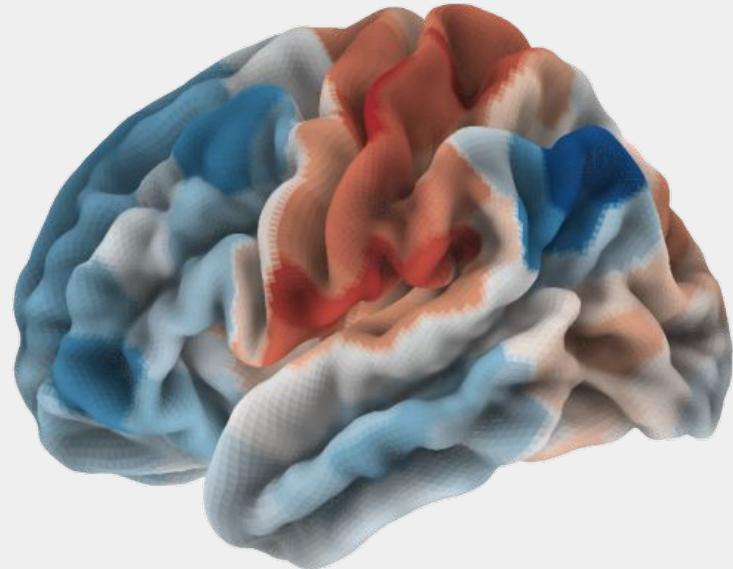


# Fundamentals of fMRI data analysis

Karolina Finc

Centre for Modern Interdisciplinary Technologies

Nicolaus Copernicus University in Toruń



PART #3: fMRI data preprocessing

# Study plan

Open science & neuroimaging



**BEFORE**

fMRI data manipulation  
in python



fMRI data  
preprocessing



Functional  
connectivity



**AFTER**



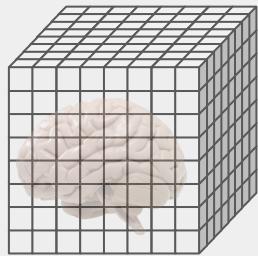
General  
Linear Model



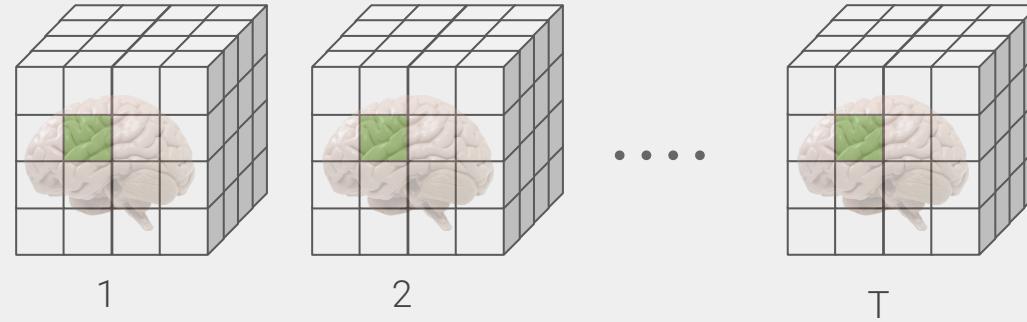
Machine Learning  
on fMRI data

# fMRI data structure

Structural data

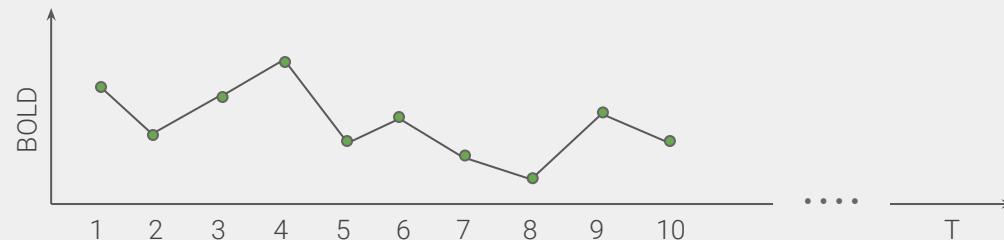


Functional data

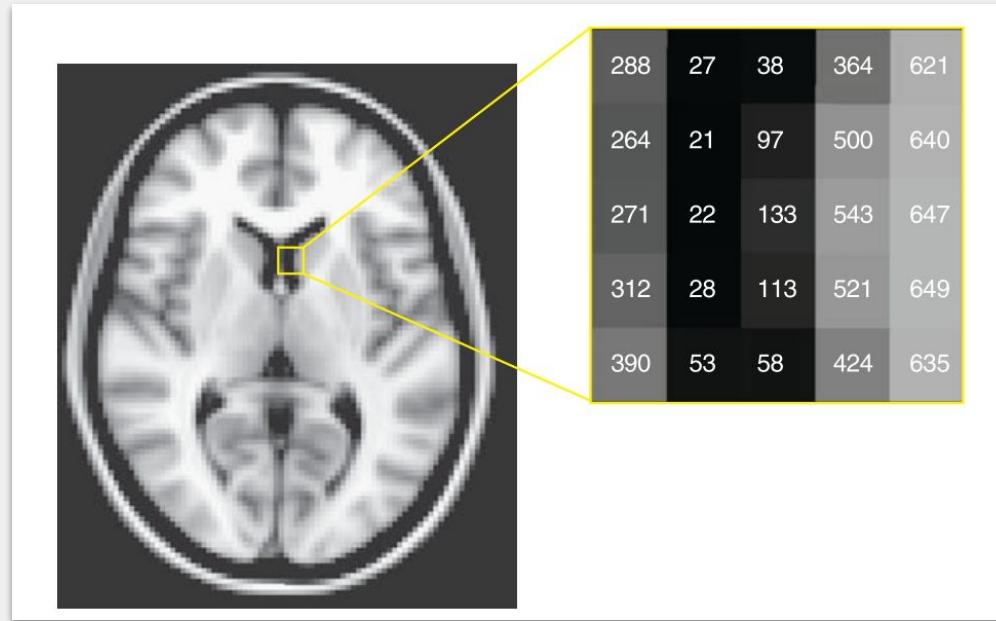


**Time series** - is a series of data points listed in time order.

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



3

Functional  
connectivity



5



4

General  
Linear Model

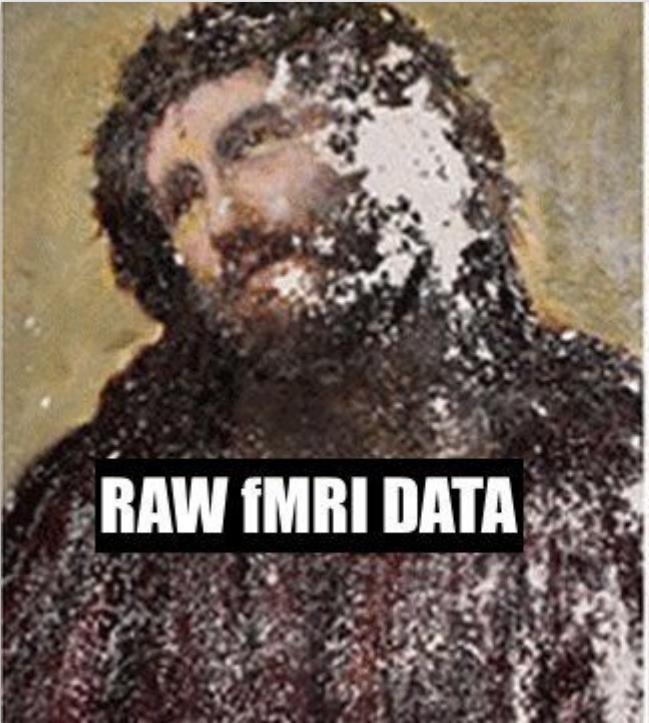


**AFTER**



Machine Learning  
on fMRI data

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?

