



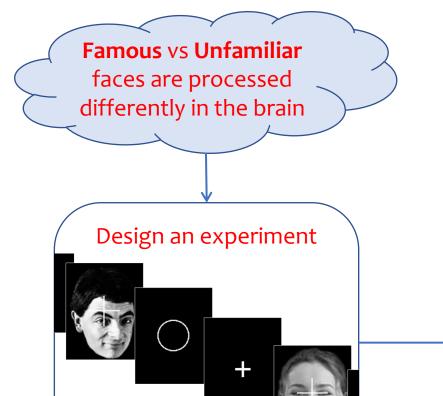
# fMRI analysis

GitHub https://github.com/dcdace/fMRI-COGNESTIC-23

Dace Apšvalka [Datza]

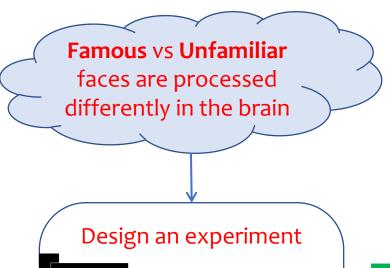


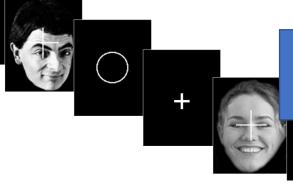
COGNESTIC, 2023





What do we do now?





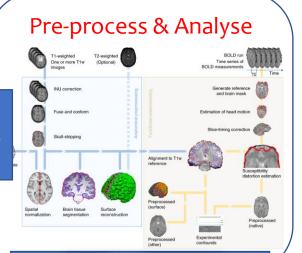
Data

Stimuli Timing Collect the MRI data



Data

Anatomical image Functional images Event details



The final push



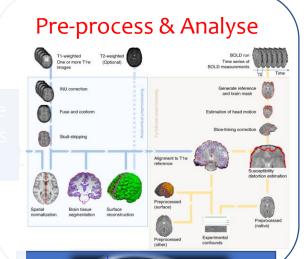


+

Data

Stimuli Timing Collect the MRI data

Anatomical imag Functional imag Event details



The final push





Pre-process

Analyse

Report

www.nature.com/scientificdata

# 

#### **SUBJECT CATEGORIES**

» Electroencephalography

-EEG

» Brain imaging

» Functional magnetic resonance imaging

» Cognitive neuroscience

## OPEN 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/.

Received: 07 April 2014 Accepted: 05 January 2015

Published: 20 January 2015

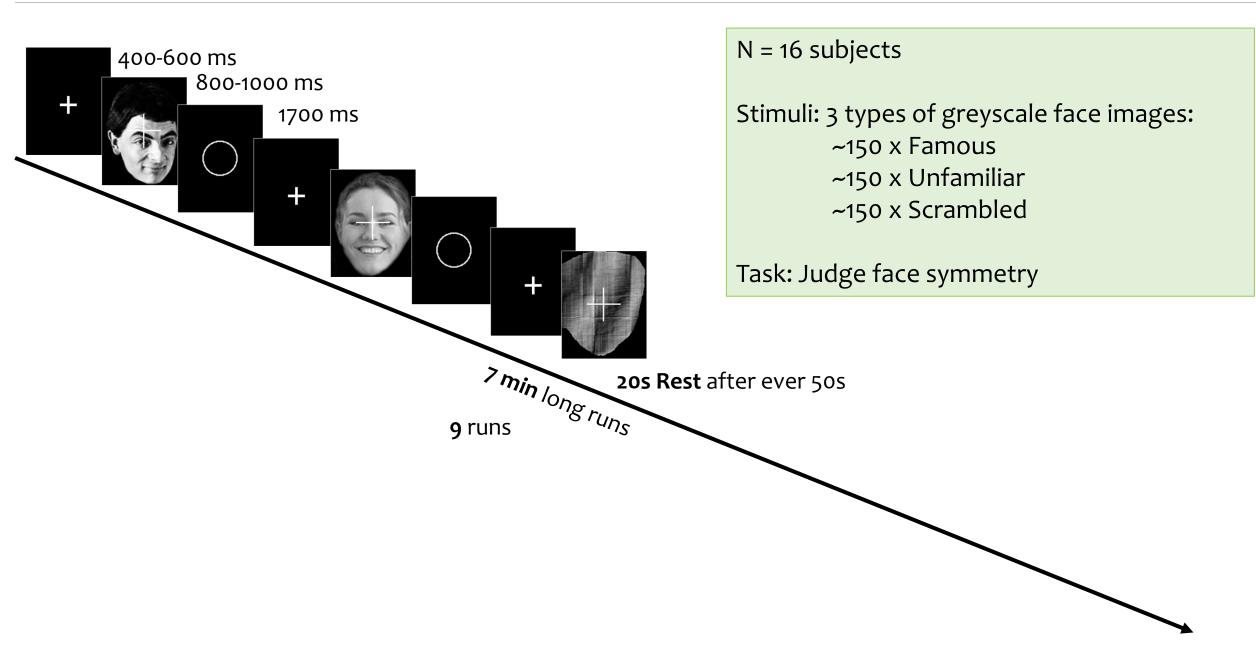
Wakeman & Henson (2015), Scientific Data, <a href="http://www.nature.com/articles/sdata20151">http://www.nature.com/articles/sdata20151</a>

