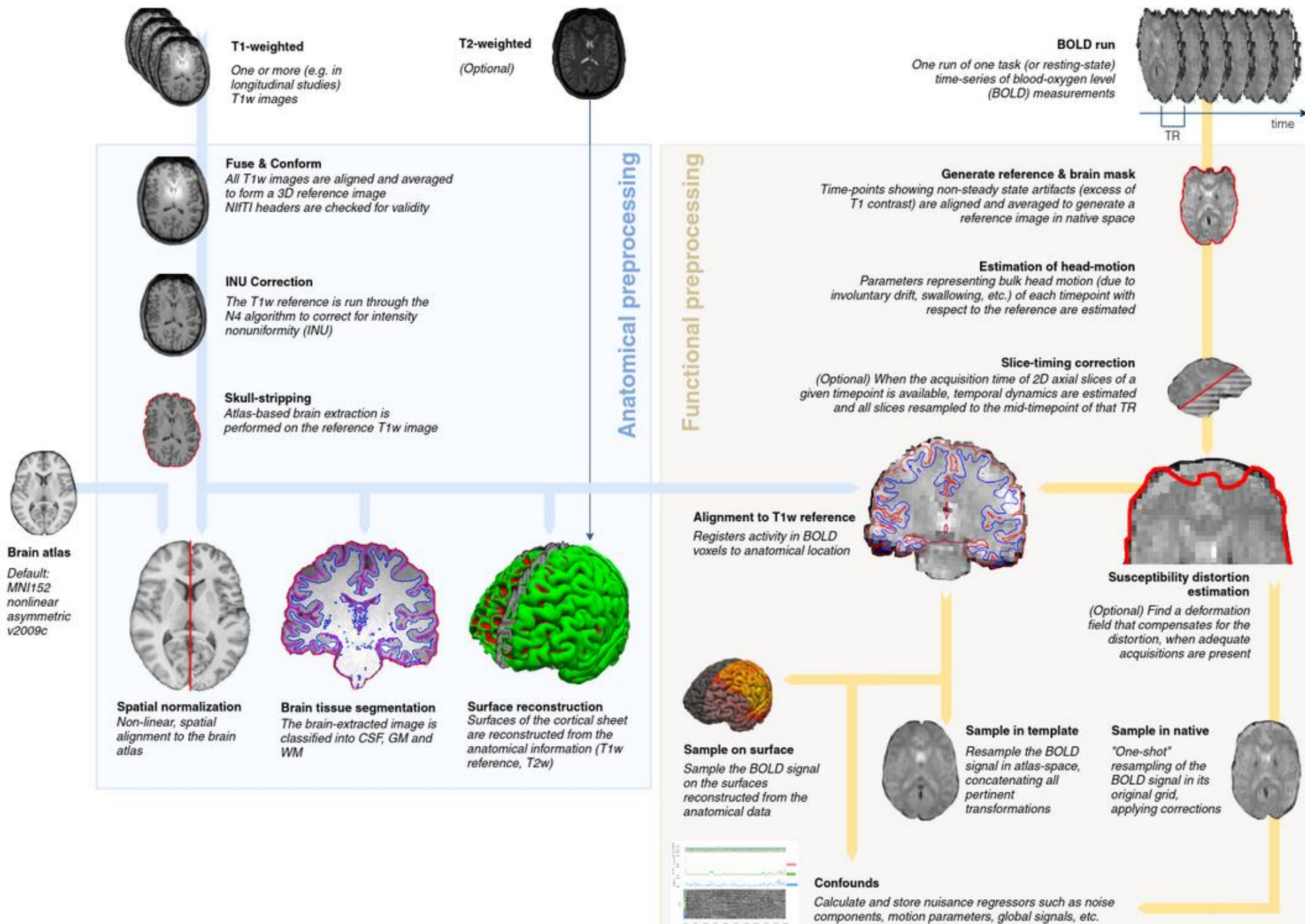
# Pre-processing tools

---

- 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.



# fMRIPrep



# ✓ Environment



**Data**  
Organise & Manage



Notebook: [nb03\\_Quality-Control-and-Preprocessing.ipynb](#)

Pre-process



# Outline

---

- Introduction
- Experimental design
- Data management
- Pre-processing
- **Statistical analysis**
- Practical demo