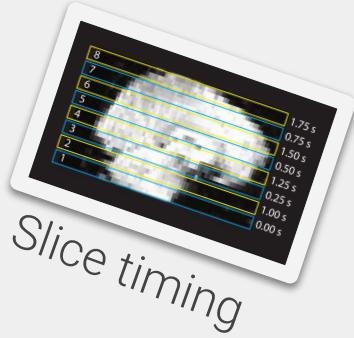
- Getting to know something about population
- Finding differences between populations
- Tracking brain changes during lifespan/learning etc.



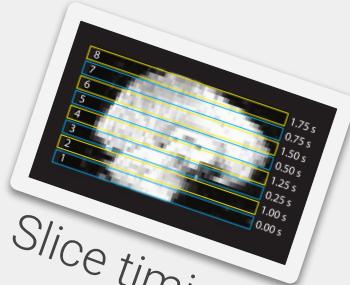
# What wrong about raw fMRI data?



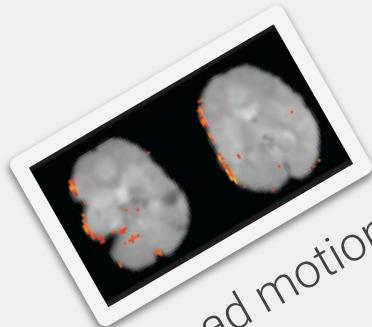
# Problems of raw fMRI data



# Problems of raw fMRI data

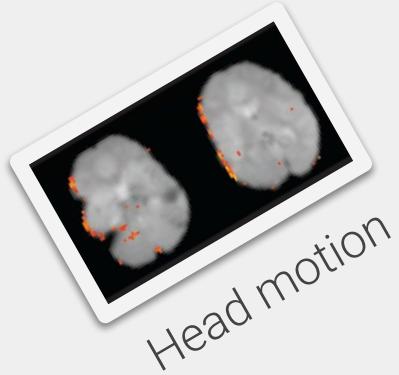
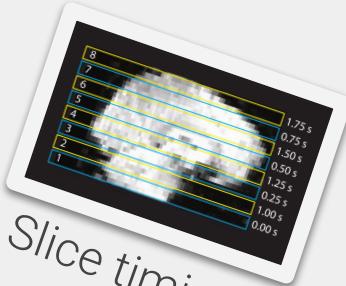


