



MRC Cognition  
and Brain  
Sciences Unit



UNIVERSITY OF  
CAMBRIDGE

# fMRI analysis

Dace Apšvalka  
[Datza]



@dcdace



dcdace.net

• Sep, 2022

# Materials

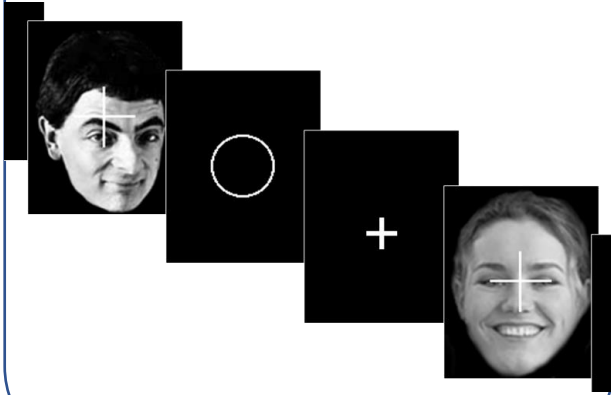
---



<https://github.com/dcdace/COGNESTIC-fMRI>

**Famous vs Unfamiliar**  
faces are processed  
differently in the brain

Design an experiment



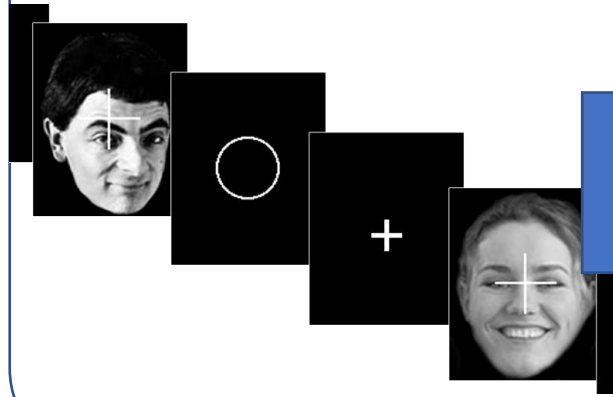
Collect the MRI data



What do we  
do now?

**Famous vs Unfamiliar**  
faces are processed  
differently in the brain

Design an experiment



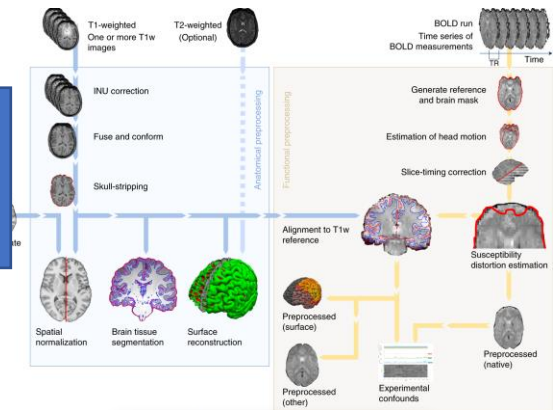
Stimuli  
Timing

Collect the MRI data

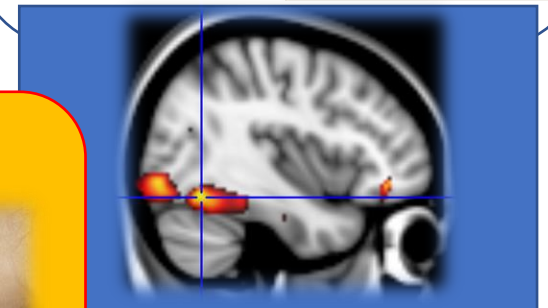


Anatomical image  
Functional images  
Event details

Pre-process & Analyse



The final push



# Environment



```
graph TD; subgraph Environment; subgraph Data_Organise_Manage [Data Organise & Manage]; PreProcess[Pre-process]; Analyse[Analyse]; Report[Report]; end; end;
```

## **Data**

Organise & Manage

Pre-process

Analyse

Report

# SCIENTIFIC DATA

OPEN

## SUBJECT CATEGORIES

- » Electroencephalography  
-EEG
- » Brain imaging
- » Functional magnetic  
resonance imaging
- » Cognitive neuroscience

Received: 07 April 2014

Accepted: 05 January 2015

Published: 20 January 2015

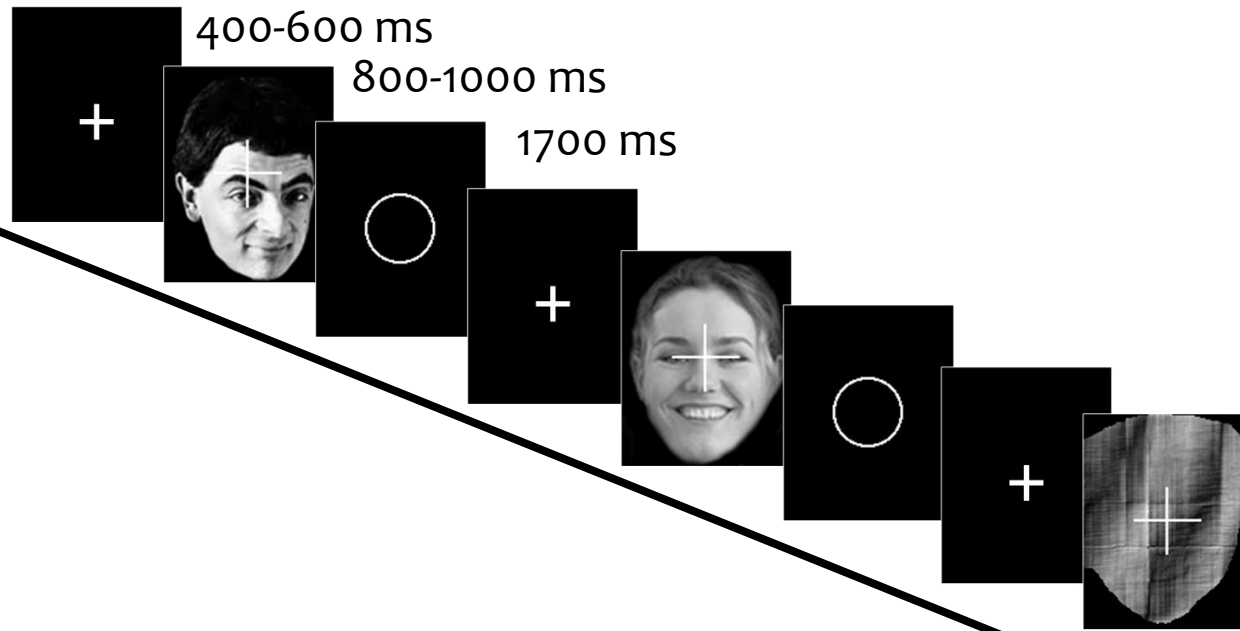
## A multi-subject, multi-modal human neuroimaging dataset

Daniel G. Wakeman<sup>1,2</sup> & Richard N. Henson<sup>2</sup>

We describe data acquired with multiple functional and structural neuroimaging modalities on the same nineteen healthy volunteers. The functional data include Electroencephalography (EEG), Magnetoencephalography (MEG) and functional Magnetic Resonance Imaging (fMRI) data, recorded while the volunteers performed multiple runs of hundreds of trials of a simple perceptual task on pictures of familiar, unfamiliar and scrambled faces during two visits to the laboratory. The structural data include T1-weighted MPRAGE, Multi-Echo FLASH and Diffusion-weighted MR sequences. Though only from a small sample of volunteers, these data can be used to develop methods for integrating multiple modalities from multiple runs on multiple participants, with the aim of increasing the spatial and temporal resolution above that of any one modality alone. They can also be used to integrate measures of functional and structural connectivity, and as a benchmark dataset to compare results across the many neuroimaging analysis packages. The data are freely available from <https://openfmri.org/>.

