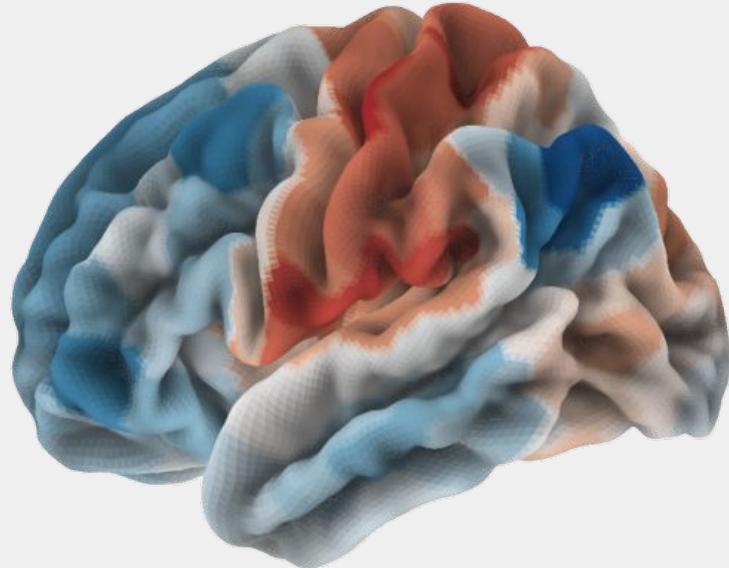


Fundamentals of fMRI data analysis

Karolina Finc

Centre for Modern Interdisciplinary Technologies
Nicolaus Copernicus University in Toruń



COURSE #3: **fMRI data preprocessing** | 16th November 2020

Study plan

Open science & neuroimaging



BEFORE

fMRI data manipulation
in python



fMRI data
preprocessing



Functional
connectivity



AFTER



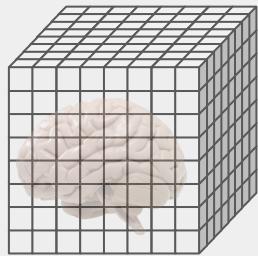
General
Linear Model



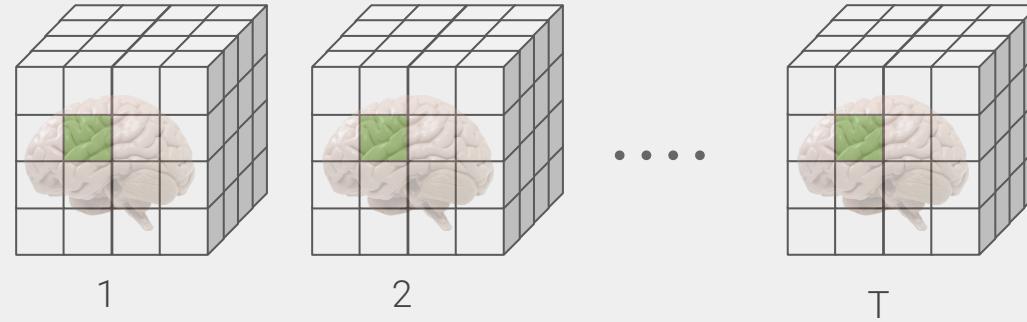
Machine Learning
on fMRI data

fMRI data structure

Structural data



Functional data

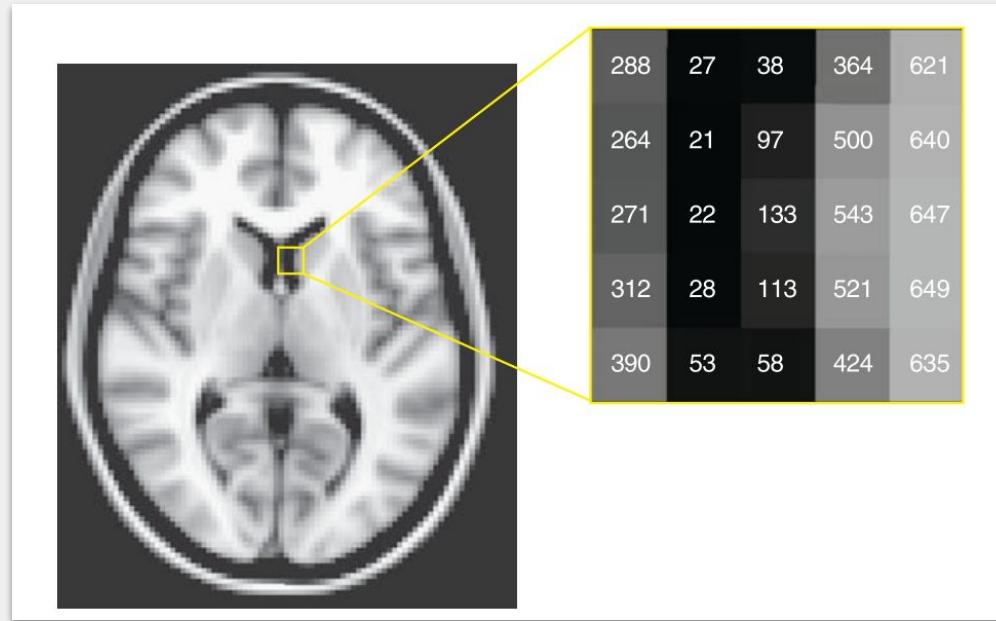


Time series - is a series of data points listed in time order.

Every voxel has its own time-series.