*Slice timing*

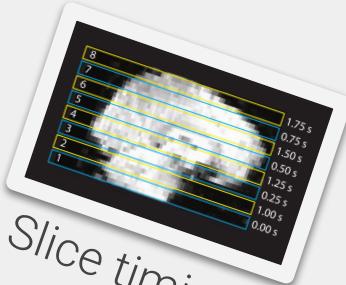


*Head motion*

# Problems of raw fMRI data



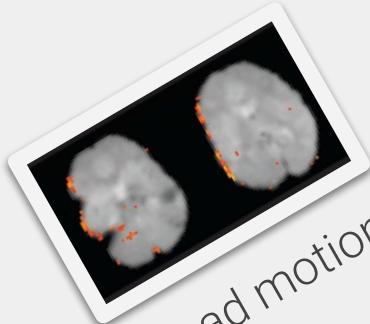
# Problems of raw fMRI data



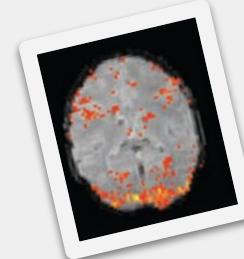
Slice timing



Brain differences

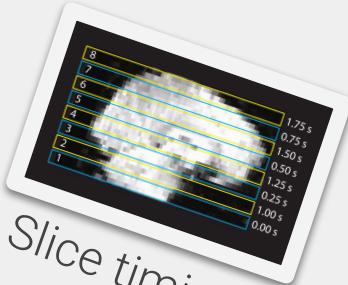


Head motion



Noise

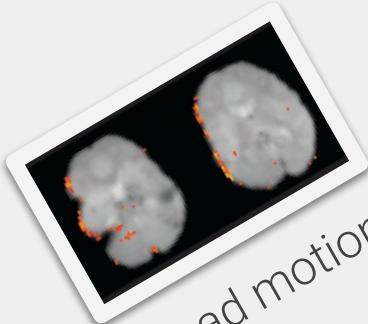
# Problems of raw fMRI data



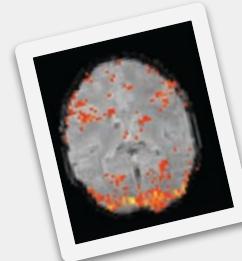
*Slice timing*



*Brain differences*



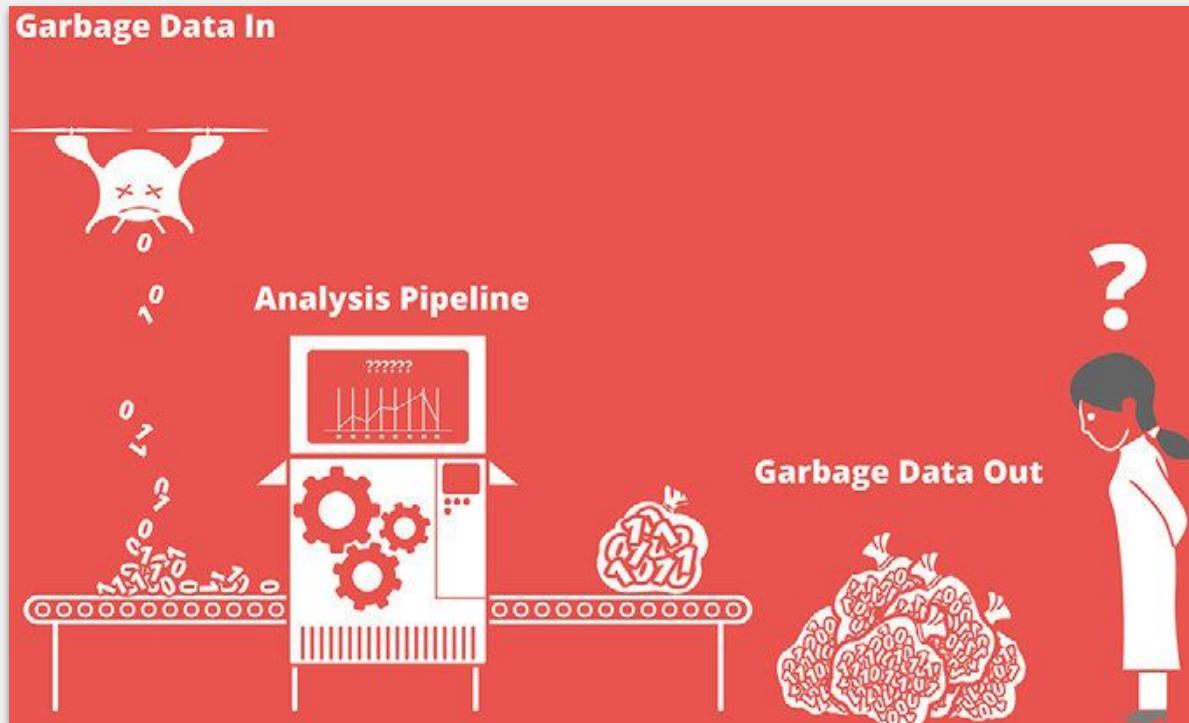
*Head motion*



*Noise*

*... and many others!*

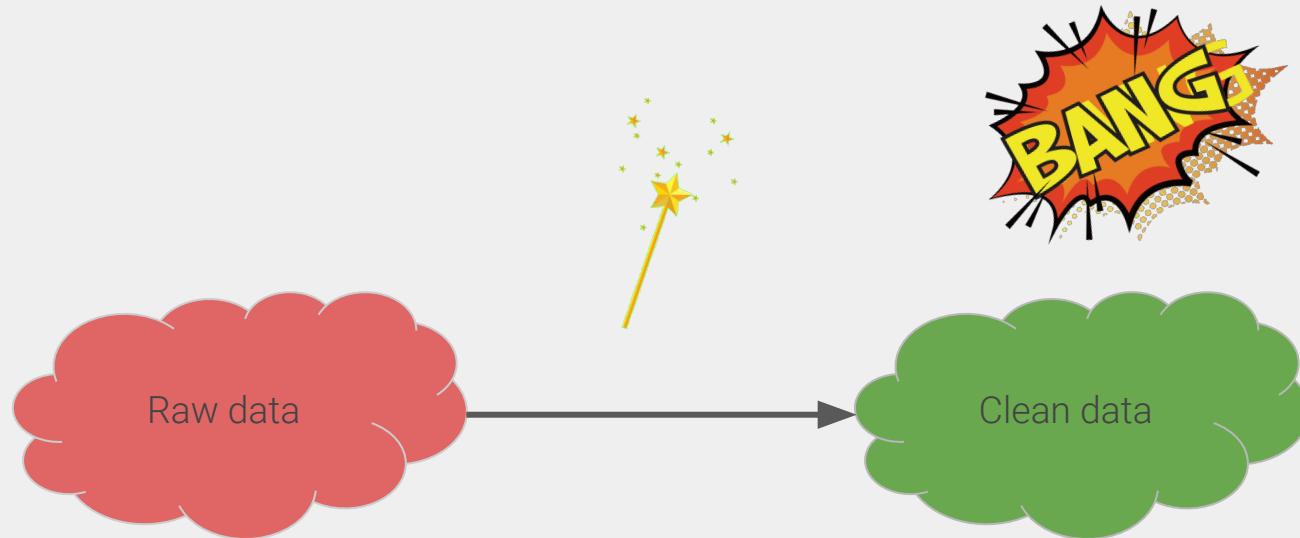
# Garbage in, garbage out



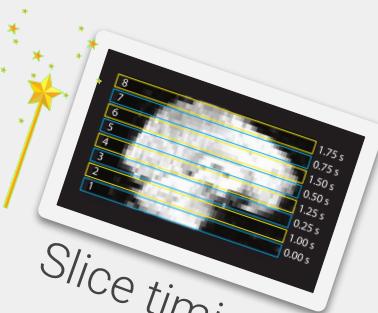
# How to fix this?



# How to fix this?



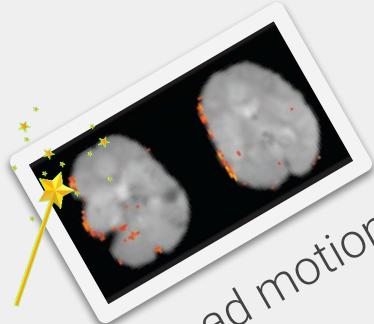
# Preprocessing



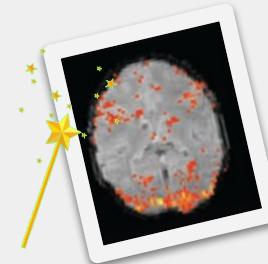
Slice timing



Brain differences



Head motion

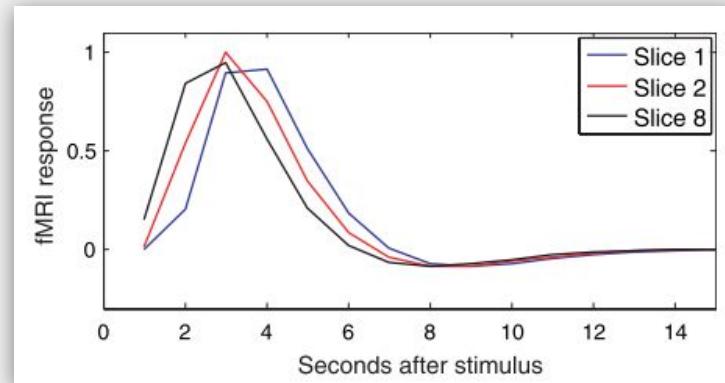


Noise

# Slice timing correction



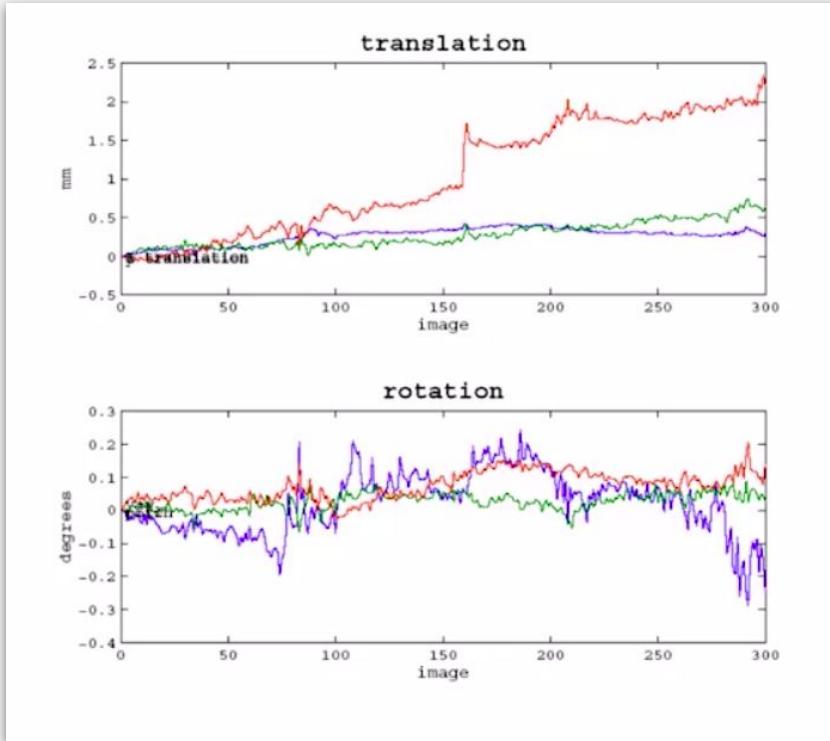
Interleaved acquisition



**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.

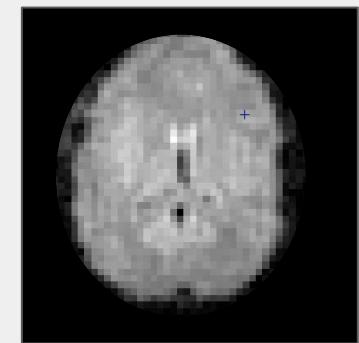
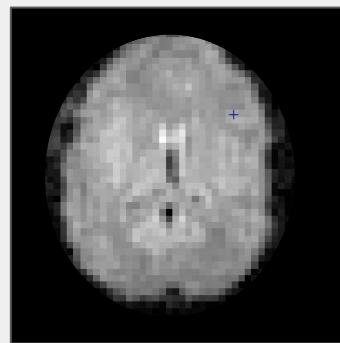
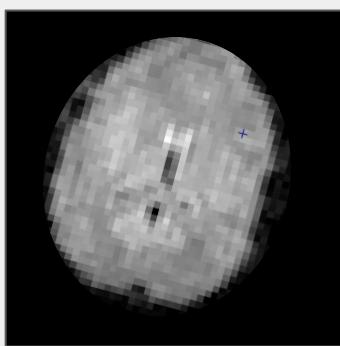
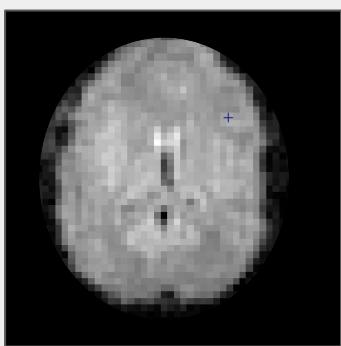
Typically each slice is interpolated to either the first time-point or the middle MR image.