- Been used in many methods projects and publications, as well as tutorials (e.g. “multimodal” dataset in SPM12 manual)
- Here we will analyse it from the very root – the raw DICOM images

# Experiment: Face Recognition



N = 16 subjects

Stimuli: 3 types of greyscale face images:

~150 x Famous

~155 x Unfamiliar

~150 x Scrambled

Task: Judge face symmetry

7 min long runs  
9 runs  
20s Rest after ever 50s



# Environment

Let's see the [01\\_Analysis\\_Environment.ipynb](#) notebook

# Environment

**Data**

Organise & Manage

fMRI file formats

# Anatomical (T1w) image & Functional (T2\*/BOLD) image

Collect the data

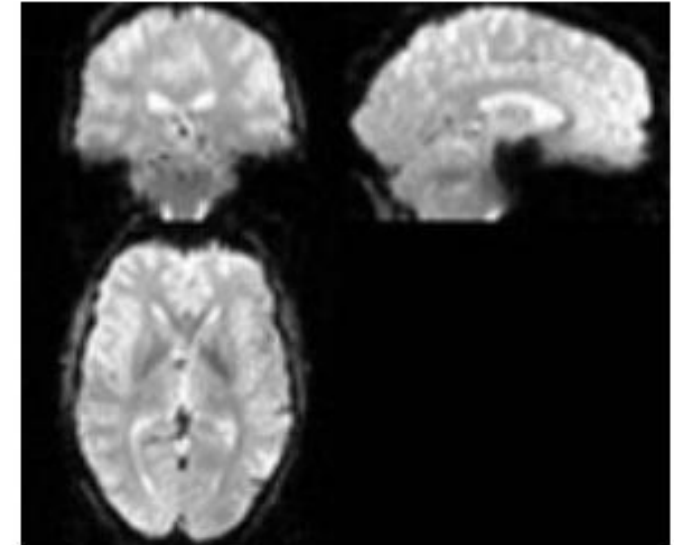


- **DICOM** - Digital Imaging and Communications in Medicine (.dcm)
  - Raw data standard for storing and communicating medical images
  - Contains a **header** (meta data) and the actual **image** itself
  - A separate file for each **slice** (2D format)

Why is  
anatomical scan  
collected only  
once?

Need to convert to NifTI

**functional scan**  
A brain image  
(slice-by-slice)  
selected every  
2s > 100 times



- **NifTI** – Neuroimaging Informatics Technology Initiative (.nii, .nii.gz)
  - Standardised representation of brain images, cross-platform, cross-software
  - Contains **header** and **image**
  - 3D or 4D files (all slices/volumes in a single file)

Collect the data



## Anatomical (T1w) image & Functional (T2\*/BOLD) image

- sub-01\_T1w.nii
- sub-01\_run-01\_bold.nii
- sub-01\_run-02\_bold.nii
- sub-02\_T1w.nii
- sub-02\_run-01\_bold.nii
- sub-02\_run-02\_bold.nii
- ...
- sub-100\_T1w.nii
- sub-100\_run-01\_bold.nii
- sub-100\_run-02\_bold.nii
- and even more files

How should we  
organise our files?