Brain image is a matrix of numbers



Study plan

Open science & neuroimaging



BEFORE

fMRI data manipulation
in python



fMRI data
preprocessing



Functional
connectivity



AFTER



General
Linear Model



Machine Learning
on fMRI data

Study plan

Open science & neuroimaging

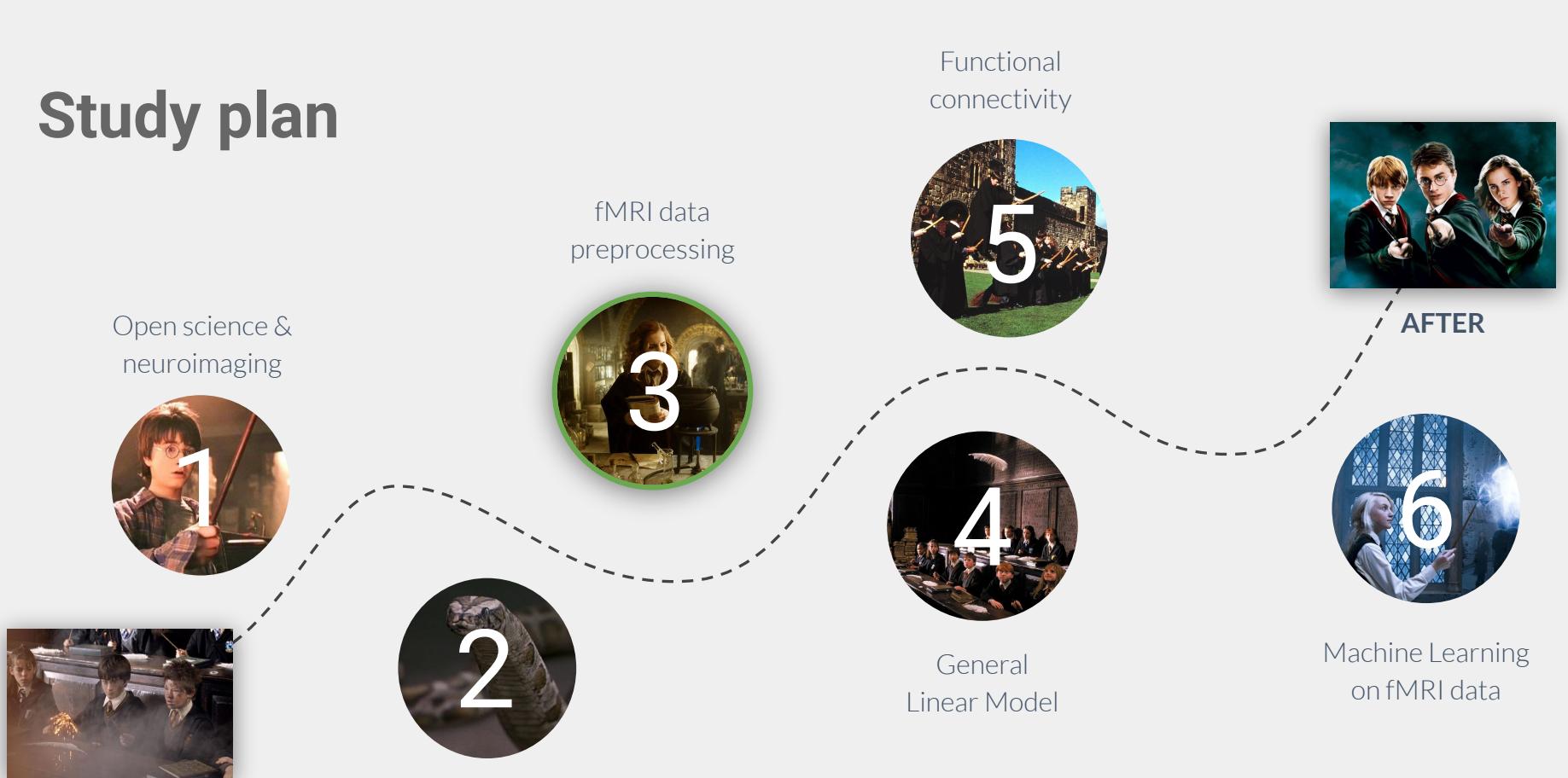


BEFORE

fMRI data manipulation
in python



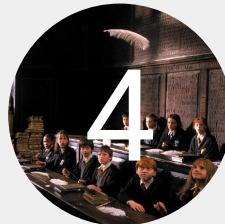
fMRI data
preprocessing



Functional
connectivity



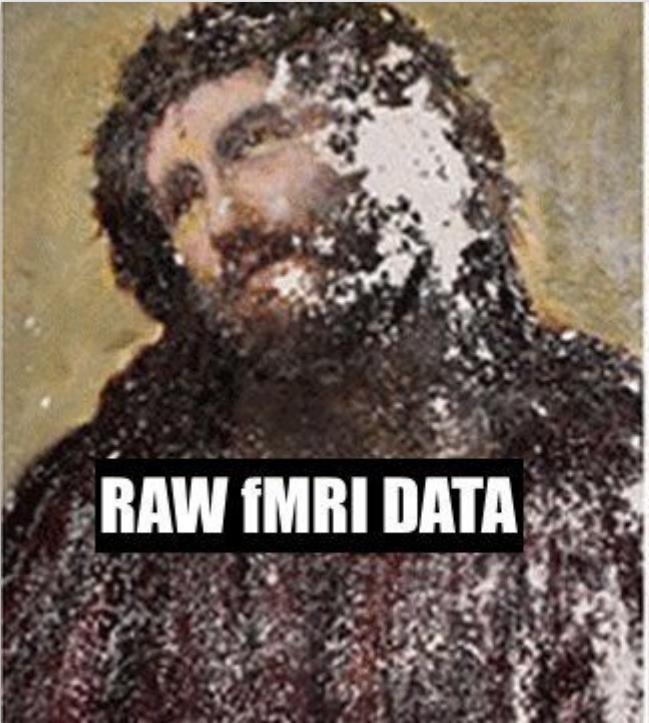
AFTER



General
Linear Model



Machine Learning
on fMRI data



RAW fMRI DATA



CLEANED fMRI DATA

CENTRO DE ESTUDIOS BORJANOS

What is fMRI analysis for?



What is fMRI analysis for?

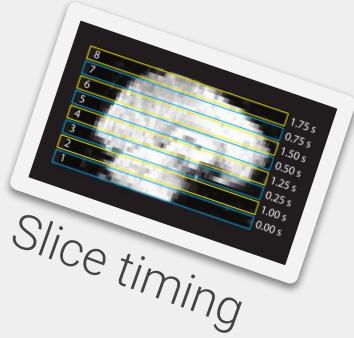
- Getting to know something about population
- Finding differences between populations
- Tracking brain changes during lifespan/learning etc.



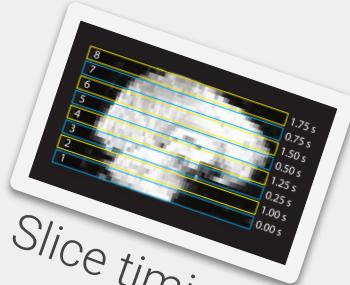
What wrong about raw fMRI data?



Problems of raw fMRI data



Problems of raw fMRI data

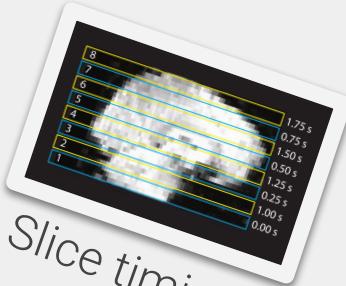


Slice timing



Head motion

Problems of raw fMRI data



Slice timing

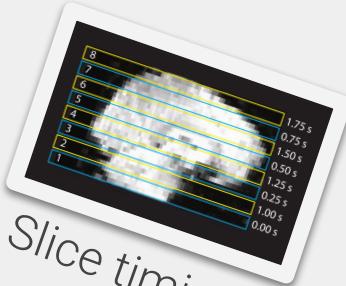


Brain differences



Head motion

Problems of raw fMRI data



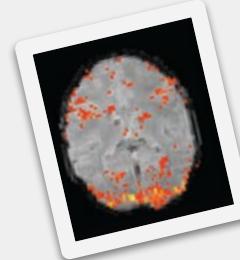
Slice timing



Brain differences

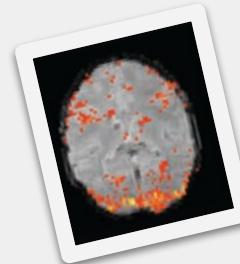
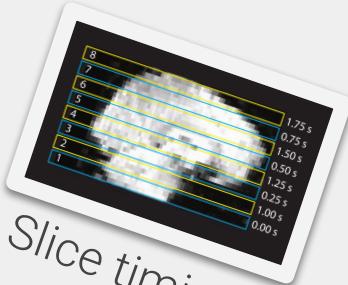


Head motion



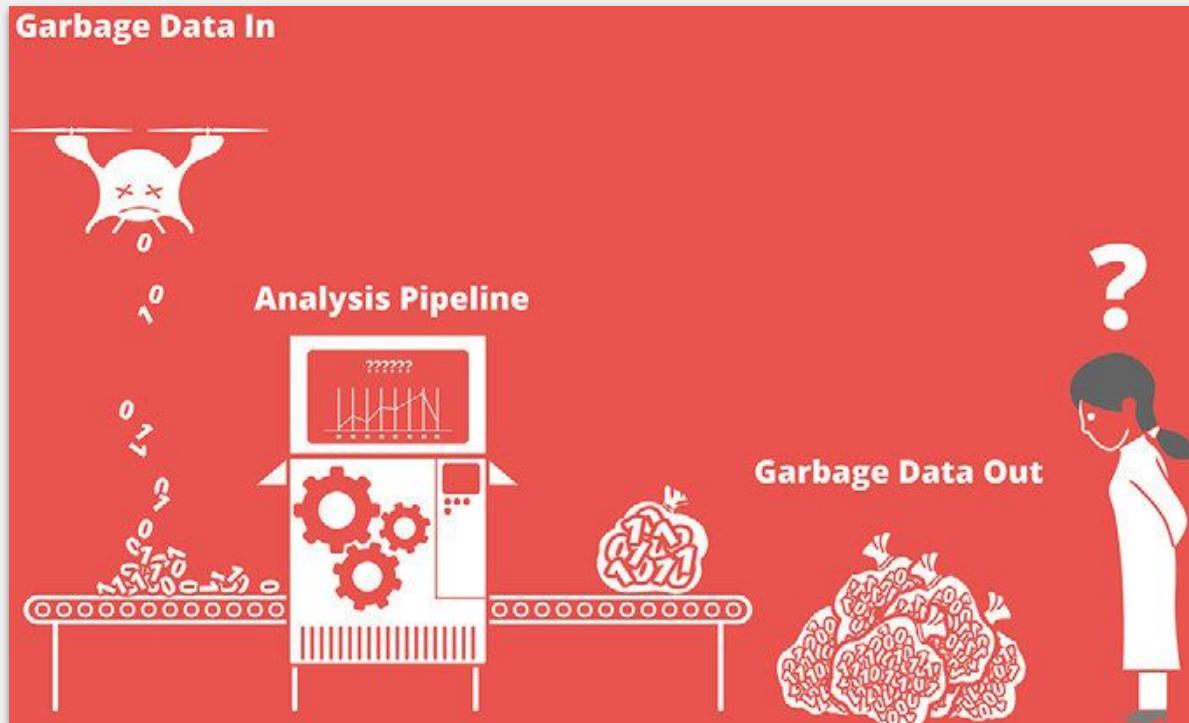
Noise

Problems of raw fMRI data



... and many
others!