# Motion correction



- 3 rotations
- 3 translations

# Motion correction

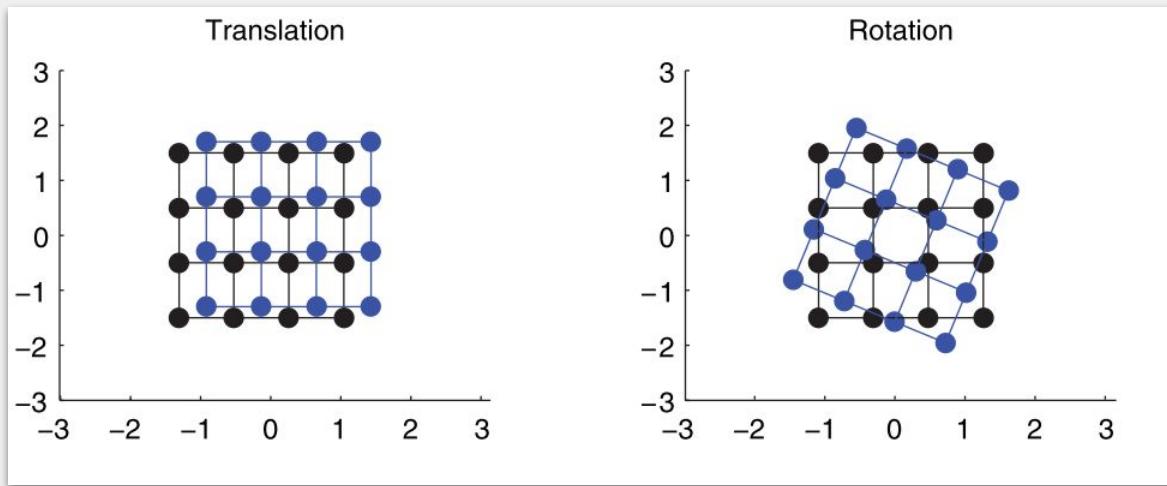


*"I'm particularly interested in Transfiguration, you know, turning something into something else, of course, it's supposed to be very difficult"*

—Hermione Granger regarding transformation



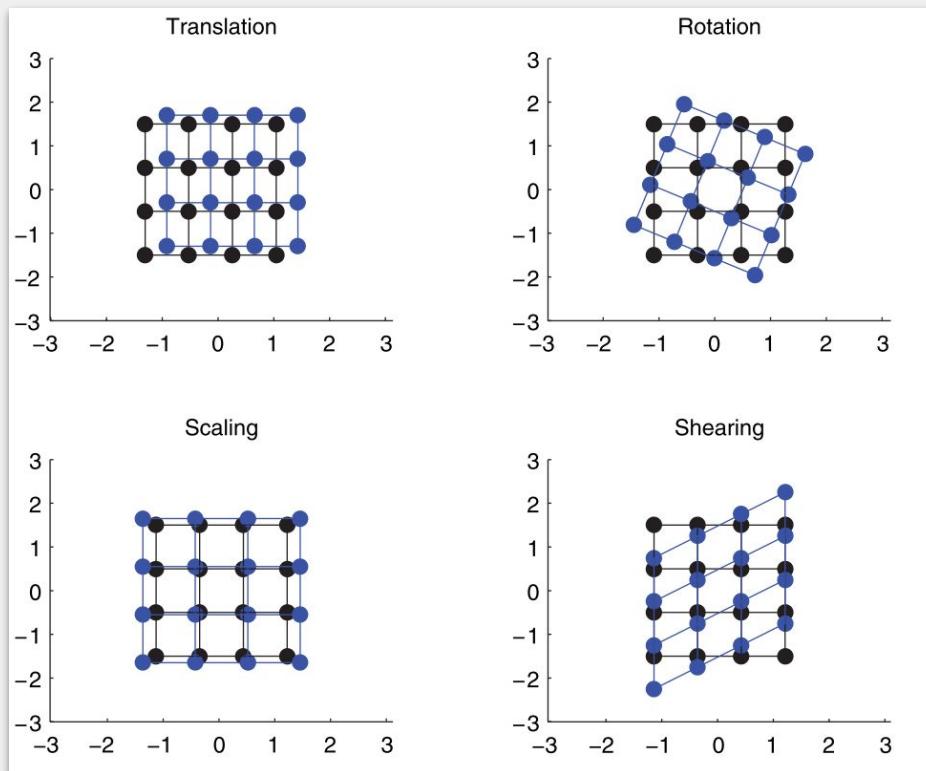
# Rigid body transformation



Does not change the shape and size of image.

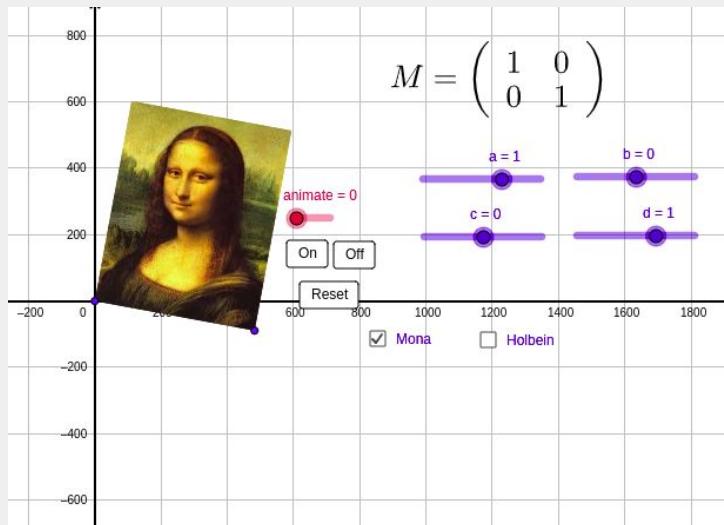
6 parameters: 3 translations and 3 rotations.