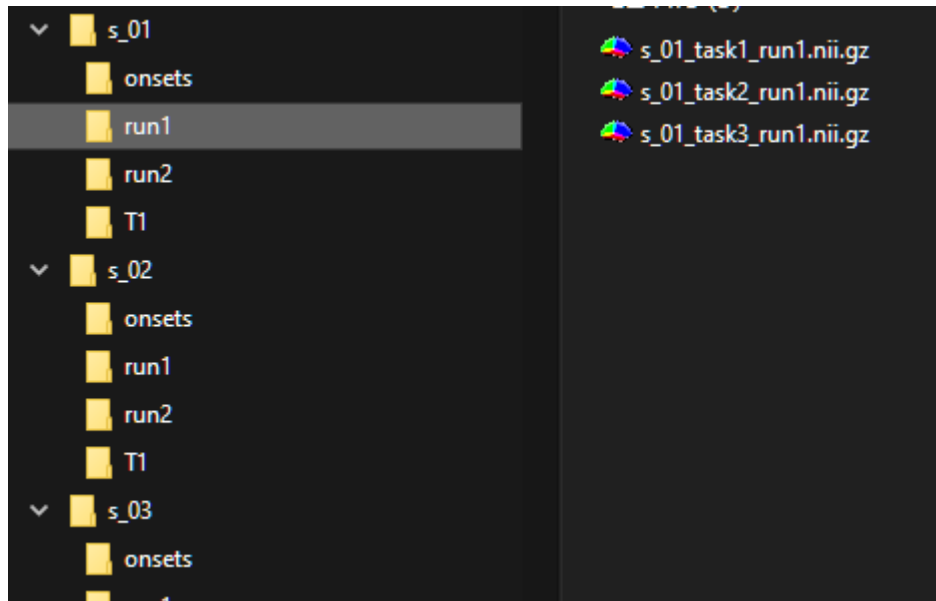
# File organisation

# fMRI terminology

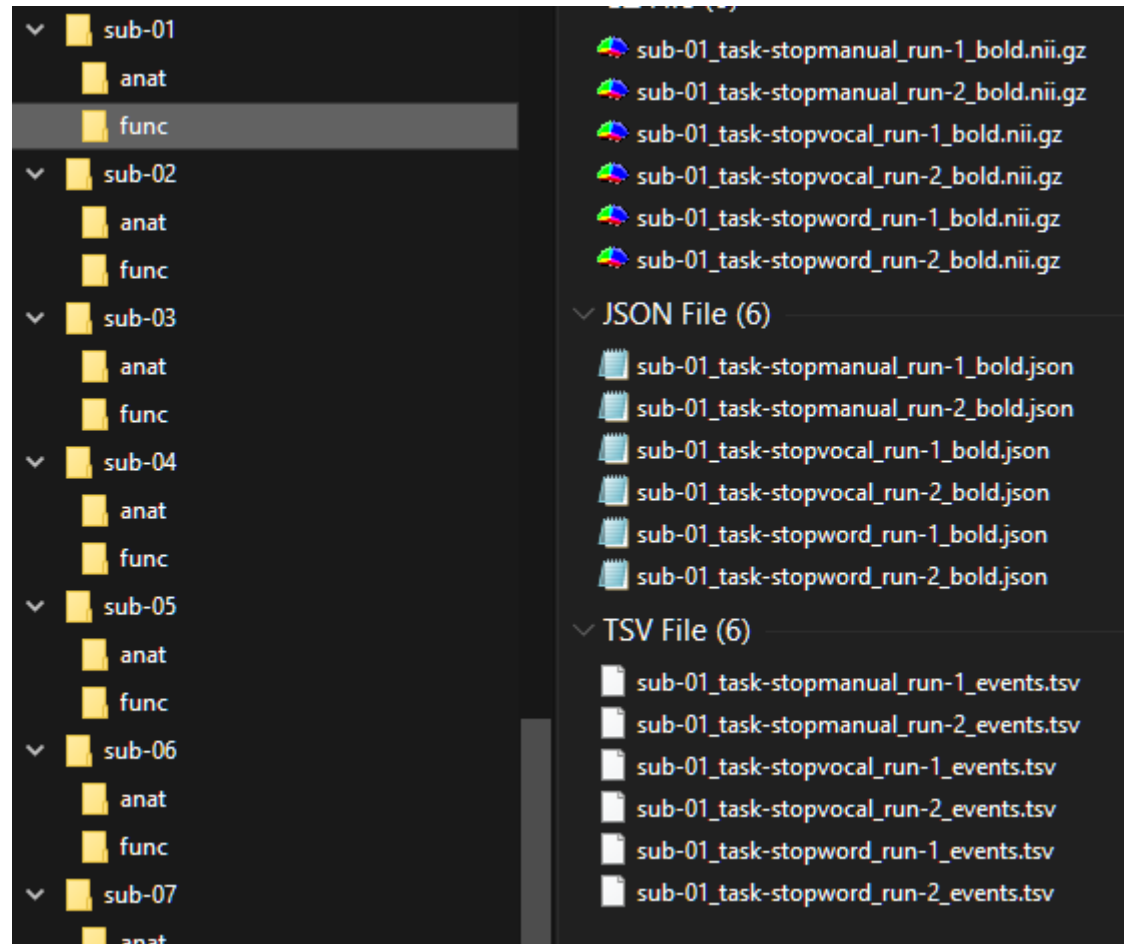
---

- **Session**
  - The time that the subject enters the scanner until they leave the scanner. This will usually include multiple scanning runs with different pulse sequences, including anatomical, functional, etc. Participant can be invited for a follow up session, next day or even later. That will then be Session 2.
- **Run**
  - A period of temporally continuous data acquisition using a single pulse sequence. Functional acquisitions are often split into multiple runs (5-10min) with brief breaks in between.
- **Volume**
  - A single 3D image acquired as part of a run. There is 1 anatomical volume and > 100 functional volumes.
- **Condition**
  - A set of task features that are created to engage a particular mental state. E.g., look at faces (condition 1), or look at houses (condition 2).
- **Trial**
  - A temporally isolated period during which a particular condition is presented, or a specific behaviour is observed. E.g., the first occurrence of the 'faces' condition is trial\_1, the second occurrence is trial\_2.
- **Event**
  - A trial can consist of multiple subunits. E.g., viewing faces trial may include pressing a button if you saw this face in the previous trials. Or working memory task may contain encoding, delay, retrieval. These subunits are labelled as 'events' and the 'trial' is defined as an overarching task.
- **Block (or an 'epoch')**
  - A temporarily contiguous period when a subject is presented with a particular condition.

## Example 1



## Example 2





# fMRI data management

---

- **Problems with heterogeneity in data management**
  - Difficult for others (and you!) to understand your data and keep track of changes
  - Scripts have to be adapted (can't be easily reused)
  - Huge effort to automate workflows and no way to automatically validate data sets
  - Sharing data becomes a hustle

Wouldn't it be much easier if everybody organised the files in the same way?

# fMRI data management

- A standardised way for organising & describing neuroimaging data

## Brain Imaging Data Structure - **BIDS**



Stanford | Center for Reproducible Neuroscience

- Documentation: <https://bids-specification.readthedocs.io/en/latest/>



## SCIENTIFIC DATA

OPEN

SUBJECT CATEGORIES

» Data publication and  
archiving  
» Research data

### The brain imaging data structure, a format for organizing and describing outputs of neuroimaging experiments

Krzysztof J. Gorgolewski<sup>1</sup>, Tibor Auer<sup>2</sup>, Vince D. Calhoun<sup>3,4</sup>, R. Cameron Craddock<sup>5,6</sup>, Samir Das<sup>7</sup>, Eugene P. Duff<sup>8</sup>, Guillaume Flandin<sup>9</sup>, Satrajit S. Ghosh<sup>10,11</sup>, Tristan Glatard<sup>7,12</sup>, Yaroslav O. Halchenko<sup>13</sup>, Daniel A. Handwerker<sup>14</sup>, Michael Hanke<sup>15,16</sup>, David Keator<sup>17</sup>, Xiangrui Li<sup>18</sup>, Zachary Michael<sup>19</sup>, Camille Maumet<sup>20</sup>, B. Nolan Nichols<sup>21,22</sup>, Thomas E. Nichols<sup>23,24</sup>, John Pellmar<sup>5</sup>, Jean-Baptiste Poline<sup>24</sup>, Ariel Rokem<sup>25</sup>, Gunnar Schaefer<sup>1,26</sup>, Vanessa Sochat<sup>27</sup>, William Triplett<sup>1</sup>, Jessica A. Turner<sup>3,28</sup>, Gaël Varoquaux<sup>29</sup> & Russell A. Poldrack<sup>1</sup>

Received: 18 December 2015

Accepted: 19 May 2016

Published: 21 June 2016

RESEARCH ARTICLE

### BIDS apps: Improving ease of use, accessibility, and reproducibility of neuroimaging data analysis methods

Krzysztof J. Gorgolewski<sup>1\*</sup>, Fidel Alfaro-Almagro<sup>2</sup>, Tibor Auer<sup>3</sup>, Pierre Bellec<sup>4,5</sup>, Mihai Capota<sup>6</sup>, M. Mallar Chakravarty<sup>7,8</sup>, Nathan W. Churchill<sup>9</sup>, Alexander Li Cohen<sup>10</sup>, R. Cameron Craddock<sup>11,12</sup>, Gabriel A. Devenyi<sup>7,8</sup>, Anders Eklund<sup>13,14,15</sup>, Oscar Esteban<sup>1</sup>, Guillaume Flandin<sup>16</sup>, Satrajit S. Ghosh<sup>17,18</sup>, J. Swaroop Guntupalli<sup>19</sup>, Mark Jenkinson<sup>2</sup>, Anisha Keshavan<sup>20</sup>, Gregory Kiar<sup>21,22</sup>, Franziskus Liem<sup>23</sup>, Pradeep Reddy Raamana<sup>24,25</sup>, David Raffelt<sup>26</sup>, Christopher J. Steele<sup>7,8</sup>, Pierre-Olivier Quirion<sup>15</sup>, Robert E. Smith<sup>26</sup>, Stephen C. Strother<sup>24,25</sup>, Gaël Varoquaux<sup>27</sup>, Yida Wang<sup>6</sup>, Tal Yarkoni<sup>28</sup>, Russell A. Poldrack<sup>1</sup>