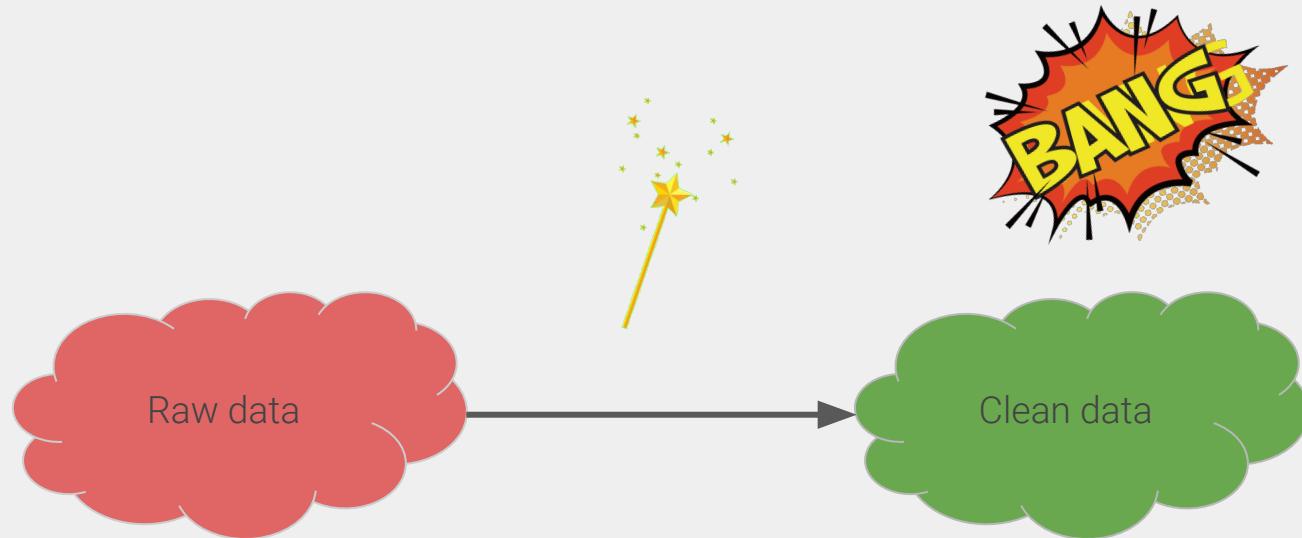
Garbage in, garbage out



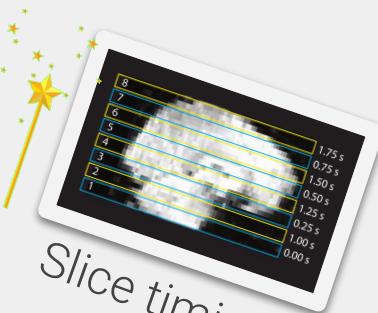
How to fix this?



How to fix this?



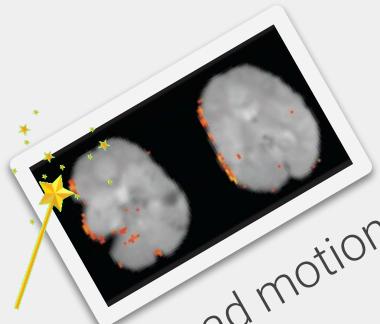
Preprocessing



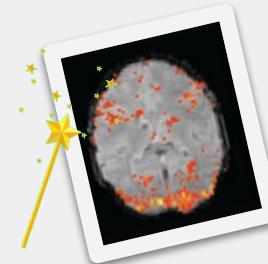
Slice timing



Brain differences

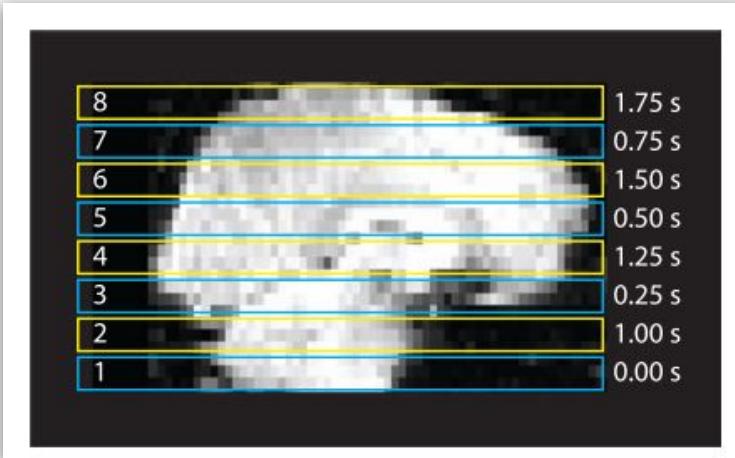


Head motion

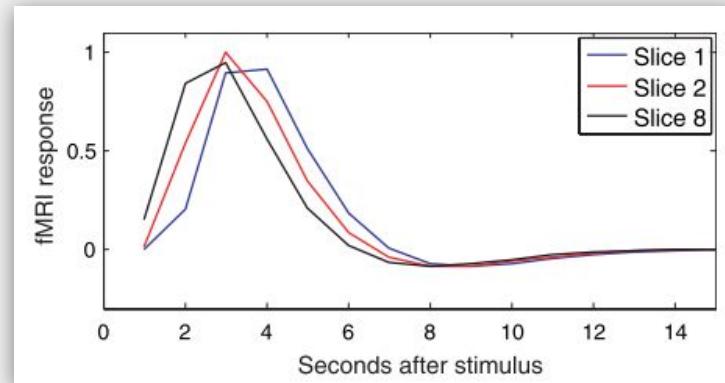


Noise

Slice timing correction



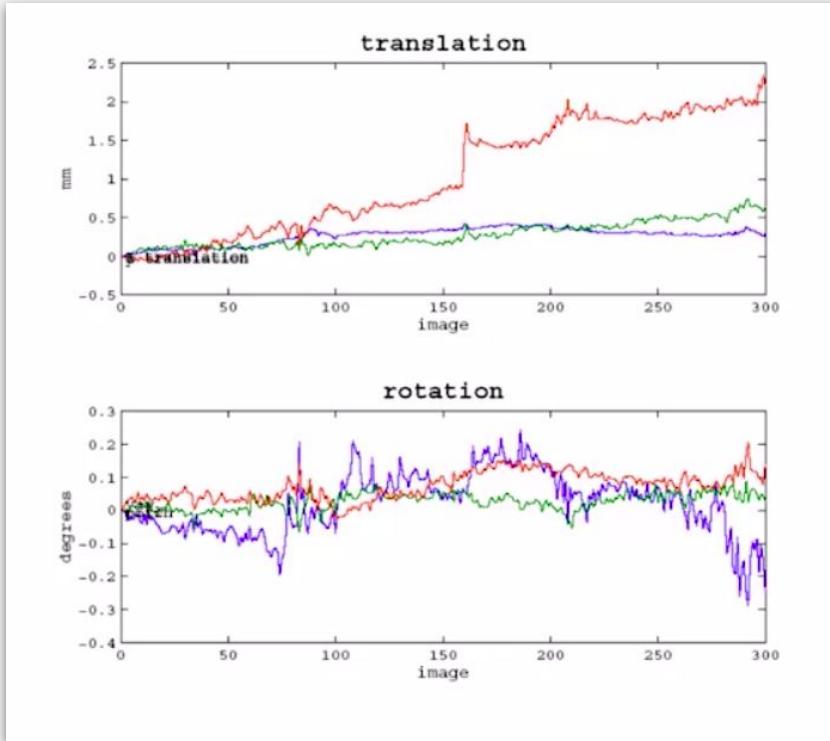
Interleaved acquisition



Temporal interpolation – the estimation of a value of a signal at a time point that was not originally collected, using data from nearby time points.

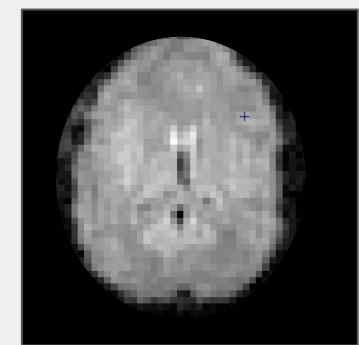
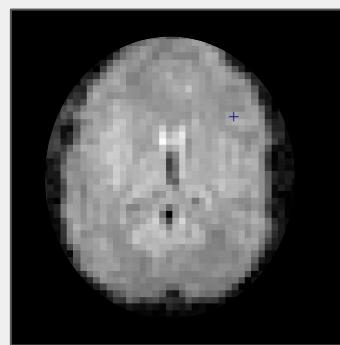
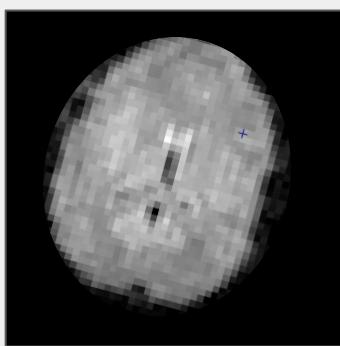
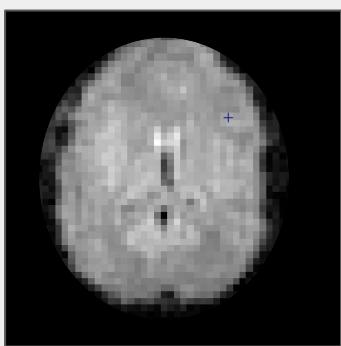
Typically each slice is interpolated to either the first time-point or the middle MR image.