# Affine transformations



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

# Linear transformations magic!

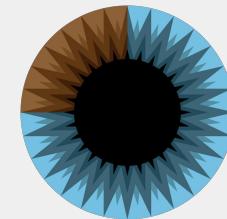


# GeoGebra

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

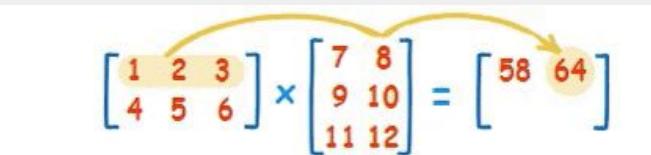


<https://www.khanacademy.org/math/linear-algebra/matrix-transformation/s/linear-transformations/a/visualizing-linear-transformations>



[https://www.youtube.com/channel/UCYO\\_jabesuFRV4b17AJtAw](https://www.youtube.com/channel/UCYO_jabesuFRV4b17AJtAw)

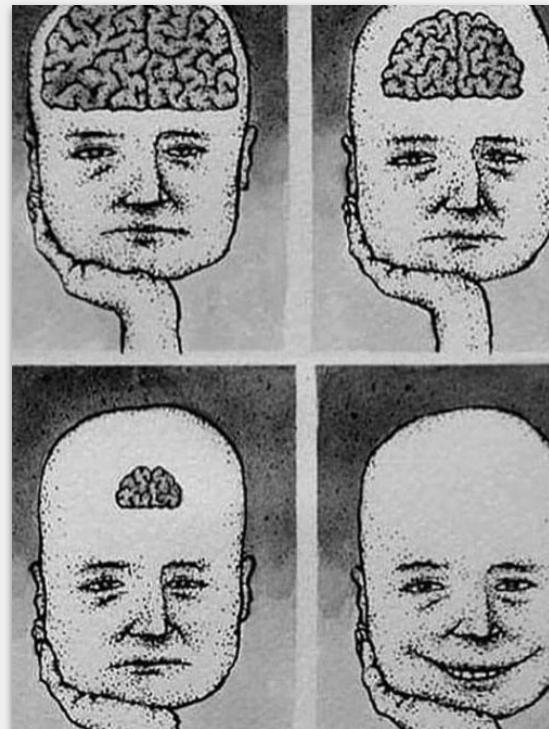
# Matrix multiplication

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


# Normalization

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

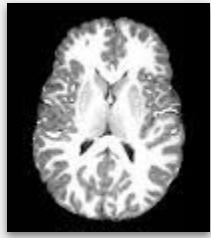
**Normalization** - stretching, squeezing and warping each brain to the “standard brain”.



# What's a “standard brain”?

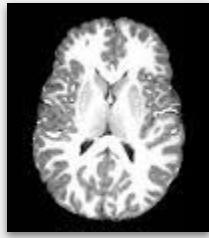


# Standard brain: template



Original image  
Native space

# Standard brain: template



Original image  
Native space

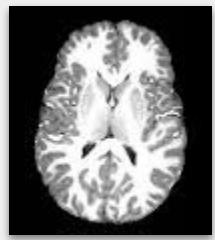


Template image  
Standard space

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.

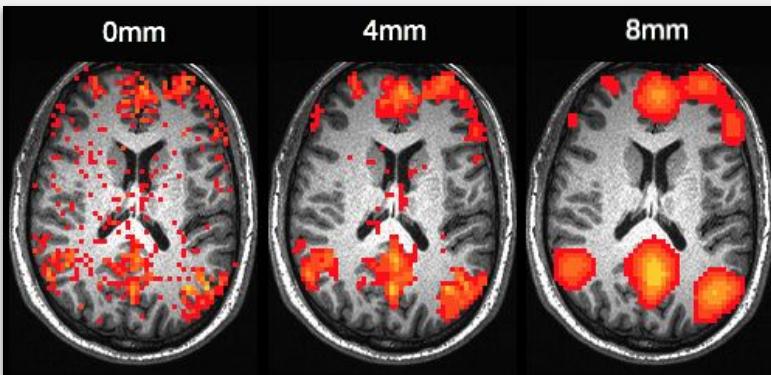
<https://www.lead-dbs.org/about-the-mni-spaces/>

# Smoothing

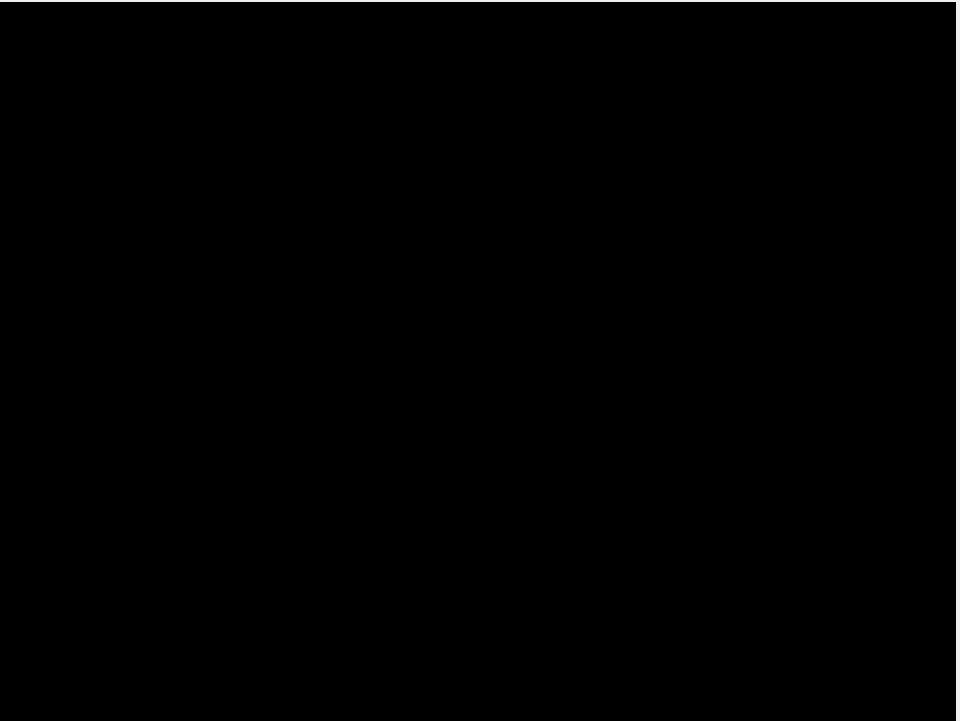


- Can increase signal-to-noise ratio and remove artifacts.
- Can blur anatomical brain differences.
- May increase validity of the statistical analysis.

**But!** It reduces the image resolution.



# Gaussian kernel

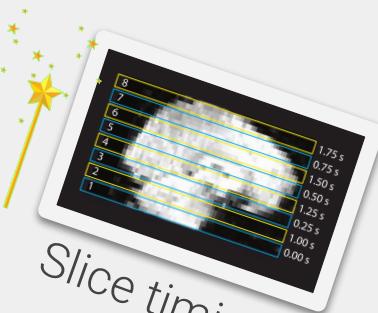


For each data point we generate a new value that is some function of the original value at that point and the surrounding data points (for Gaussian smoothing, the function that is used is our Gaussian curve).

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.