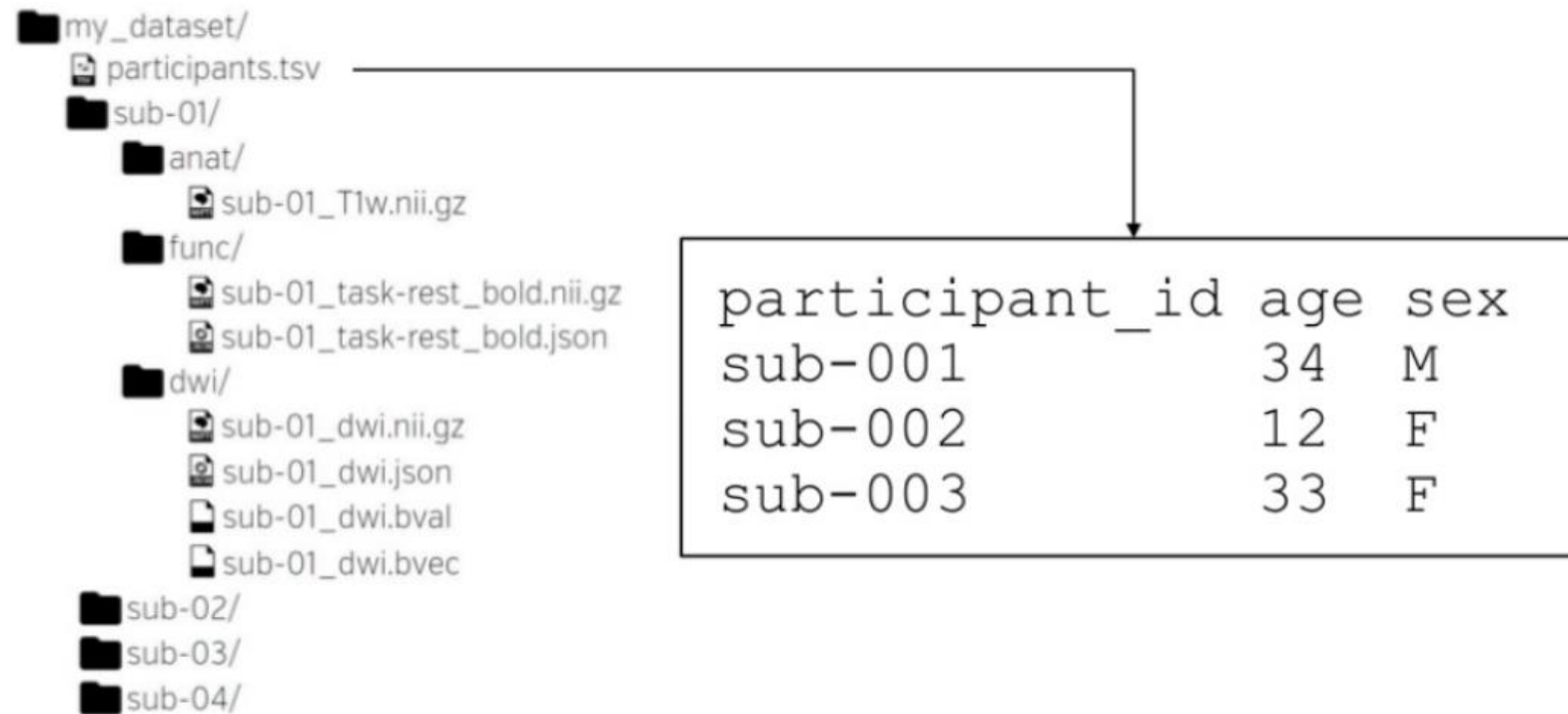
- **Benefits of BIDS**

- Easy for other people to work on your data (for collaborations or contract changes)
- Growing number of data analysis software packages that understand BIDS
- Databases, such as OpenNeuro and LORIS etc., accept and export datasets organised according to BIDS
- Validation tools that can check your dataset integrity and let you easily spot missing values