Motion correction



- 3 rotations
- 3 translations

Motion correction

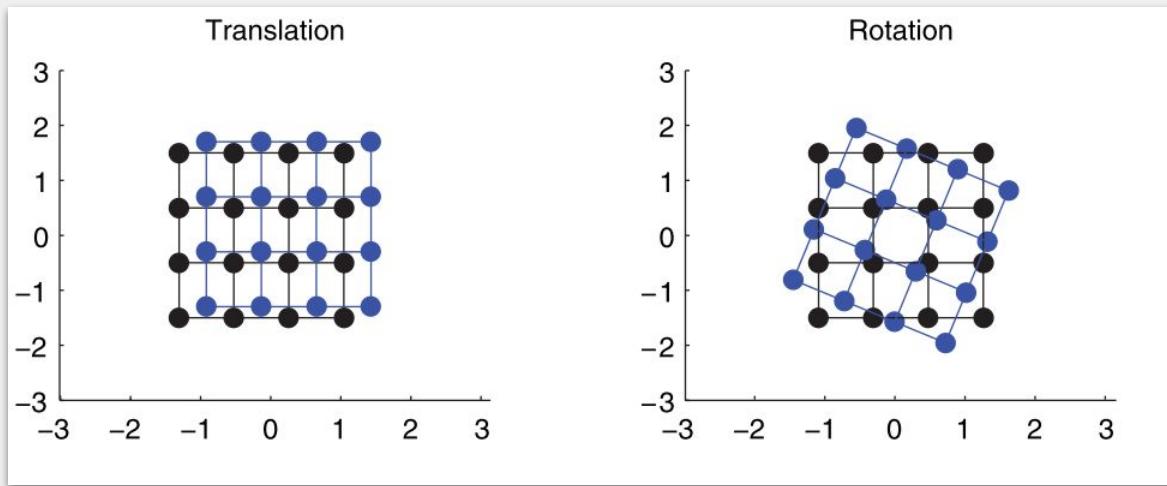


"I'm particularly interested in Transfiguration, you know, turning something into something else, of course, it's supposed to be very difficult"

—Hermione Granger regarding transformation



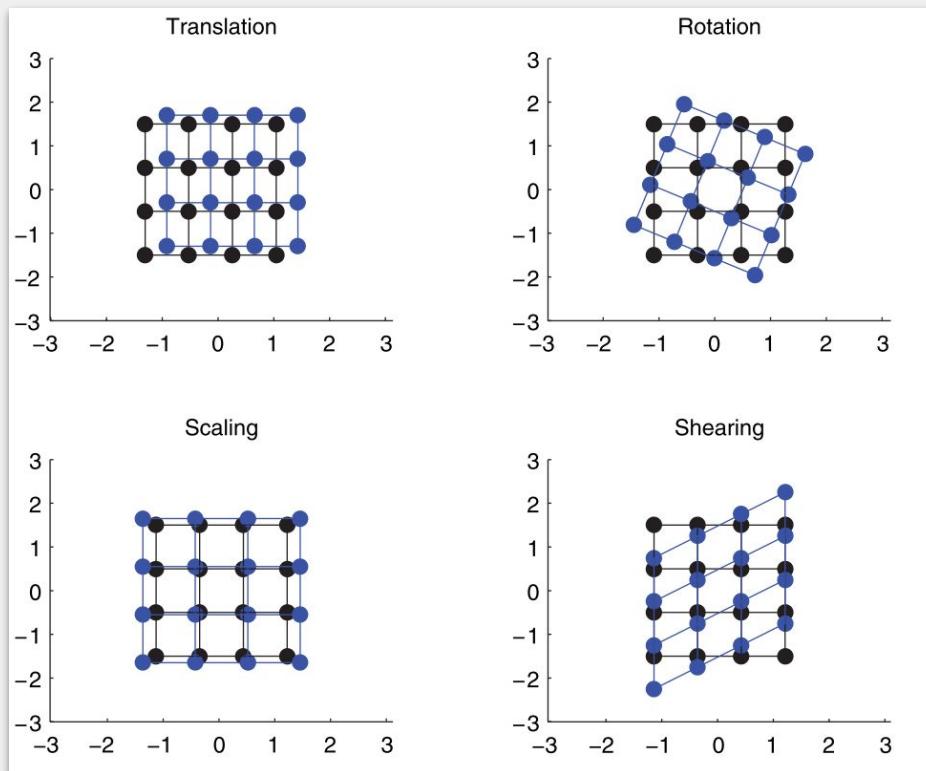
Rigid body transformation



Does not change the shape and size of image.

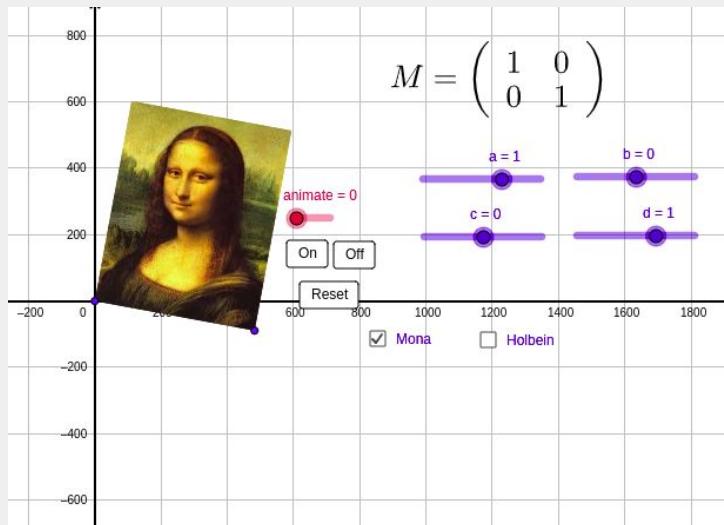
6 parameters: 3 translations and 3 rotations.

Affine transformations



12 parameters: 3 translations, 3 rotations, scaling and shearing.

Linear transformations magic!

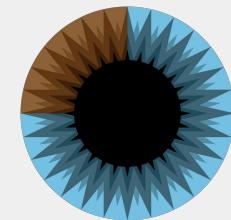


GeoGebra

<https://www.geogebra.org/m/pDU4peV5>



<https://www.khanacademy.org/math/linear-algebra/matrix-transformation/s/linear-transformations/a/visualizing-linear-transformations>



https://www.youtube.com/channel/UCYO_jabesuFRV4b17AJtAw

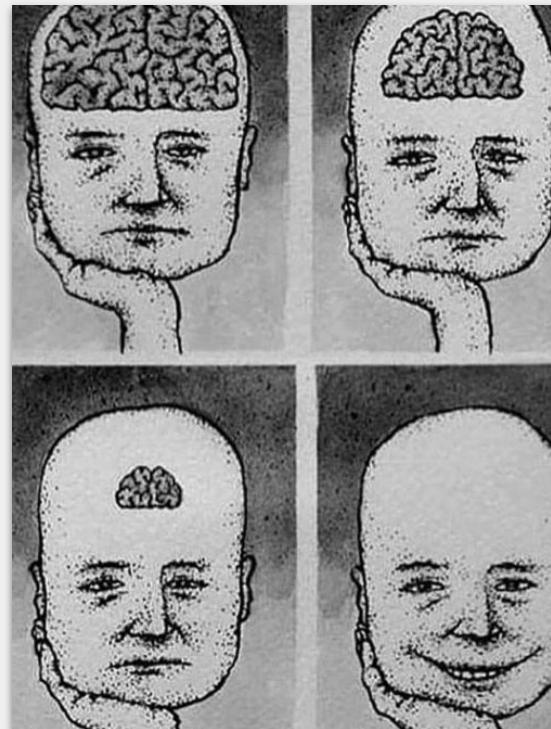
Matrix multiplication

$$\begin{bmatrix} 1 & 2 & 3 \\ 4 & 5 & 6 \end{bmatrix} \times \begin{bmatrix} 7 & 8 \\ 9 & 10 \\ 11 & 12 \end{bmatrix} = \begin{bmatrix} 58 & 64 \end{bmatrix}$$

Normalization

Brain size can differ (up to 30%).
Brain shape can differ.