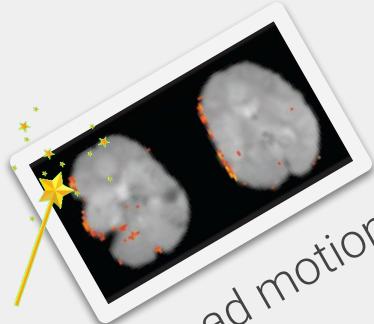
# Preprocessing



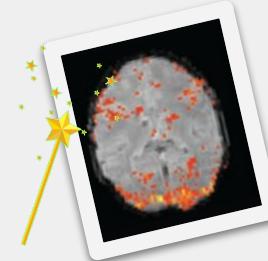
Slice timing



Brain differences

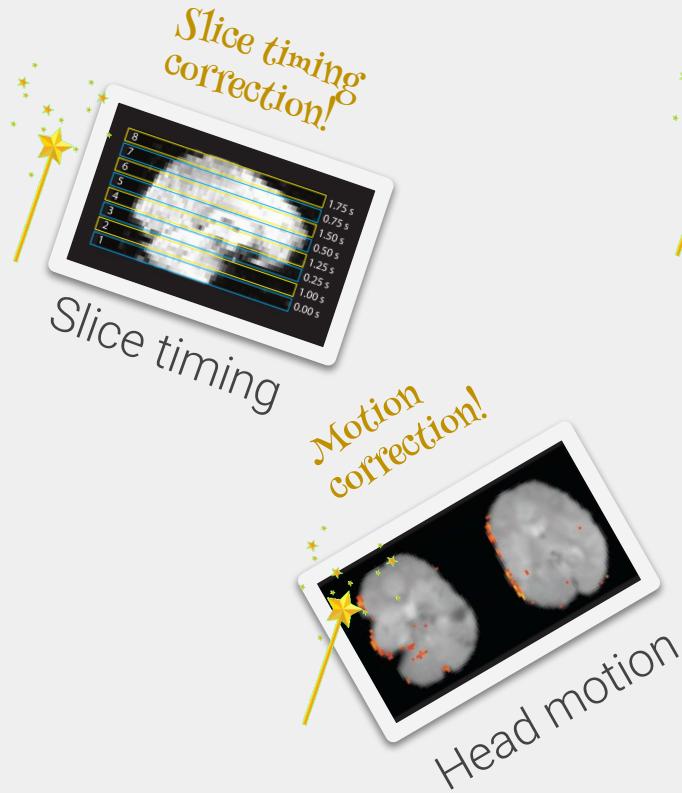


Head motion

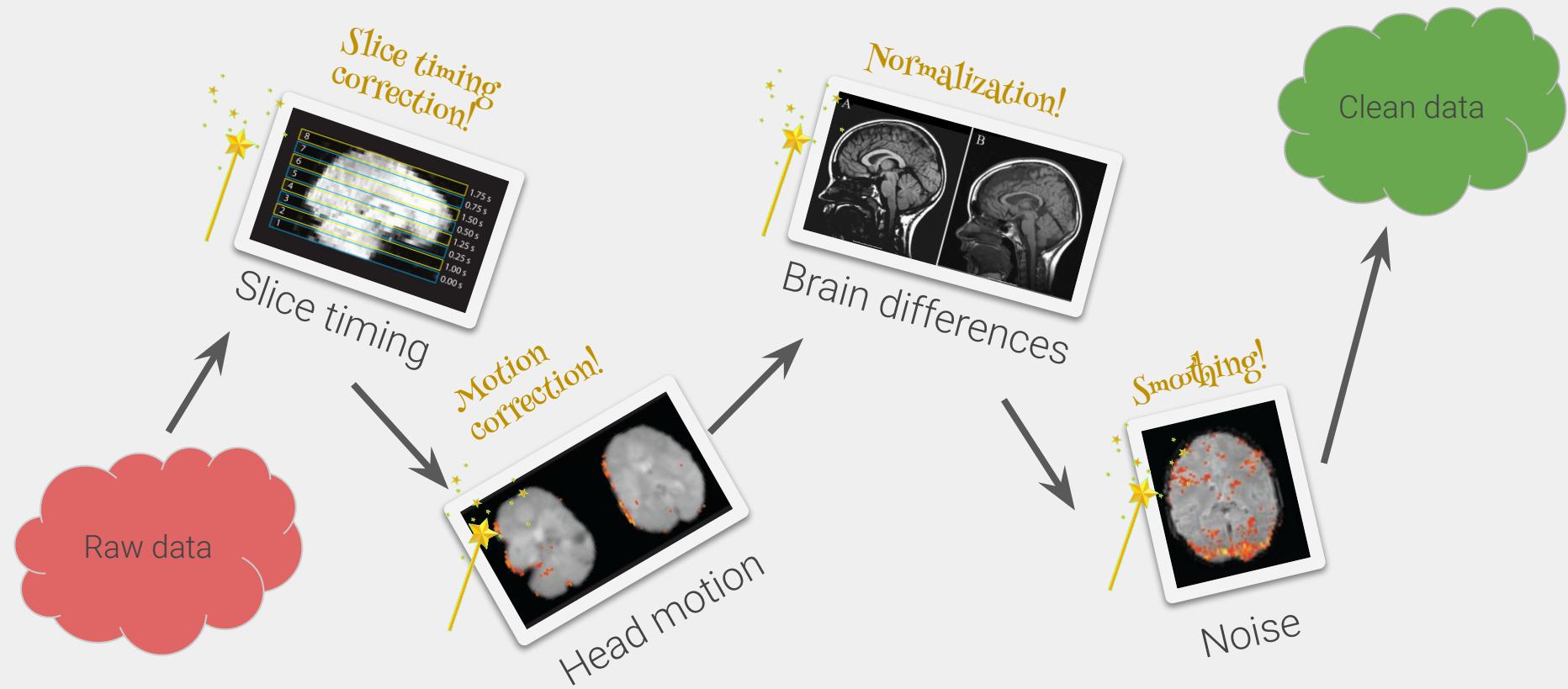


Noise

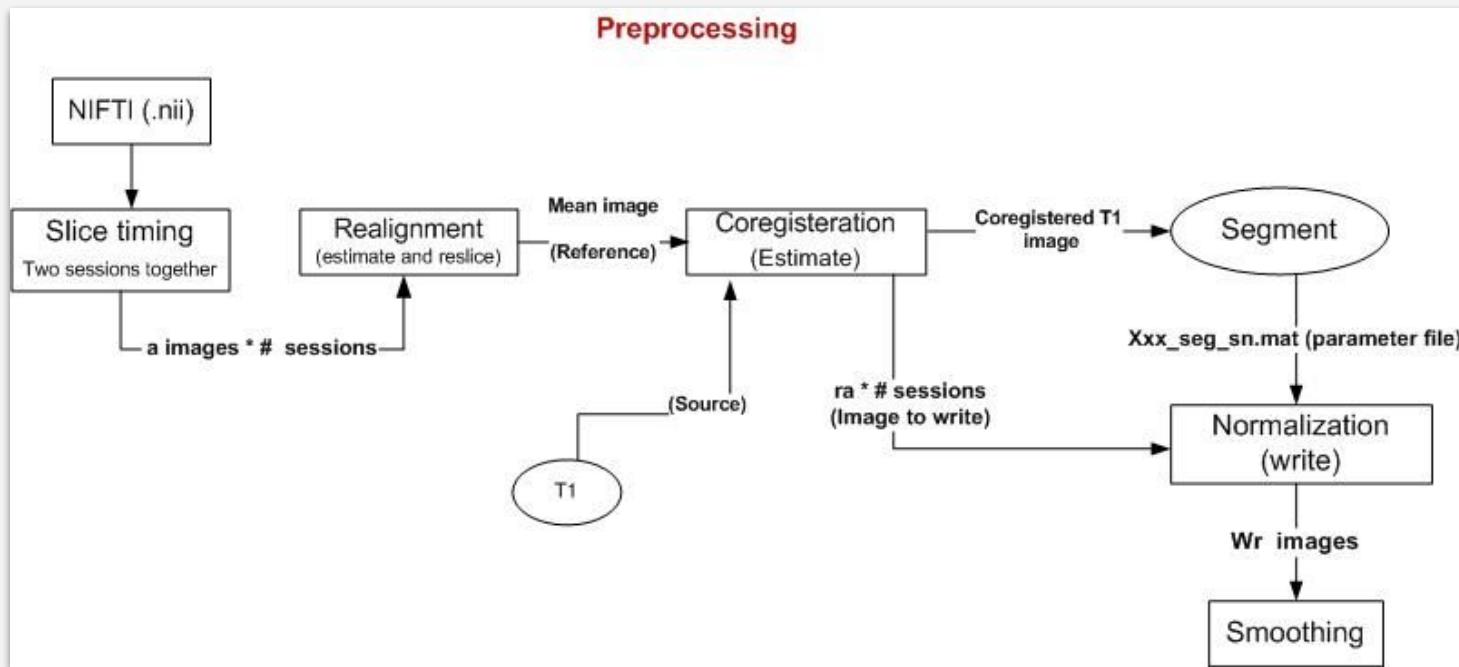
# Preprocessing



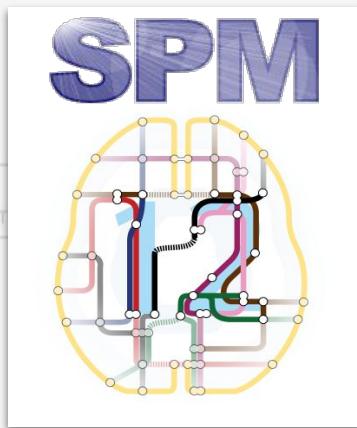
# Preprocessing workflow / pipeline



# Preprocessing workflow / pipeline



# Software



Segment  
(Reslice)