#### **Example Dataset**

• 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**





Pre-process

Analyse

Report

#### PROGRAMMING LANGUAGES



A low-level programming language providing a command line user interface for Unix-like operating systems (e.g., Linux, macOS).

Used to automate repetitive tasks and manage system processes and resources.



A high-level, general-purpose programming language. **License-free** – good for reproducible & open code.



A high-level programming language designed for engineers and scientists.

**Requires a license.** Provides loads of useful resources for Neuroimaging analysis.

#### PROGRAMMING LANGUAGES



A low-level programming language providing a command line user interface for Unix-like operating systems (e.g., Linux, macOS).

Used to automate repetitive tasks and manage system processes and resources.

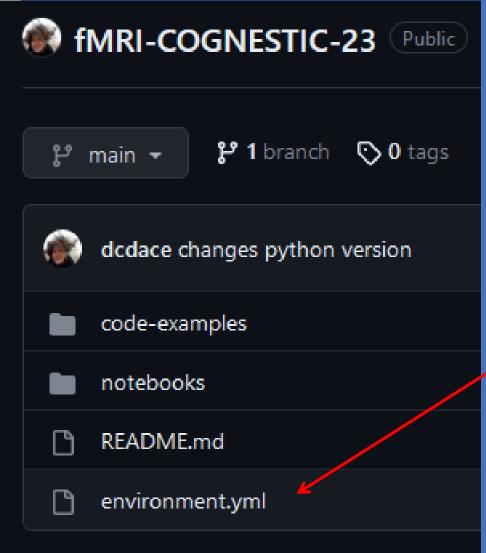


A high-level, general-purpose programming language. **License-free** – good for reproducible & open code.



A high-level programming language designed for engineers and scientists.

**Requires a license.** Provides loads of useful resources for Neuroimaging analysis.



#### PACKAGE MANAGER



Conda is an open-source, cross-platform, language-agnostic package manager and environment management system.

With conda, you can use environments that have different versions of Python and packages installed in them.

You can, for example, create your **fMRI analysis environment** that includes packages needed for your analysis work.

```
name: fMRI
       channels:
         - conda-forge
         - defaults
       dependencies:
         - python=3.10.7
         - ipython
         - jupyter
         - matplotlib
         - numpy
         - pandas
         - pip
12
13
         - pytest
         - scikit-image
         - scikit-learn
         - scipy
         - seaborn
         - pip:
           - atlasreader
           - heudiconv==0.13.1
           - nibabel
           - niflow-nipype1-workflows
22
           - nilearn
23
           - nipy
           - nipype
           - nistats
           - pybids
            - plotly
```

#### vironment



Conda is an open-source, cross-platform, language-agnostic package manager and environment management system.

With conda, you can use environments that have different versions of Python and packages installed in them.