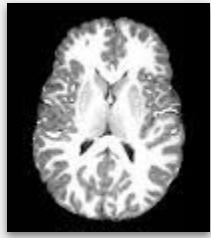
Normalization - stretching, squeezing and warping each brain to the “standard brain”.



What's a “standard brain”?

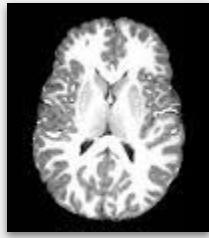


Standard brain: template



Original image
Native space

Standard brain: template



Original image
Native space

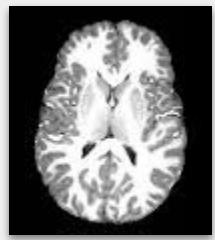


Template image
Standard space

Talairach (1967) - based on single subject.
Montreal National Institute (MNI) - combination of MRI scans.

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

Standard brain: template



Original image
Native space



Template image
Standard space



Normalized image
Standard space

Linear (affine) and nonlinear transformations, dysmorphic transformations, surface based methods.

Talairach (1967) - based on single subject.
Montreal National Institute (MNI) - combination of MRI scans.

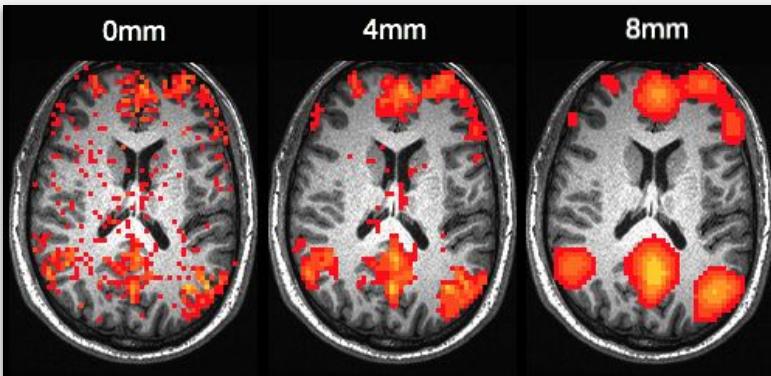
<https://www.lead-dbs.org/about-the-mni-spaces/>

Smoothing

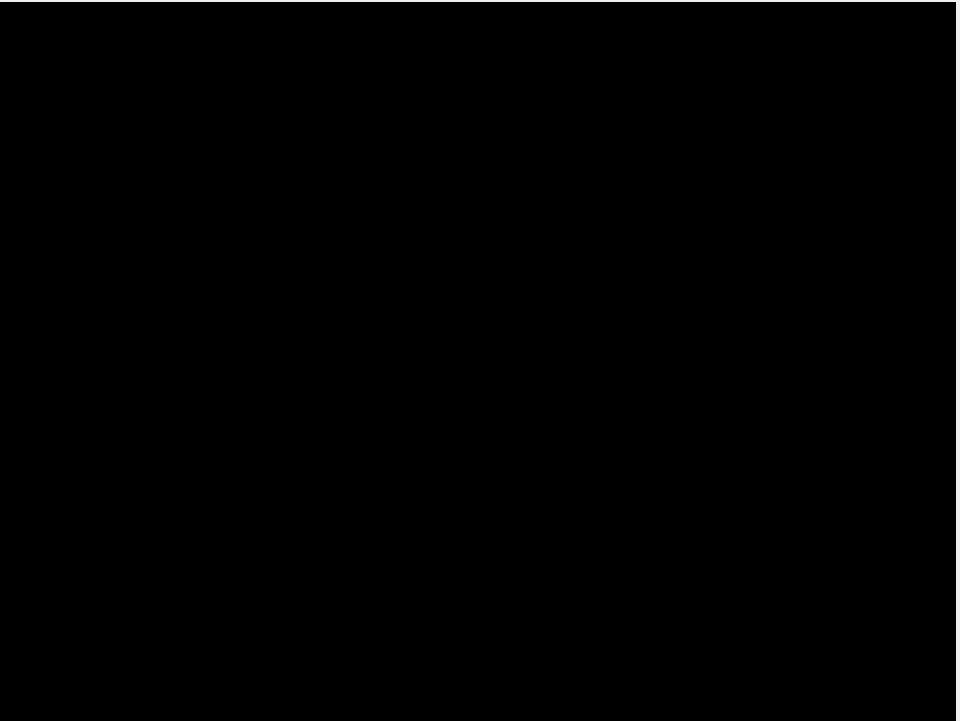


- Can increase signal-to-noise ratio and remove artifacts.
- Can blur anatomical brain differences.
- May increase validity of the statistical analysis.

But! It reduces the image resolution.



Gaussian kernel

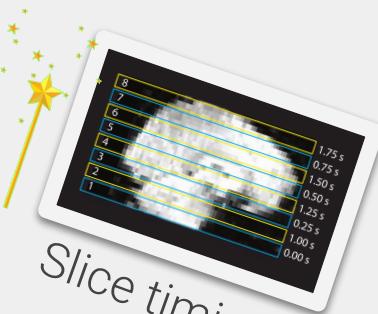


For each data point we generate a new value that is some function of the original value at that point and the surrounding data points (for Gaussian smoothing, the function that is used is our Gaussian curve).

The **kernel** for smoothing – defines the shape of the function that is used to take the average of the neighboring points.

Full Width at Half Maximum (FWHM) – the width of the kernel, at half of the maximum of the height of the Gaussian.