(Source)

ra \* # sessions  
(Image to write)

Segment

Xxx\_seg\_sn.mat (parameter file)

Normalise  
(write)

Wr im

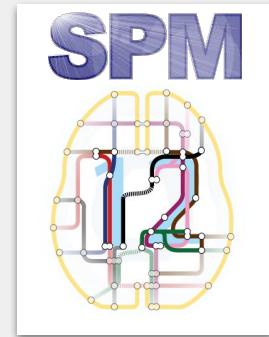
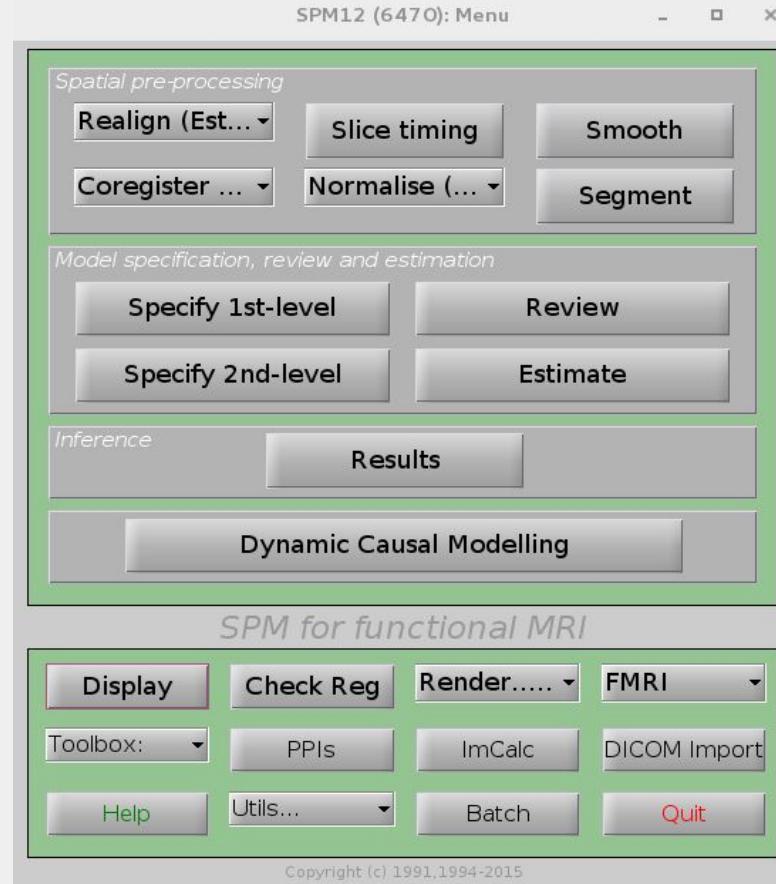