You can, for example, create your fMRI analysis environment that includes packages needed for your analysis work.

```
name: cognestic23
     channels:
       - conda-forge
       - defaults
     dependencies:
       - dcm2niix
       - python==3.10.7
       - ipython
       - jupyter
       - matplotlib
11
       - numpy
12
       - pandas
       - pip
       - pytest
       - scikit-image
       - scikit-learn
       - scipy
       - seaborn
       - pip:
         - atlasreader
21
         - heudiconv==0.13.1
         - nibabel
         - niflow-nipype1-workflows
         - nilearn
         - nipy
         - nipype
         - nistats
         - nltools
         - nxviz
         - mne
         - mne-bids
         - mne-bids-pipeline
         - mne-connectivity
         - plotly
         - pybids
         - python-louvain
         - rsatoolbox
```

#### vironment



For this Summer School, we have shared with you the **COGNESTIC environment** that you'd need to do the things we will do in most of the workshops.

This environment contains packages not only for the fMRI, but also for other workshops, e.g., EEG/MEG.

Normally, you would have separate environments for different types of projects. But in this case, let's treat COGNESTIC as one mega project.

The COGNESTIC environment is available in your cognestic23 notebook materials as a file environment.yml (/ Win,yml, Mac.yml).

```
name: cognestic23
     channels:
       - conda-forge
       - defaults
     dependencies:
       - dcm2niix
       - python==3.10.7
       - ipython
       - jupyter
       - matplotlib
11
       - numpy
12
       - pandas
13
       - pip
       - pytest
       - scikit-image
       - scikit-learn
       - scipy
       - seaborn
       - pip:
         - atlasreader
         - heudiconv==0.13.1
21
         - nibabel
         - niflow-nipype1-workflows
         - nilearn
         - nipy
         - nipype
         - nistats
         - nltools
         - nxviz
         - mne
         - mne-bids
         - mne-bids-pipeline
         - mne-connectivity
         - plotly
         - pybids
         - python-louvain
         - rsatoolbox
```

#### vironment



You can create an environment from an environment file

conda env create -f environment.yml

or from scratch

conda create -n cognestic23 python=3.10 jupyter [and other packages]

#### PROGRAMMING LANGUAGES







#### PACKAGE MANAGER



#### **CODE EDITOR**

Code editors simplify and speed up typing of source code. They also support running and debugging the code.

The best editors are cross-language, cross-platform and support version control.

#### PROGRAMMING LANGUAGES











#### **CODE EDITOR**



#### PROGRAMMING LANGUAGES







PACKAGE MANAGER



**CODE EDITOR** 



#### **VERSION CONTROL**



The practice of tracking and managing changes to software code - your analysis code. It allows to revert selected files back to a previous state, revert the entire project back to a previous state, compare changes over time, do collaborative coding etc.