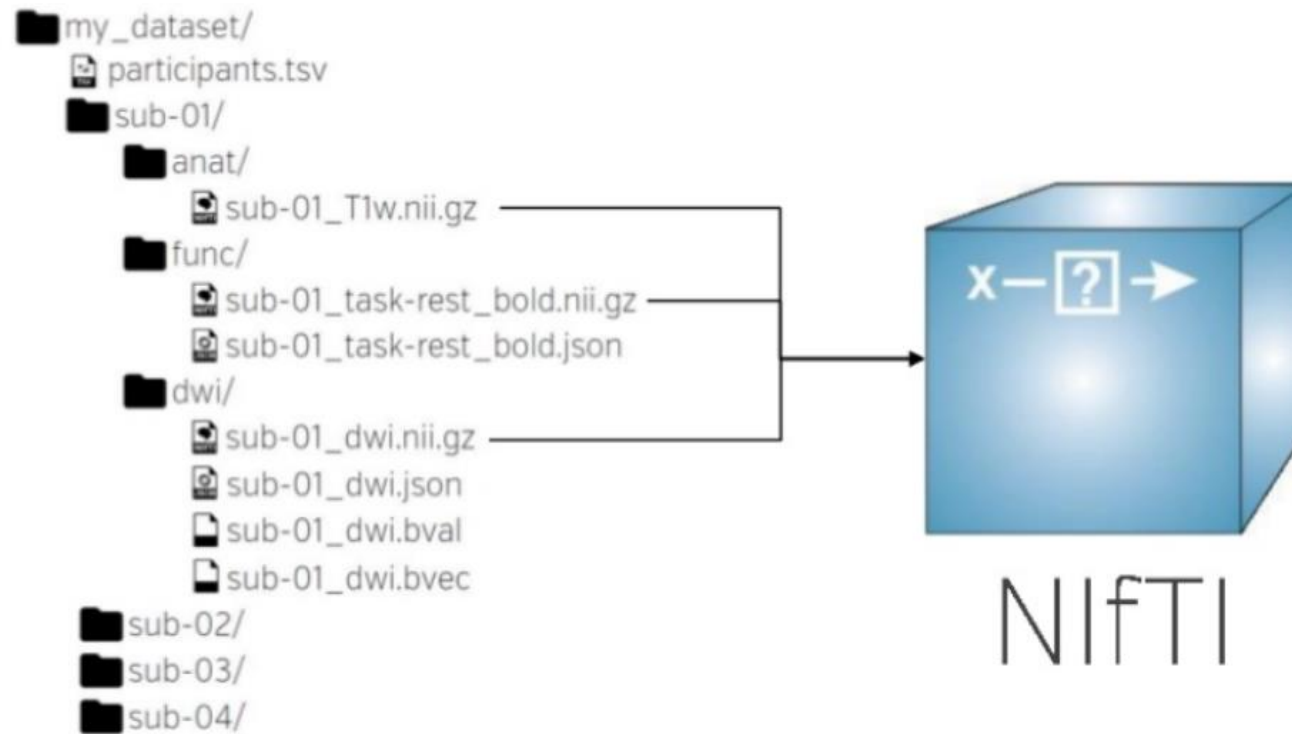
# BIDS

- Contains participant information



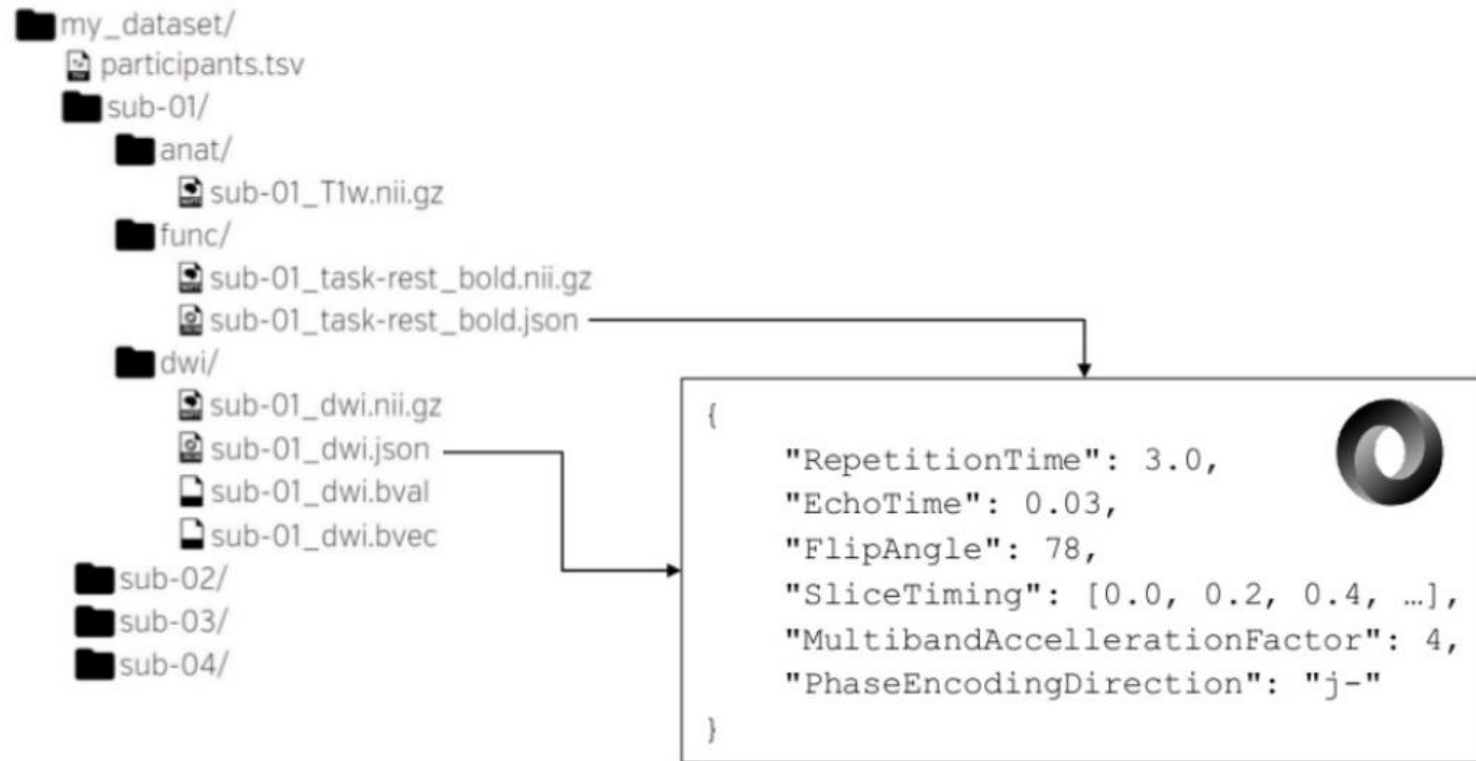
# BIDS

- Contains data files: neuroimaging/behaviour



# BIDS

- Contains study specific JSON files: sequences & paradigm



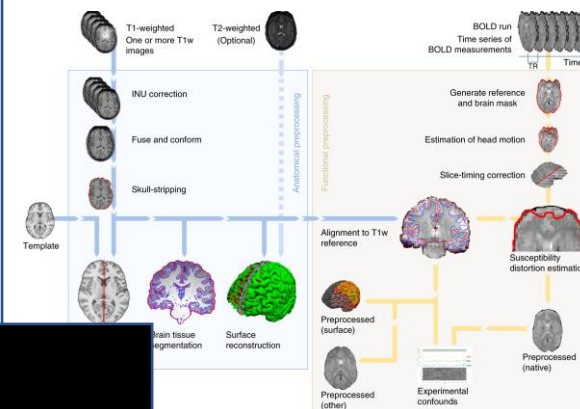
# BIDS

## Collect the data



Many BIDS converters available

## 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/
```



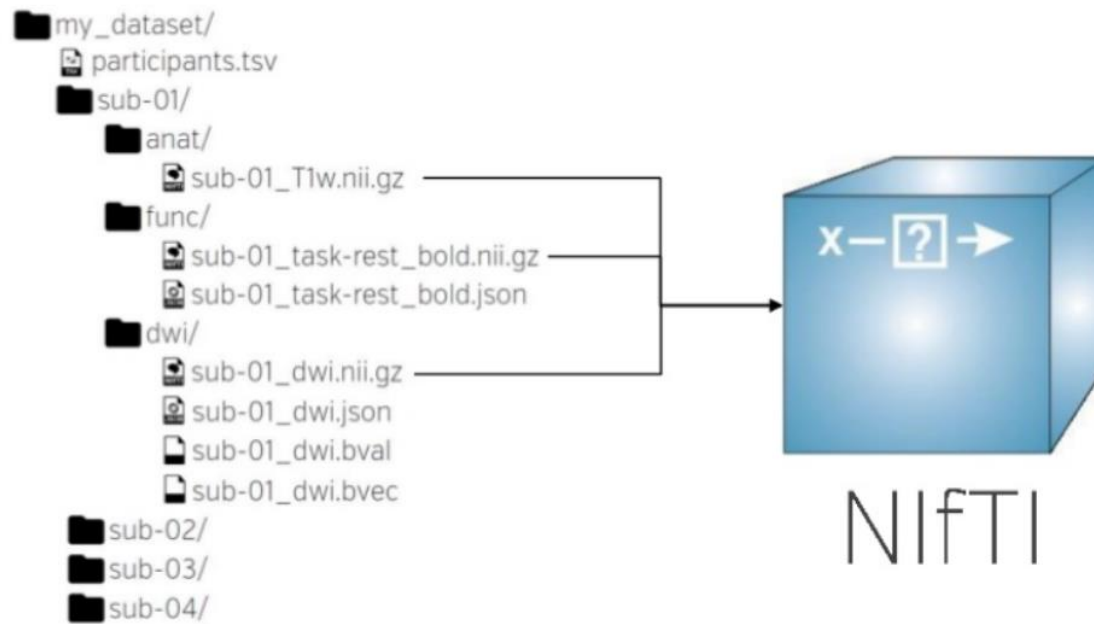
```
my_dataset/  
├── participants.tsv  
├── sub-01/  
│   ├── anat/  
│   │   └── sub-01_T1w.nii.gz  
│   ├── func/  
│   │   ├── sub-01_task-rest_bold.nii.gz  
│   │   └── sub-01_task-rest_bold.json  
│   └── dwi/  
│       ├── sub-01_dwi.nii.gz  
│       ├── sub-01_dwi.json  
│       ├── sub-01_dwi.bval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