Smooth

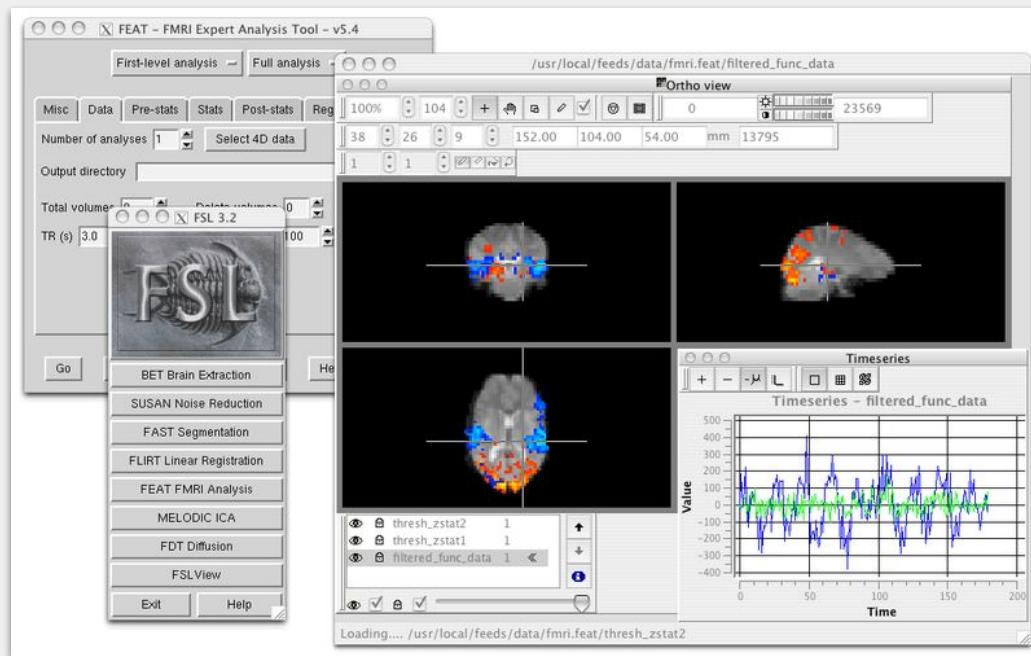


FreeSurfer

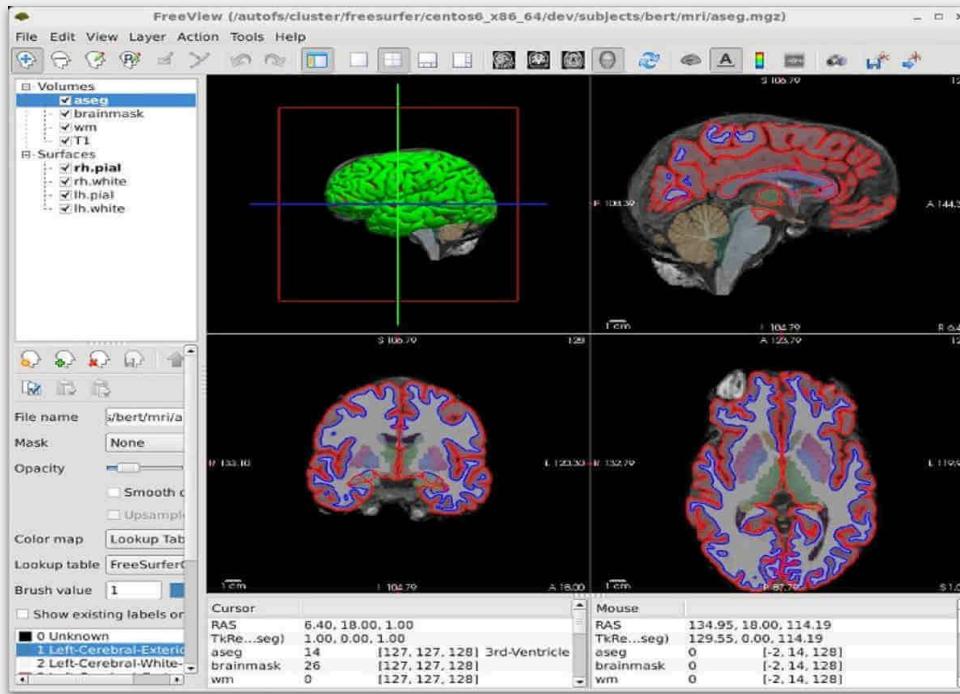
# SPM way



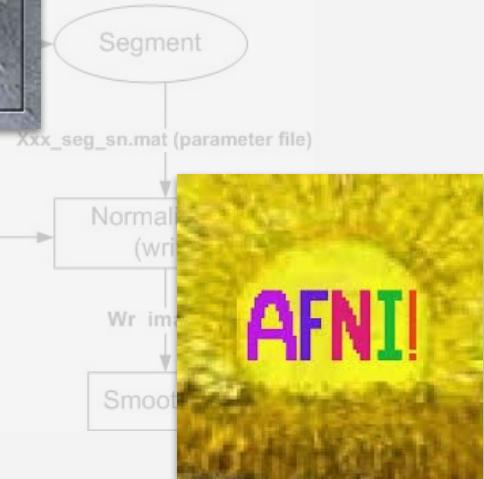
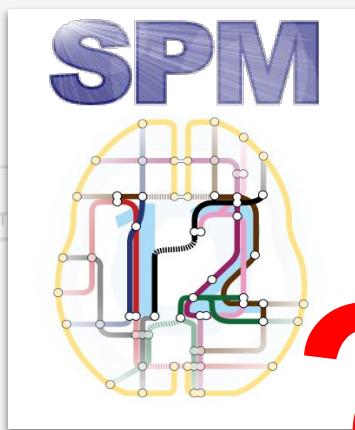
# FSL way



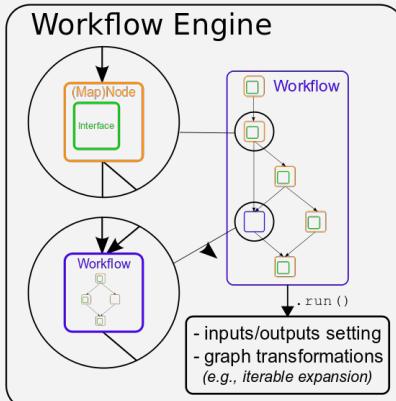
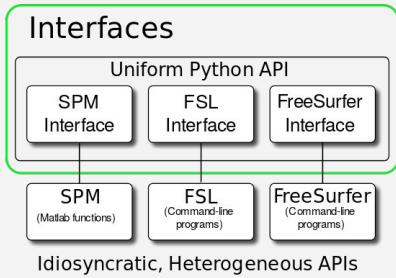
# FreeSurfer way



# Software



# Nipype



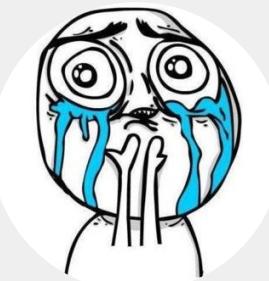
<https://giraffe.tools/pource/TimVanMourik/SomeGiraffeExample>



# 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 collection, instructions for execution and BIDS format, and a command-line example.

**Usage**

**Warning**

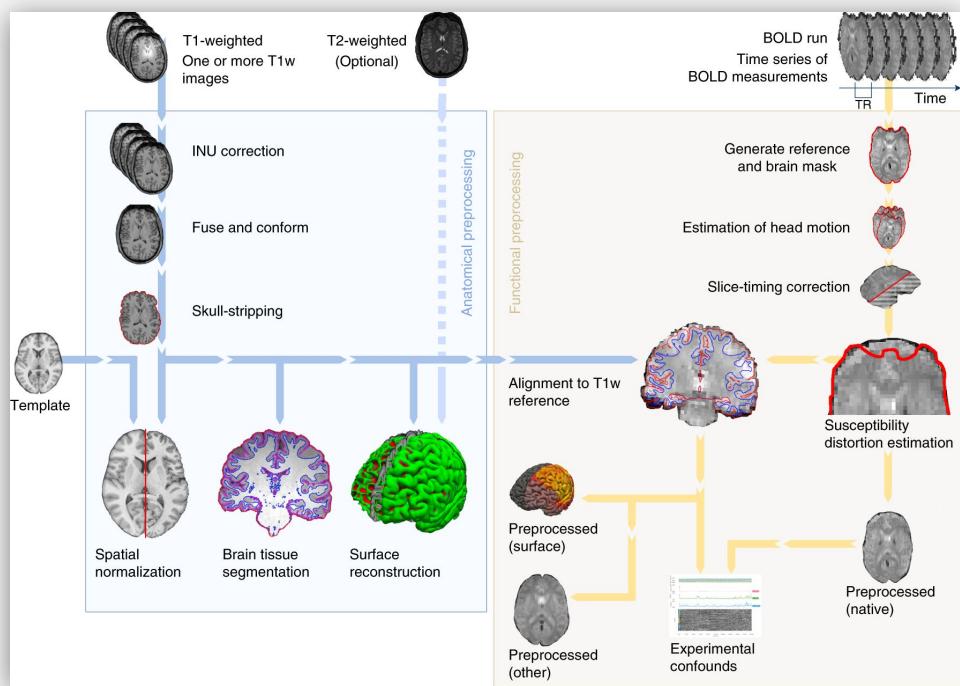
As of FMRIPREP 1.0.12, the software includes a tracking system to report usage statistics and errors. Users can opt-out using the `--notrack` command line argument.

**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/
```

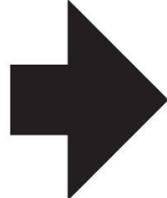


<https://fmriprep.readthedocs.io/en/stable/>

# 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
```

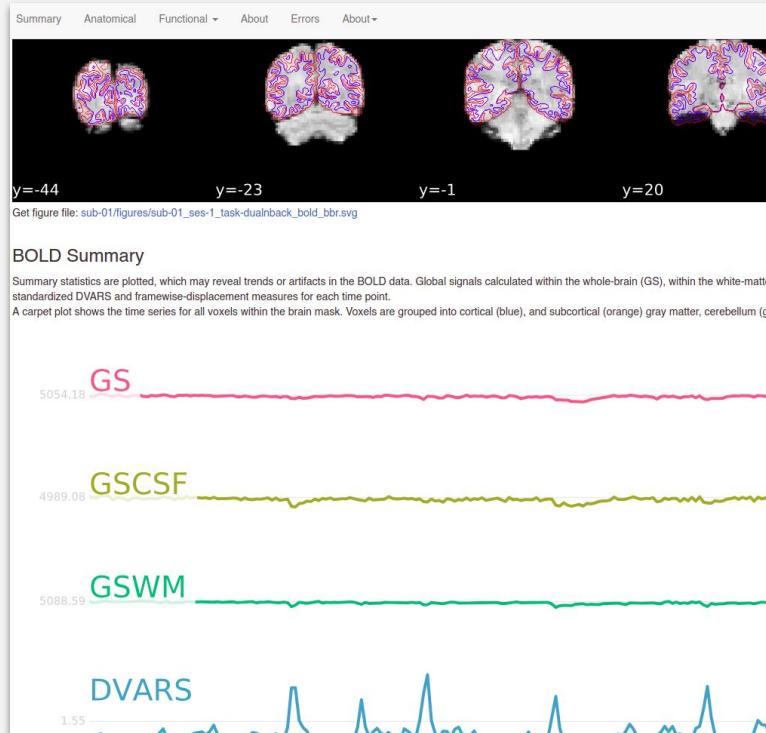
1. Convert DICOM to Nifti

<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](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



Next



## General Linear Model