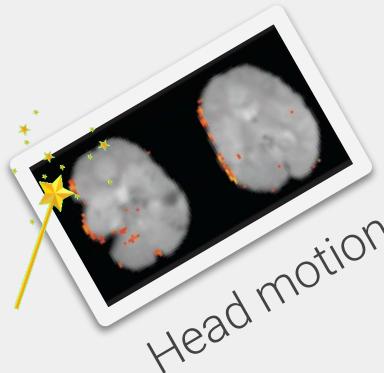
Preprocessing



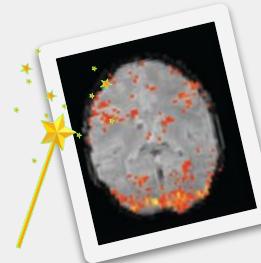
Slice timing



Brain differences

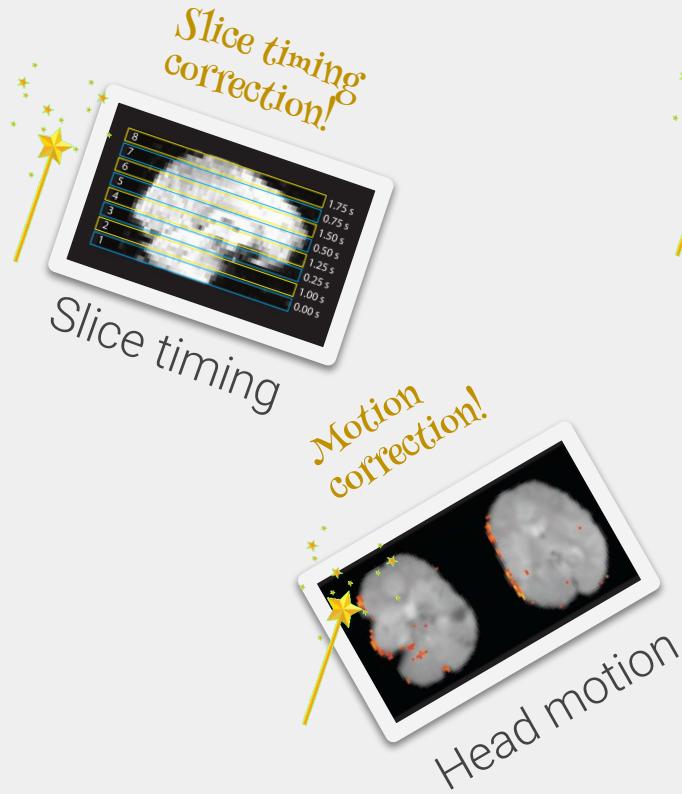


Head motion

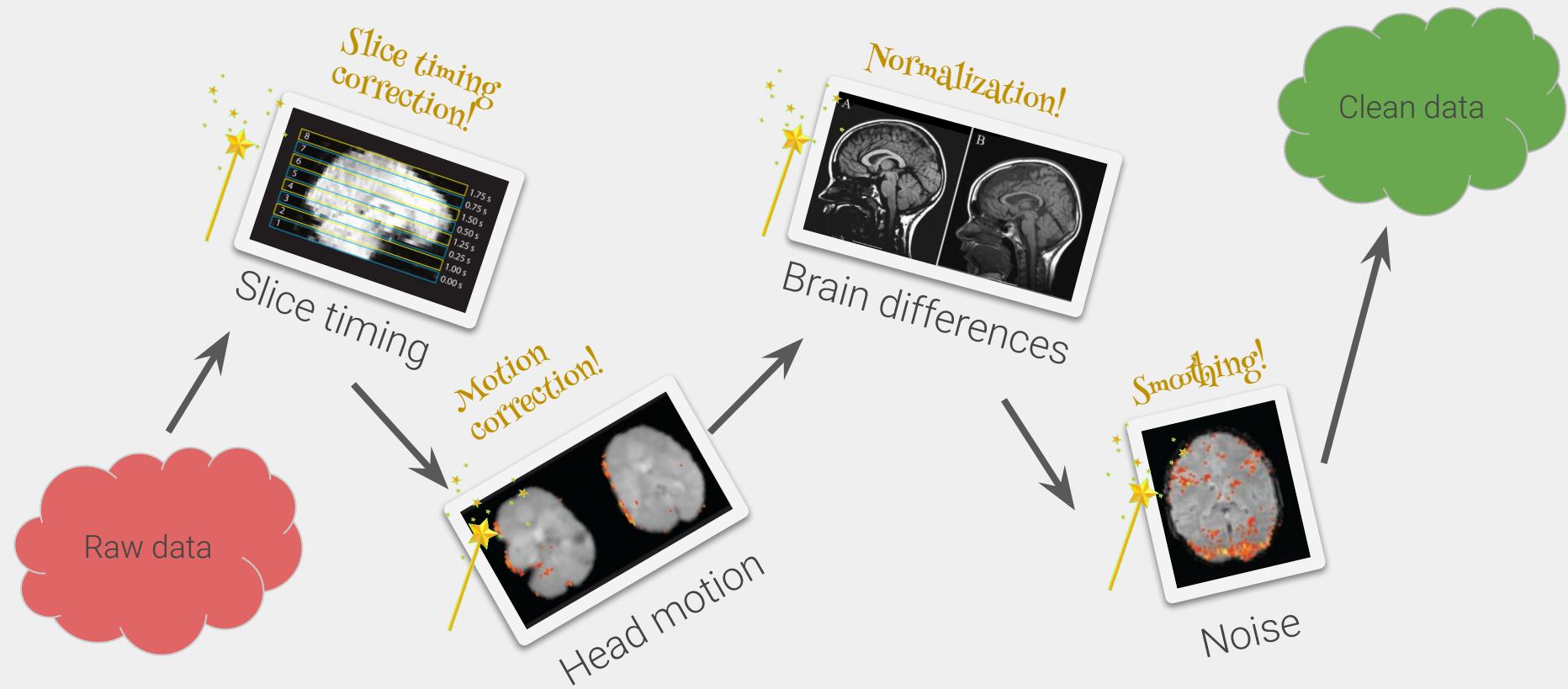


Noise

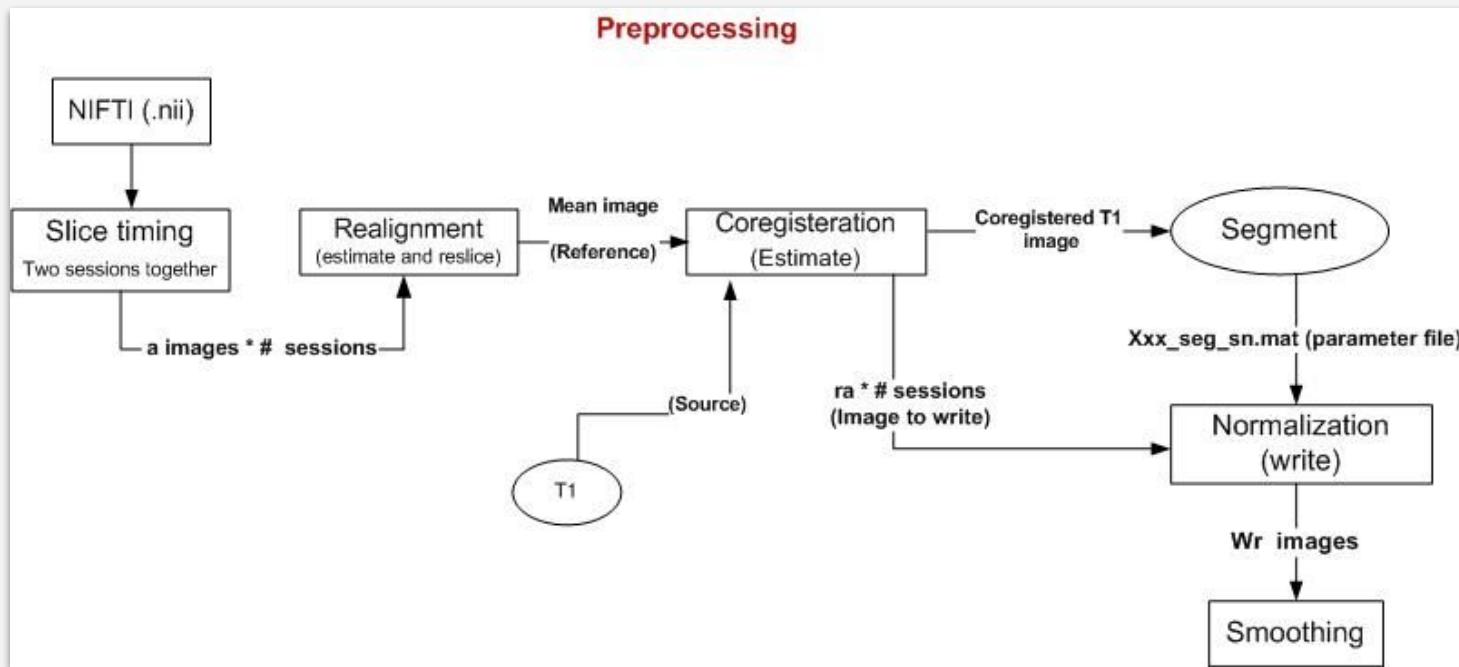
Preprocessing



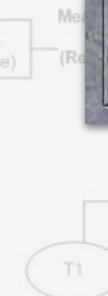
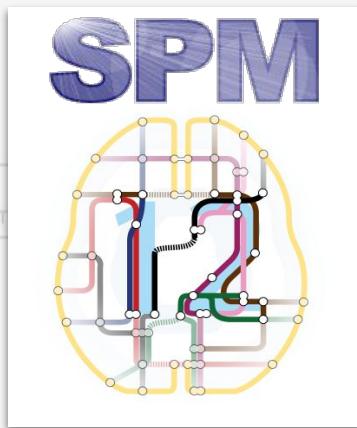
Preprocessing workflow / pipeline



Preprocessing workflow / pipeline



Software



ra * # sessions
(Image to write)

Xxx_seg_sn.mat (parameter file)

Segment

Normal
(wr)

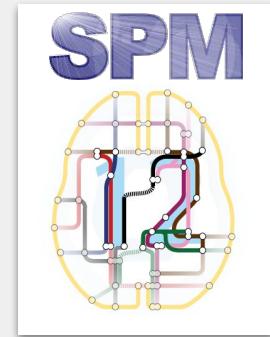
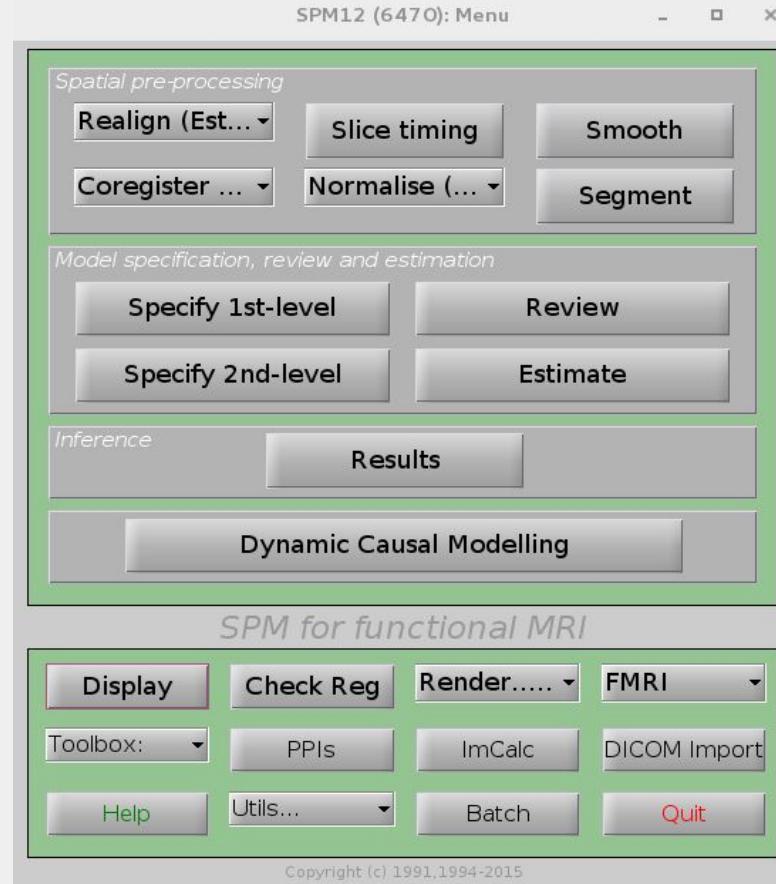
Wr im