PROGRAMMING LANGUAGES

PACKAGE MANAGER







Let's see nbo1 Analysis-Environment.ipynb notebook



**VERSION CONTROL** 

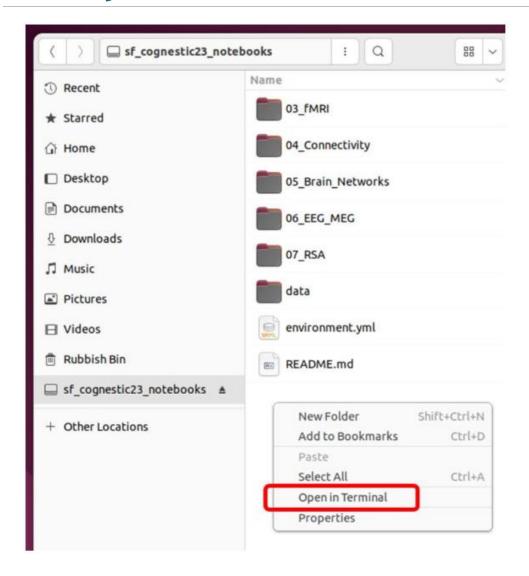




**ANALYSIS NOTEBOOK** 



## Analysis notebooks

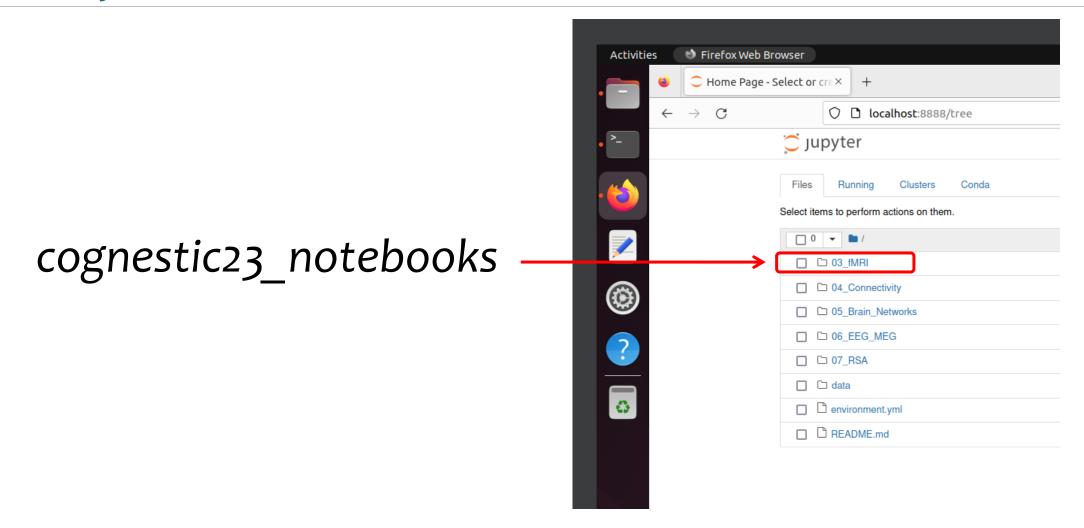


In the terminal type:

conda activate cognestic23

jupyter notebook

## Analysis notebooks



Static notebooks: <a href="https://github.com/dcdace/fMRI-COGNESTIC-23">https://github.com/dcdace/fMRI-COGNESTIC-23</a>