# Environment

## **Data** Organise & Manage

Let's see the [02-fMRI\\_Data\\_Management.ipynb](#) notebook



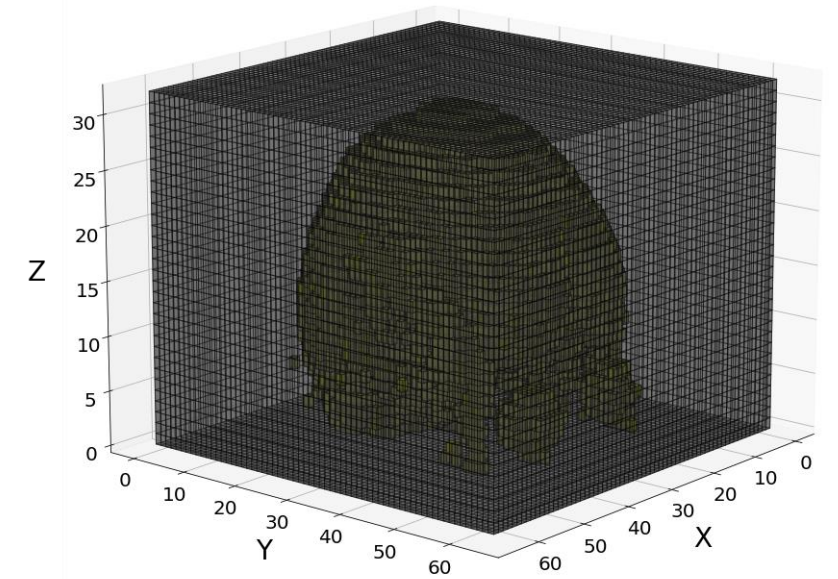
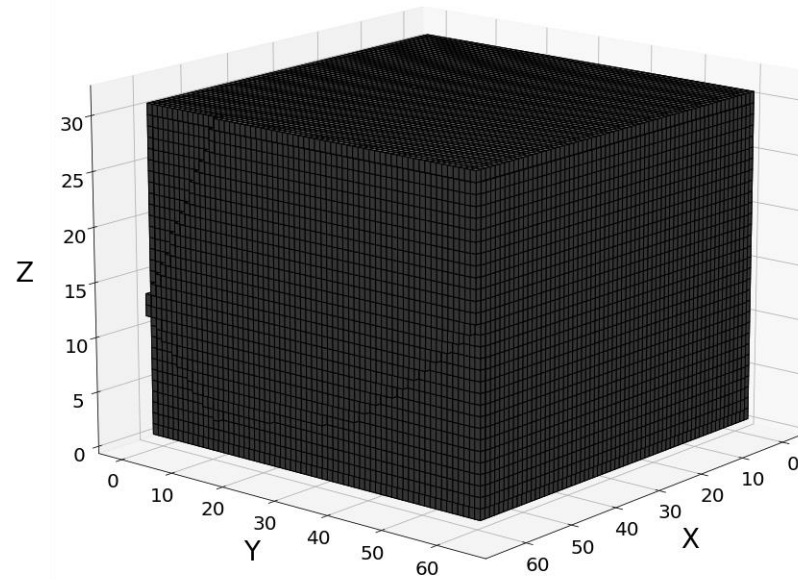


# Imaging data content

# MRI data structure

A 3D or 4D arrays of numbers

```
([[[ 0., 0., 0., ..., 0., 0., 0.],  
  [ 0., 0., 0., ..., 0., 0., 0.],  
  [ 0., 0., 0., ..., 0., 0., 0.],  
  ...,  
  [ 0., 0., 0., ..., 0., 0., 0.],  
  [ 0., 0., 0., ..., 0., 0., 0.],  
  [ 0., 0., 0., ..., 0., 0., 0.]],  
 [[ 0., 0., 0., ..., 0., 0., 0.],  
  [ 0., 25., 23., ..., 23., 32., 0.],  
  [ 0., 28., 21., ..., 25., 25., 0.],  
  ...,  
  [ 0., 26., 24., ..., 40., 20., 0.],  
  [ 0., 44., 28., ..., 30., 21., 0.],  
  [ 0., 0., 0., ..., 0., 0., 0.]],  
 [[ 0., 0., 0., ..., 0., 0., 0.],  
  [ 0., 28., 26., ..., 31., 29., 0.],  
  [ 0., 32., 30., ..., 22., 21., 0.],  
  ...,  
  [ 0., 27., 24., ..., 31., 30., 0.],  
  [ 0., 30., 23., ..., 37., 22., 0.],  
  [ 0., 0., 0., ..., 0., 0., 0.]],  
  ...],  
  ...]
```