Smooth

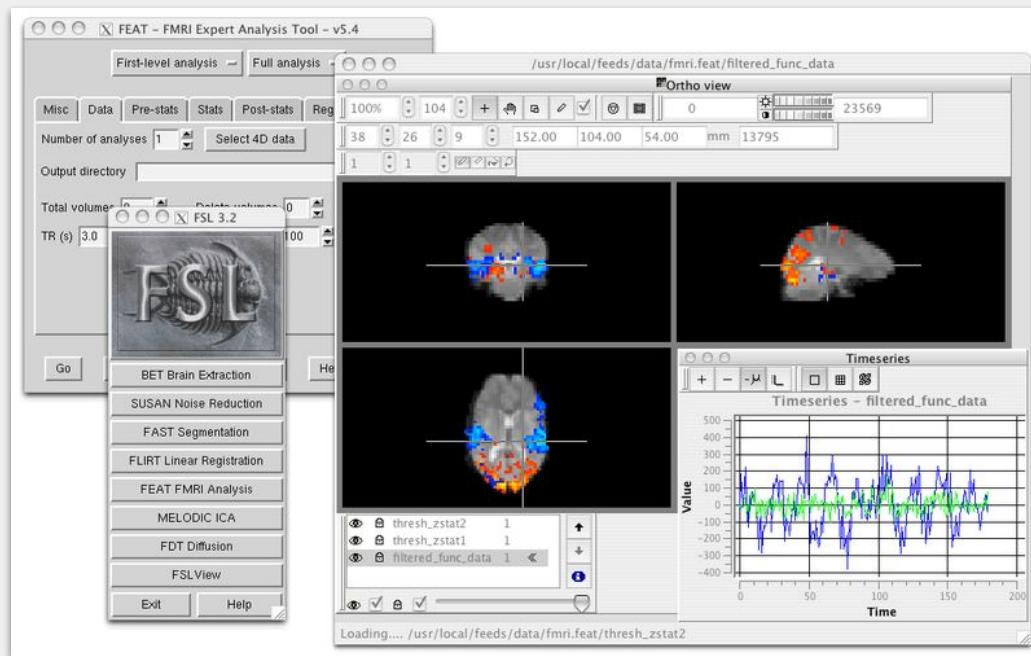


FreeSurfer

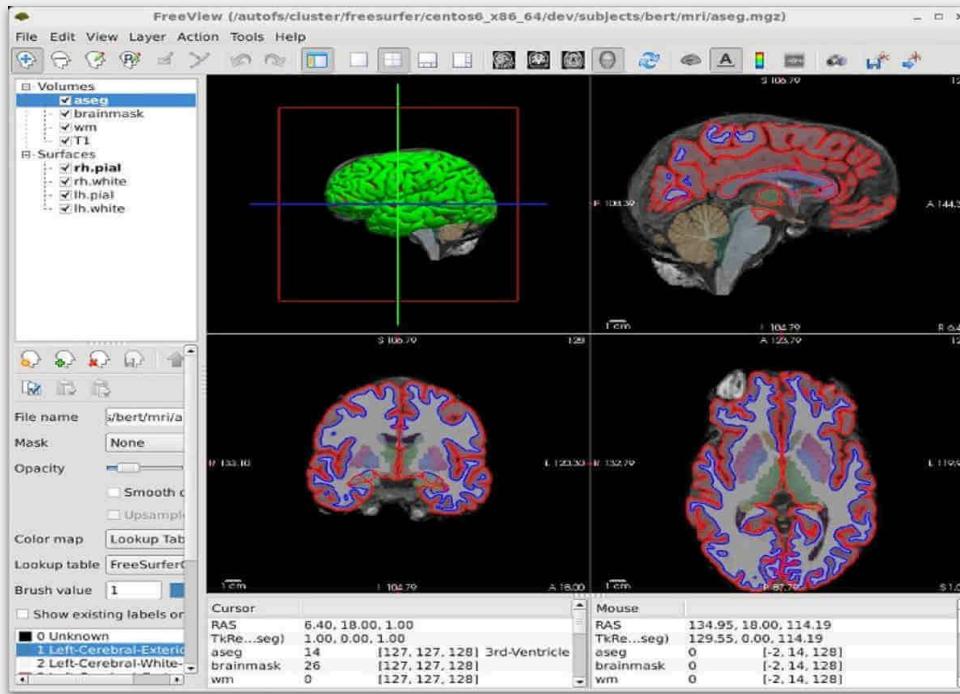
SPM way



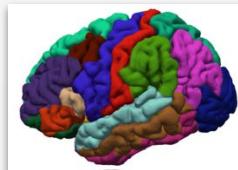
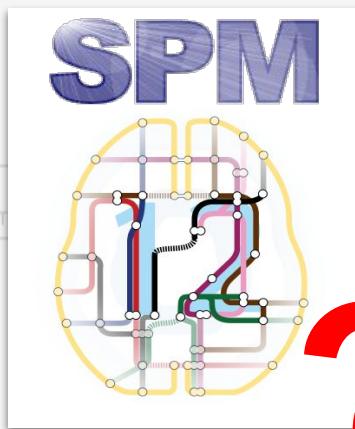
FSL way



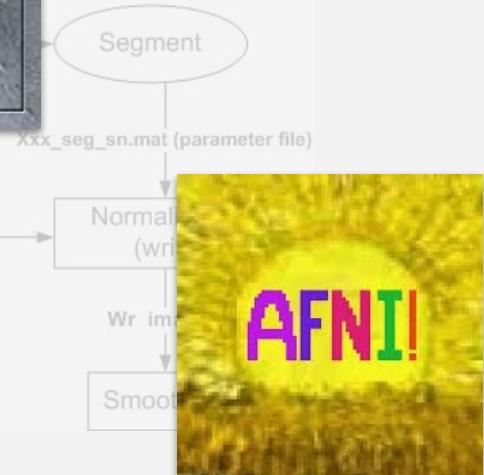
FreeSurfer way



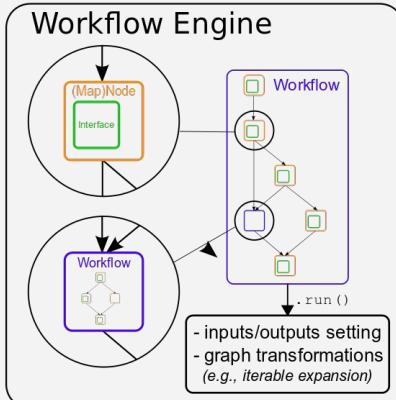
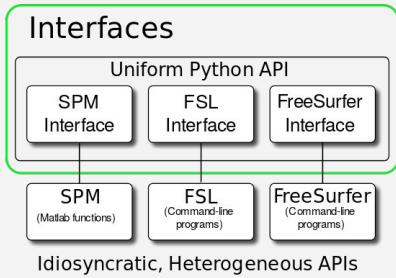
Software



FreeSurfer



Nipype



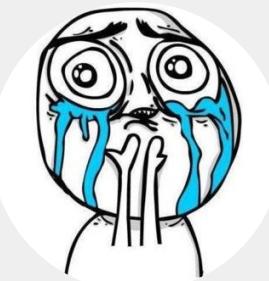
<https://giraffe.tools/pourcpine/TimVanMourik/SomeGiraffeExample>



Fast way to scientist's depression

Processing step	Reason	Options [suboptions]	Number of plausible option
Motion correction	Correct for head motion during scanning	• 'Interpolation' [linear or sinc] • 'Reference volume' [single or mean]	4
Slice timing correction	Correct for differences in acquisition timing of different slices	'No', 'before motion correction' or 'after motion correction'	3
Field map correction	Correct for distortion owing to magnetic susceptibility	'Yes' or 'no'	2
Spatial smoothing	Increase SNR for larger activations and ensure assumptions of GRF theory	'FWHM' [4 mm, 6 mm or 8 mm]	3
Spatial normalization	Warps an individual brain to match a group template	'Method' [linear or nonlinear]	2
High-pass filter	Remove low-frequency nuisance signals from data	'Frequency cut-off' [100s or 120s]	2
Head motion regressors	Remove remaining signals owing to head motion via statistical model	'Yes' or 'no' [if yes: 6/12/24 parameters or single time point 'scrubbing' regressors]	5
Haemodynamic response	Account for delayed nature of haemodynamic response to neuronal activity	• 'Basis function' ['single-gamma' or 'double-gamma'] • 'Derivatives' ['none', 'shift' or 'dispersion']	6
Temporal autocorrelation model	Model for the temporal autocorrelation inherent in fMRI signals	'Yes' or 'no'	2
Multiple-comparison correction	Correct for large number of comparisons across the brain	'Voxel-based GRF', 'cluster-based GRF', 'FDR' or 'non-parametric'	4
Total possible workflows			69,120

- Which software to select?
- Which method to select?
- Which option to select?



fMRIPrep!