**Data**Organise & Manage

Pre-process

Analyse

Report

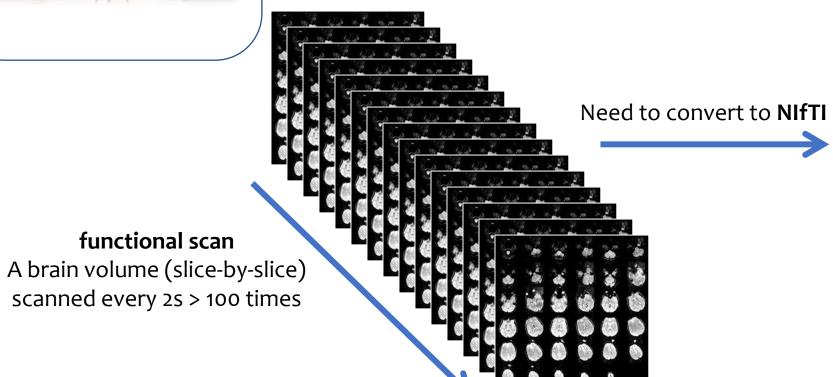
# fMRI file formats

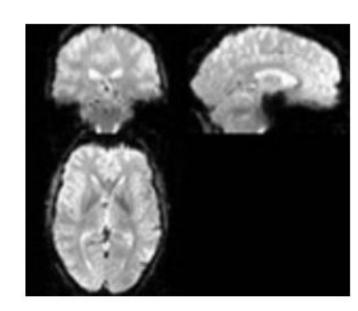
#### Collect the data



functional scan

#### **DICOM** format

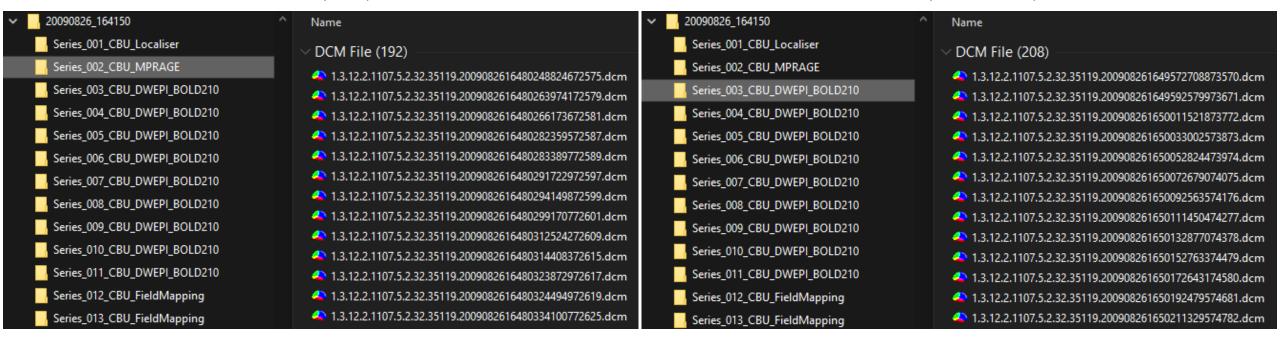






#### Anatomical (T1w) scans

#### Functional (T2\*/BOLD) scans

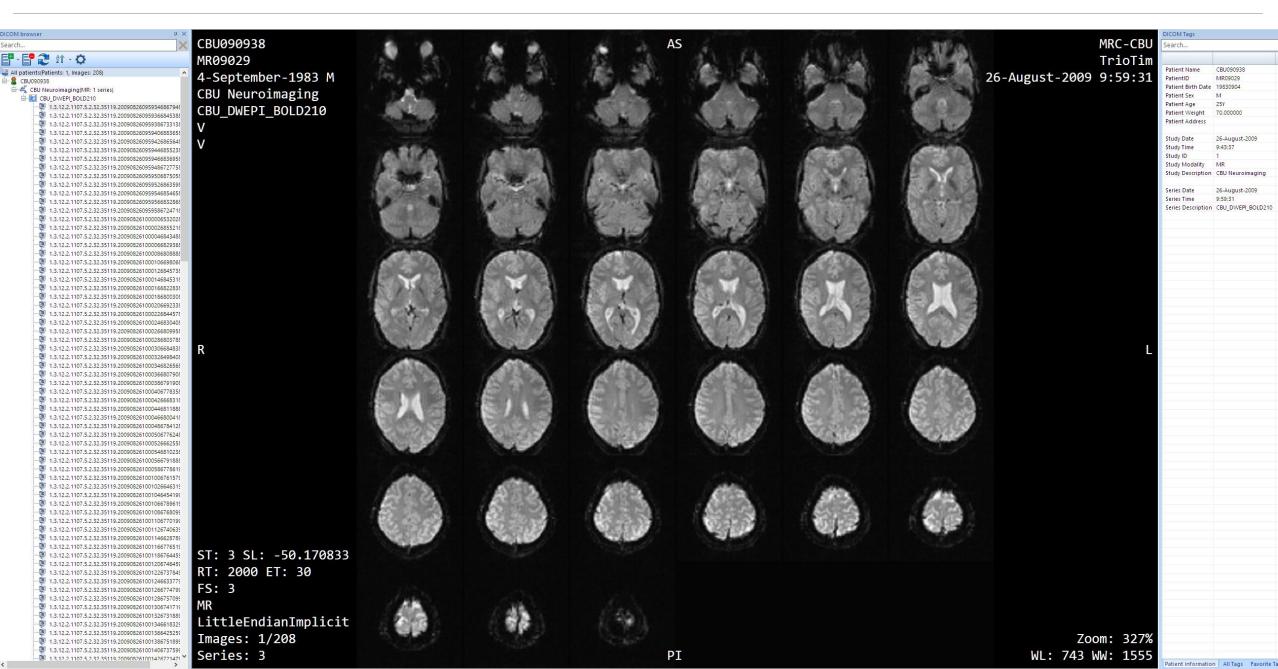


- DICOM Digital Imaging and Communications in Medicine (.dcm)
  - Raw data standard for storing and communicating medical images
  - Contains a header (meta data) and the actual image itself
  - Images are stored in **2D layers**
  - A separate file for each slice (T1w) or volume (BOLD)