# MRI data structure

A 3D or 4D arrays of numbers – intensity values

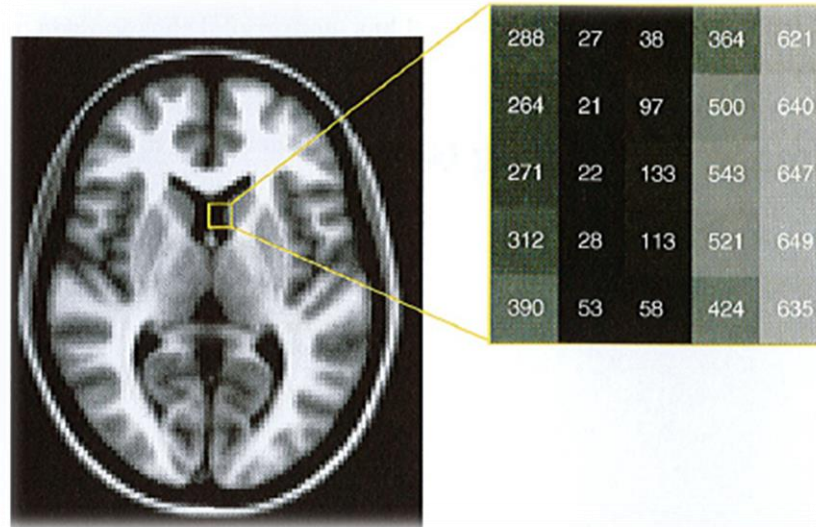
```
([[[ 0., 0., 0., ..., 0., 0., 0.],
 [ 0., 0., 0., ..., 0., 0., 0.],
 [ 0., 0., 0., ..., 0., 0., 0.],
 ...,
 [ 0., 0., 0., ..., 0., 0., 0.],
 [ 0., 0., 0., ..., 0., 0., 0.],
 [ 0., 0., 0., ..., 0., 0., 0.]],

 [[ 0., 0., 0., ..., 0., 0., 0.],
 [ 0., 25., 23., ..., 23., 32., 0.],
 [ 0., 28., 21., ..., 25., 25., 0.],
 ...,
 [ 0., 26., 24., ..., 40., 20., 0.],
 [ 0., 44., 28., ..., 30., 21., 0.],
 [ 0., 0., 0., ..., 0., 0., 0.]],

 [[ 0., 0., 0., ..., 0., 0., 0.],
 [ 0., 28., 26., ..., 31., 29., 0.],
 [ 0., 32., 30., ..., 22., 21., 0.],
 ...,
 [ 0., 27., 24., ..., 31., 30., 0.],
 [ 0., 30., 23., ..., 37., 22., 0.],
 [ 0., 0., 0., ..., 0., 0., 0.]],

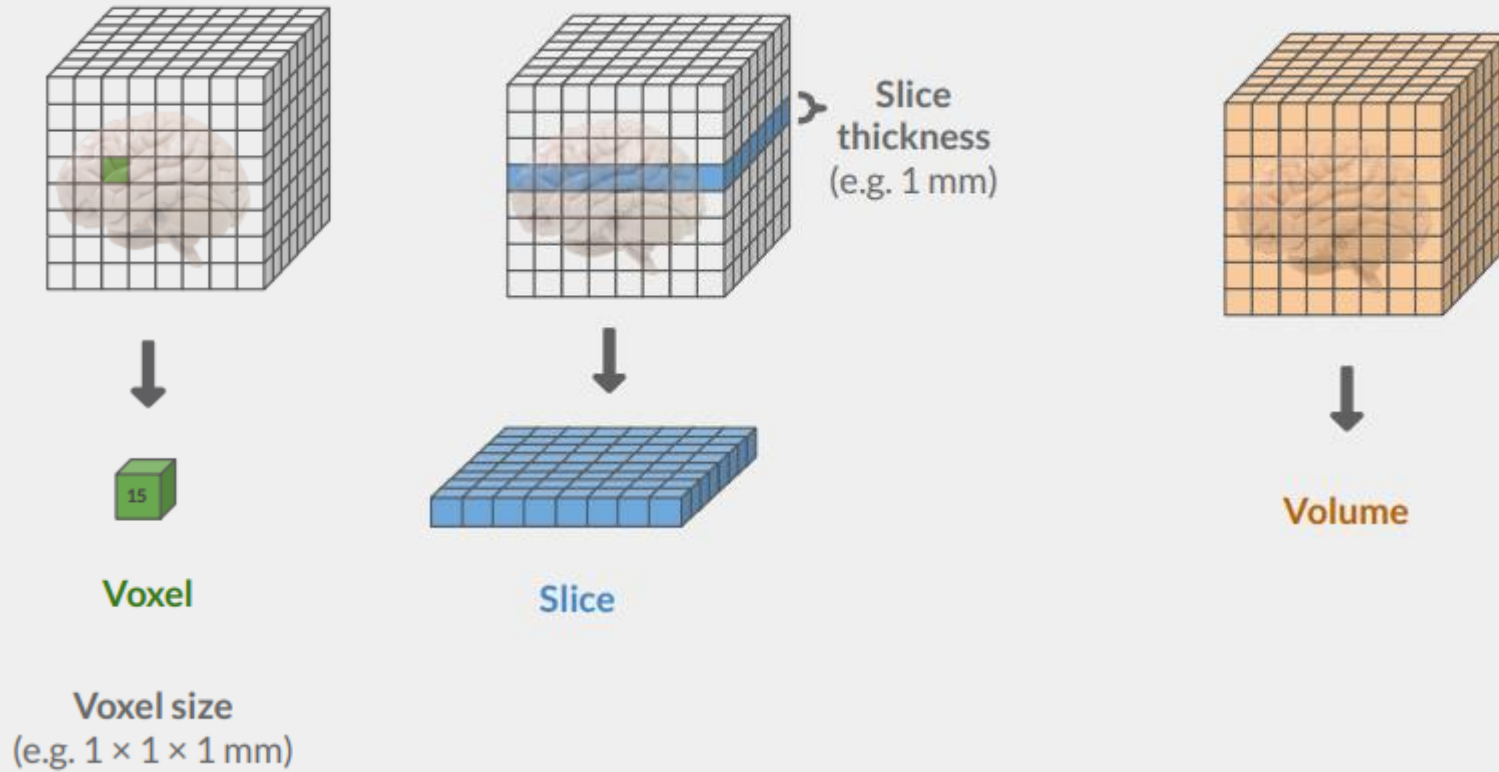
 ...,

```



*Image from Poldrack et al., 2011*

# MRI data structure



Karolina Finc

# MRI data



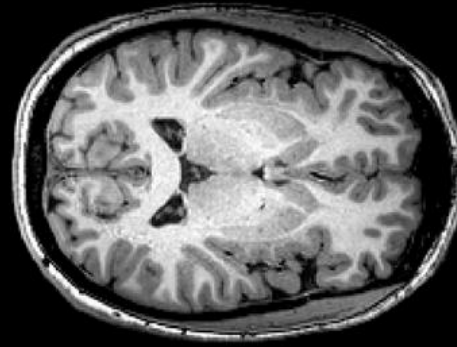


# MRI data

What determines the resolution?

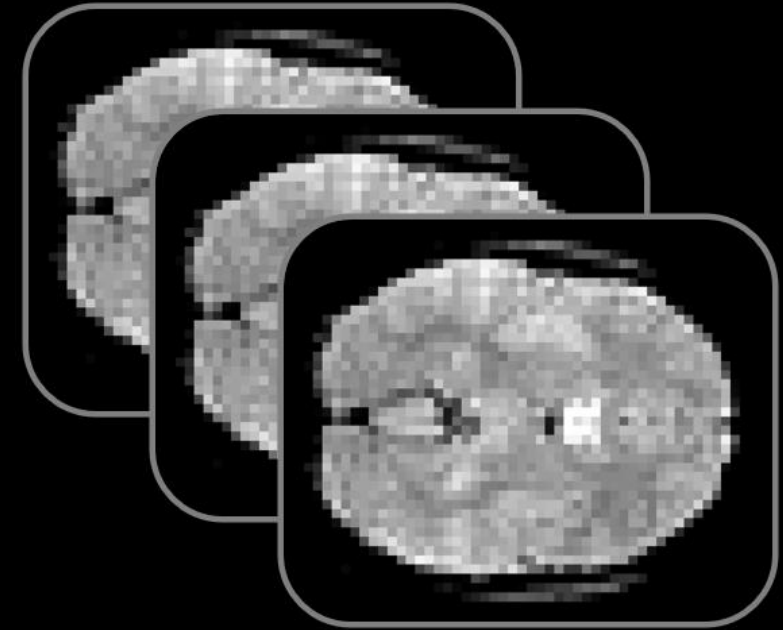
Why can't we acquire the functional images with higher resolution?