The screenshot shows the 'Usage' section of the fMRIprep stable documentation. It includes a warning about usage statistics, instructions for execution and BIDS format, and a command-line example.

Usage

Warning

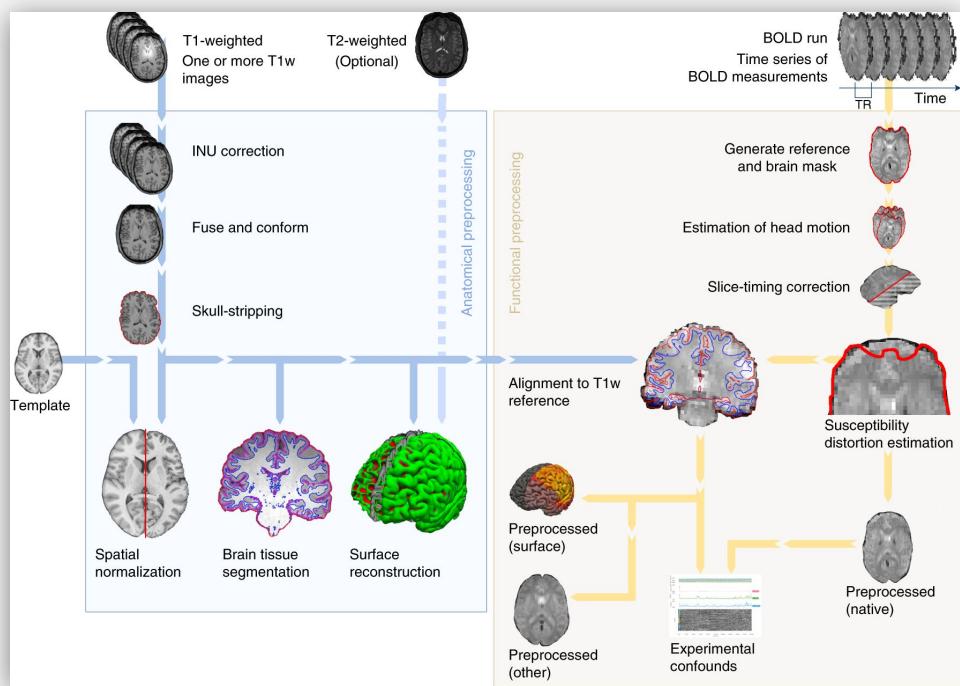
As of FMRIPREP 1.0.12, the software includes a tracking system to report usage statistics and errors. Users can opt-out using the `--notrack` command line argument.

Execution and the BIDS format

The `fmrifprep` workflow takes as principal input the path of the dataset that is to be processed. The input dataset is required to be in valid BIDS format, and it must include at least one T1w structural image and (unless disabled with a flag) a BOLD series. We highly recommend that you validate your dataset with the free, online BIDS Validator.

The exact command to run `fmrifprep` depends on the **Installation** method. The common parts of the command follow the BIDS-Apps definition. Example:

```
fmrifprep data/bids_root/ out/ participant -w work/
```

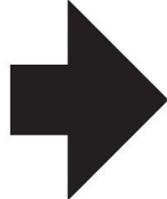


<https://fmriprep.readthedocs.io/en/stable/>

Brain Imaging Data Structure (BIDS)

```
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/
```

Website:

<https://bids.neuroimaging.io/>

BIDS validator:

<https://bids-standard.github.io/bids-validator/>

How to BIDSify fMRI data?

```
derivatives/
└── fmriprep/
    ├── dataset_description.json
    ├── logs
    ├── sub-01.html
    └── sub-01/
        ├── anat/
        │   ├── sub-01_desc-brain_mask.nii.gz
        │   ├── sub-01_dseg.nii.gz
        │   ├── sub-01_label-GM_probseg.nii.gz
        │   ├── sub-01_label-WM_probseg.nii.gz
        │   ├── sub-01_label-CSF_probseg.nii.gz
        │   ├── sub-01_desc-preproc_T1w.nii.gz
        │   ├── sub-01_space-MNI152_desc-brain_mask.nii.gz
        │   ├── sub-01_space-MNI152_dseg.nii.gz
        │   ├── sub-01_space-MNI152_label-GM_probseg.nii.gz
        │   ├── sub-01_space-MNI152_label-WM_probseg.nii.gz
        │   ├── sub-01_space-MNI152_label-CSF_probseg.nii.gz
        │   ├── sub-01_space-MNI152_desc-preproc_T1w.nii.gz
        │   ├── sub-01_from-MNI152_to-T1w_mode-image_xfm.h5
        │   ├── sub-01_from-T1w_to-MNI152_mode-image_xfm.h5
        │   └── sub-01_from-orig_to-T1w_mode-image_xfm.txt
        └── figures/
            └── func/
                ├── sub-01_task-rhymejudgment_space-MNI152_boldref.nii.gz
                └── sub-01_task-rhymejudgment_space-MNI152_desc-preproc_bold.nii.gz
```

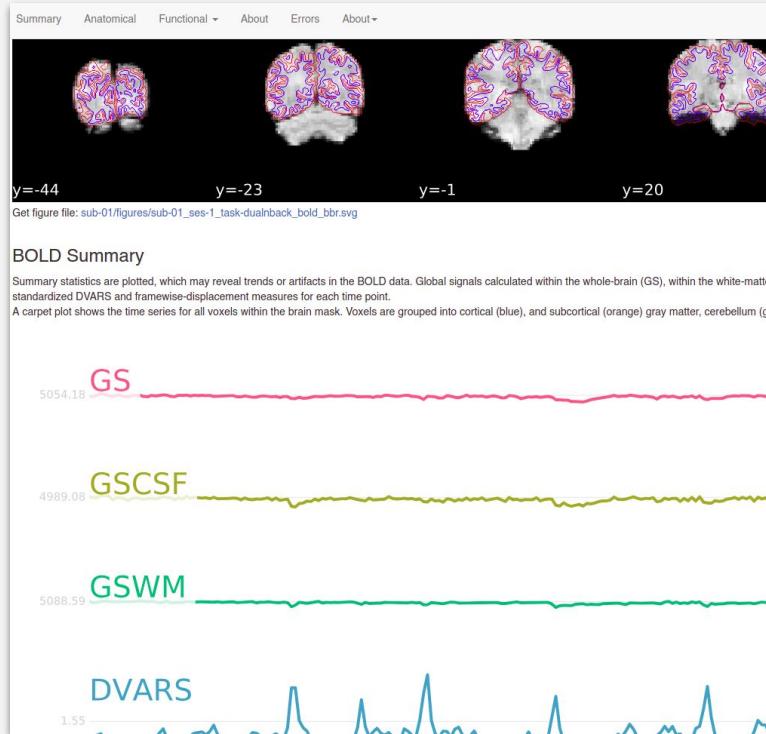
1. Convert DICOM to Nifti

<https://github.com/rordenlab/dcm2niix>

2. Create folder structure

3. Add remaining data
(dataset_desctiption, events etc.)

fMRIPrep - reports



https://fmriprep.readthedocs.io/en/stable/_static/sample_report.html#Anatomical

Homework

1. **3Blue1Brown** videos (Linear Algebra)

2. **Data Camp Classroom**

<https://www.datacamp.com/enterprise/advanced-fMRI-data-analysis/assignments>

Exploratory Data Analysis in Python

Deadline: 23-11-2020



Next



General Linear Model