#### **DICOM:** Anatomical



#### **DICOM:** Functional

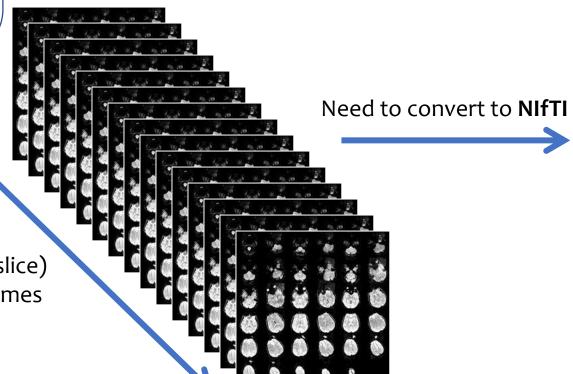


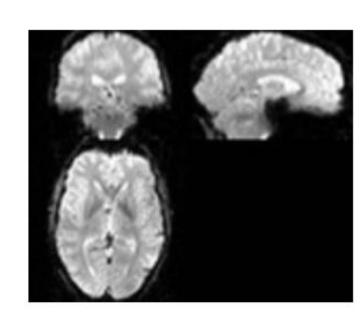
#### Collect the data



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

#### **DICOM** format





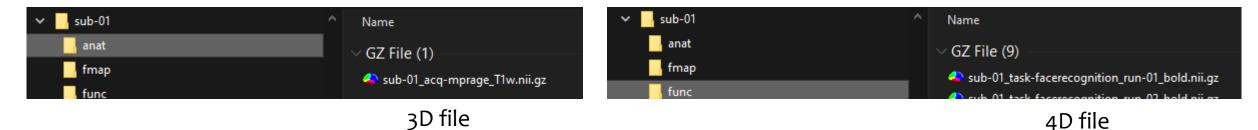
#### functional scan

A brain volume (slice-by-slice) scanned every 2s > 100 times



#### Anatomical (T1w) scans

#### Functional (T2\*/BOLD) scans



- 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)

#### DICOM vs NIFTI

- All medical vs brain images
- 2D layer files vs 3D/4D files
- More vs less metadata
  - When converting DICOM to NIfTI need to be aware of that and save all metadata that might be needed

#### DICOM to NIfTI

- Several tools are available
  - For example, dcm2niix Python package

#### Collect the data



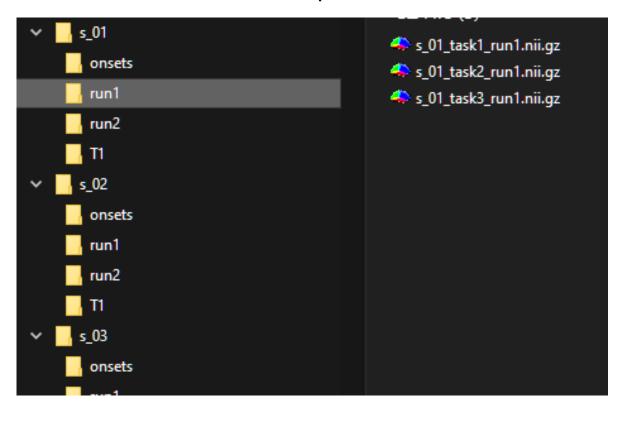
# How should we organise our files?

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

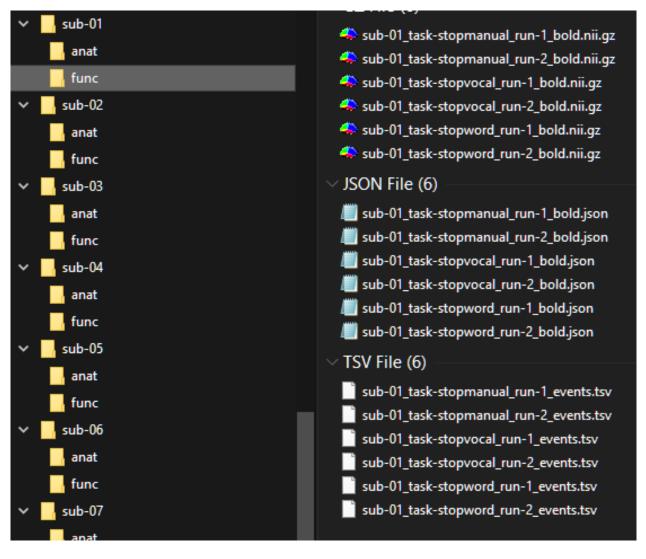
- sub-o1 T1w.nii
- sub-01 run-01 bold.nii
- sub-01\_run-02\_bold.nii
- sub-o2\_T1w.nii
- sub-02 run-01 bold.nii
- sub-02 run-02 bold.nii
- ...
- sub-100 T1w.nii
- sub-100 run-01 bold.nii
- sub-100 run-02 bold.nii
- and even more files (more sessions and tasks)

# File organisation

#### 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





Documentation: <a href="https://bids-specification.readthedocs.io/en/latest/">https://bids-specification.readthedocs.io/en/latest/</a>