high resolution **MRI**



One 3D volume

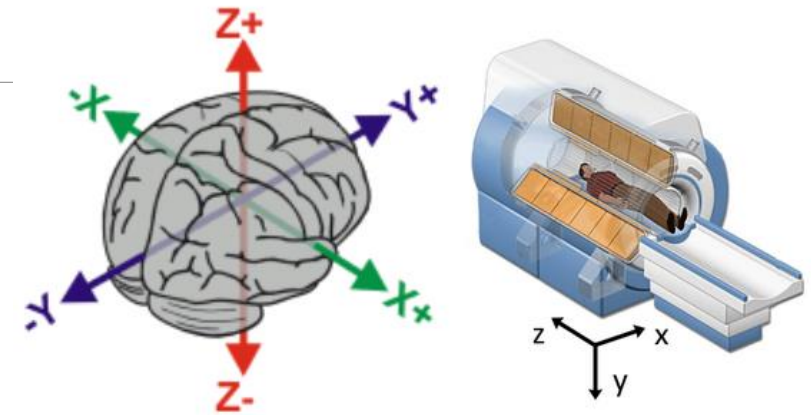
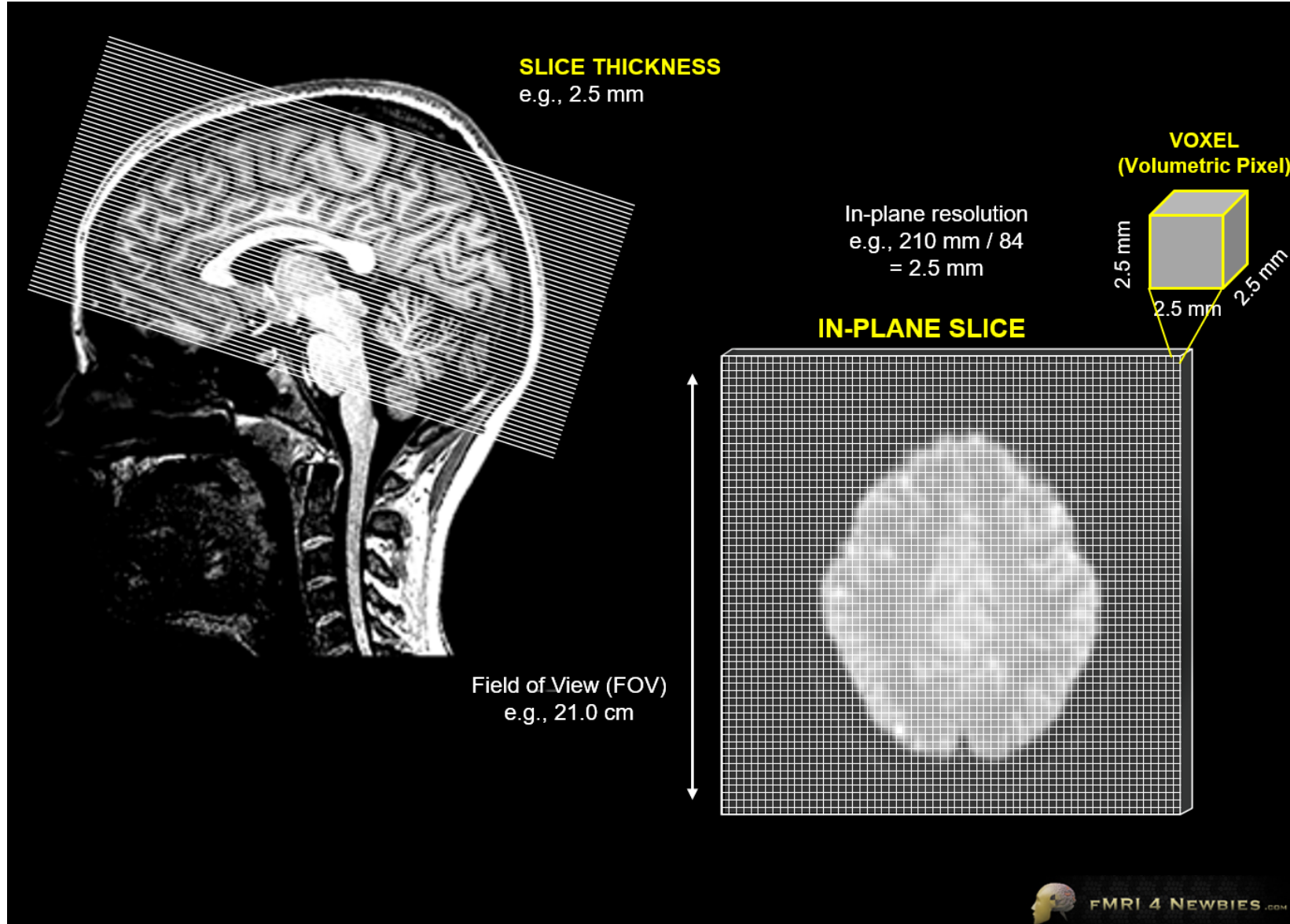
**fMRI** low resolution



series of 3D volumes (i.e., 4D data)  
(e.g., every 2 sec for 5 mins)

# fMRI data

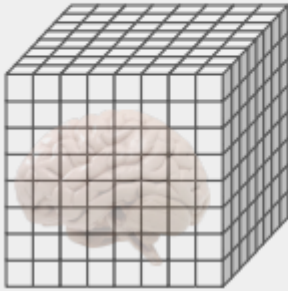
- Acquired in slices (usually axial; z-axis)



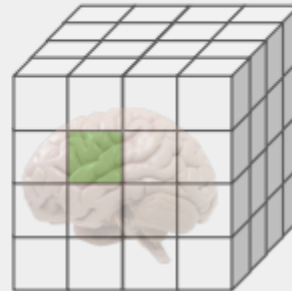
- Temporal resolution (TR) usually 1.5-3s
- Modern sequences allow acquiring multiple slices at the same time
- Typically 30-50 slices acquired
- More slices = longer TR

# MRI data structure

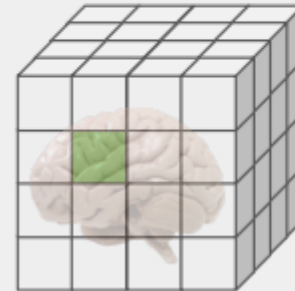
Structural data



Functional data

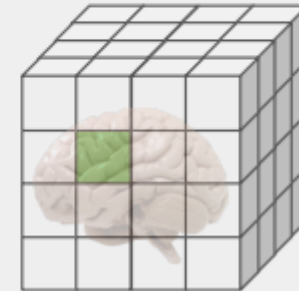


1



2

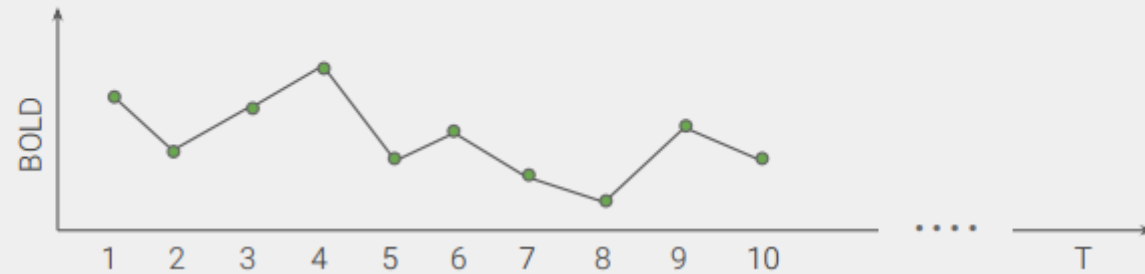
...



T

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

Every voxel has its own time-series.



....

T

Karolina Finc



# Environment

## **Data** Organise & Manage

Let's check the [Hands-On\\_02\\_Neuroimaging\\_data\\_manipulation](#) notebook