#### SCIENTIFIC DATA (1011)10 (1011)110 (

SUBJECT CATEGORIES » Data publication and

**OPEN**: The brain imaging data structure, a format for organizing and experiments

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>, Received: 18 December 2015 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>20,23</sup>, John Pellman<sup>6</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>3,26</sup> Published: 21 June 2016 Gaël Varoquaux29 & Russell A. Poldrack1





#### 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 Capotă<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

#### 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

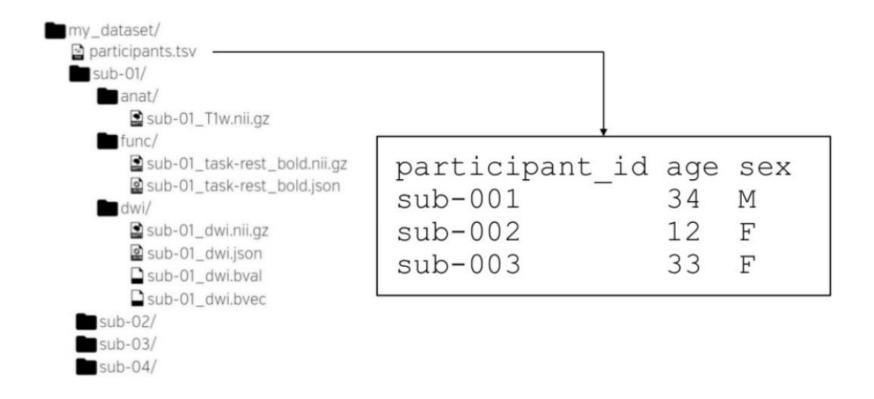




 Validation tools that can check your dataset integrity and let you easily spot missing values

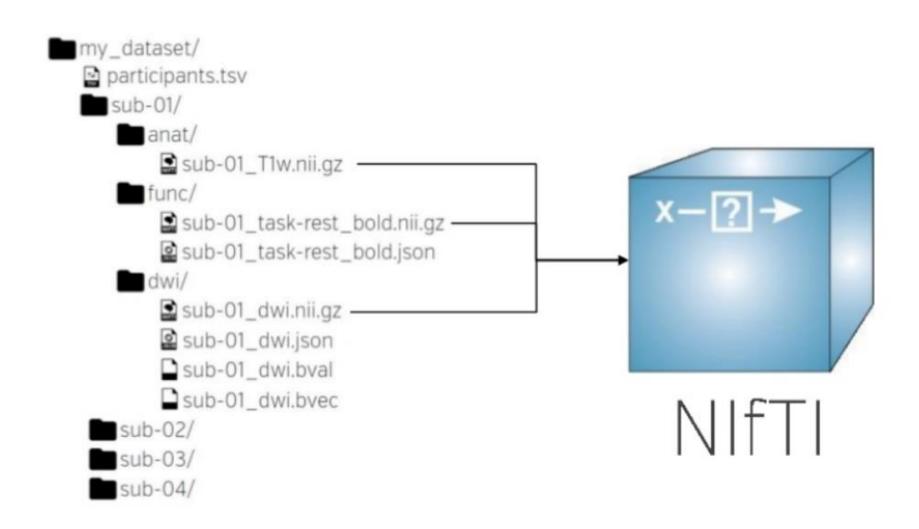
#### **BIDS**

Contains participant information



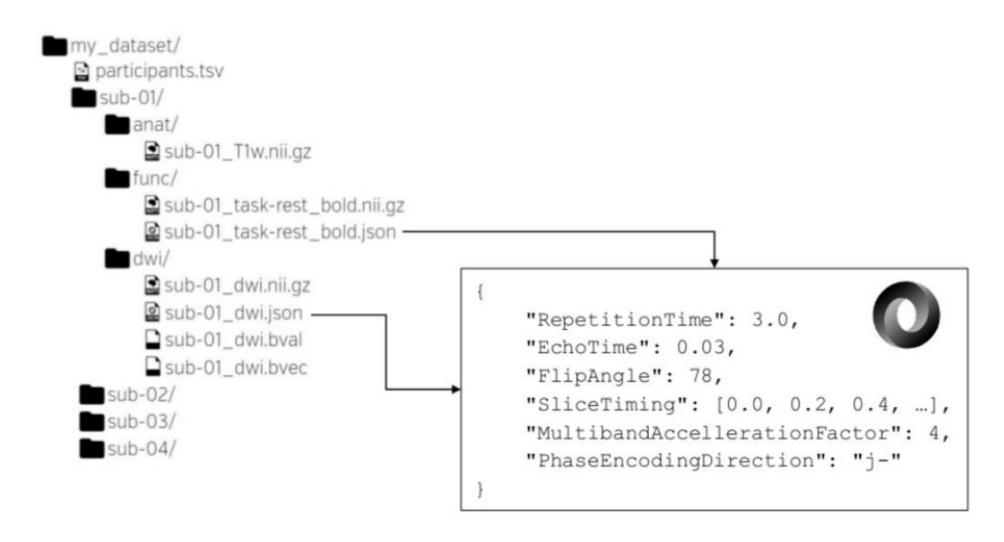
#### BIDS

• Contains data files



#### **BIDS**

Contains study specific JSON (metadata) files



### DICOM → BIDS

Collect the data



1208200617178\_22/

1208200617178\_23/

1208200617178 24/ 1208200617178\_25/

□ 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

Many BIDS converters available

**HeuDiConv** (Heuristic Dicom Conversion) provides sophisticated and flexible creation of BIDS datasets.

my dataset/

sub-01/

participants.tsv

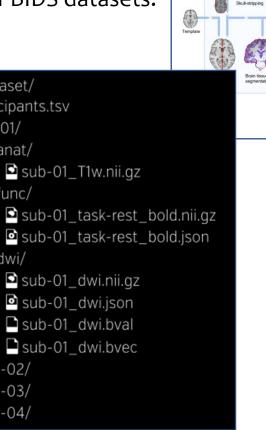
anat/

func/

dwi/

sub-02/ sub-03/

sub-04/



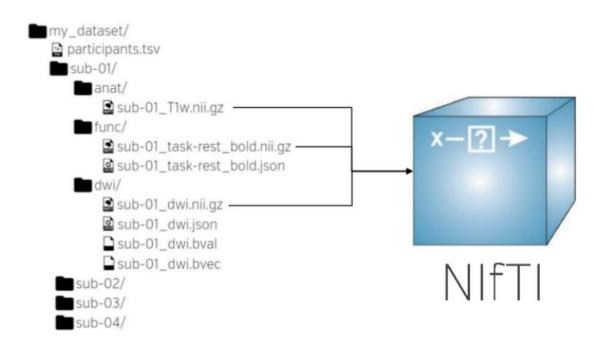
Pre-process & Analyse

# Environment

# **Data**Organise & Manage

Let's see the <a href="mailto:nbox">nbox</a>\_Data-Management.ipynb notebook

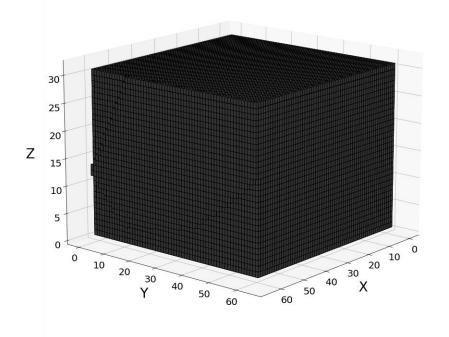


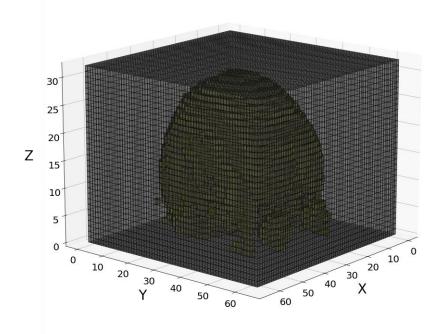


# Imaging data content

#### 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.]],
```





...,

#### 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.]],
 ...,
```

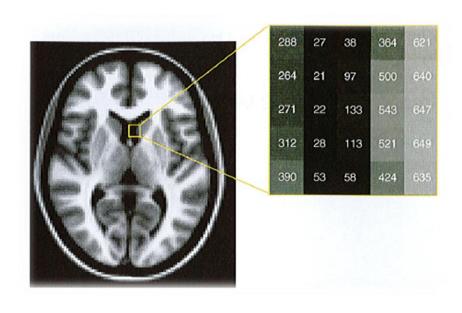
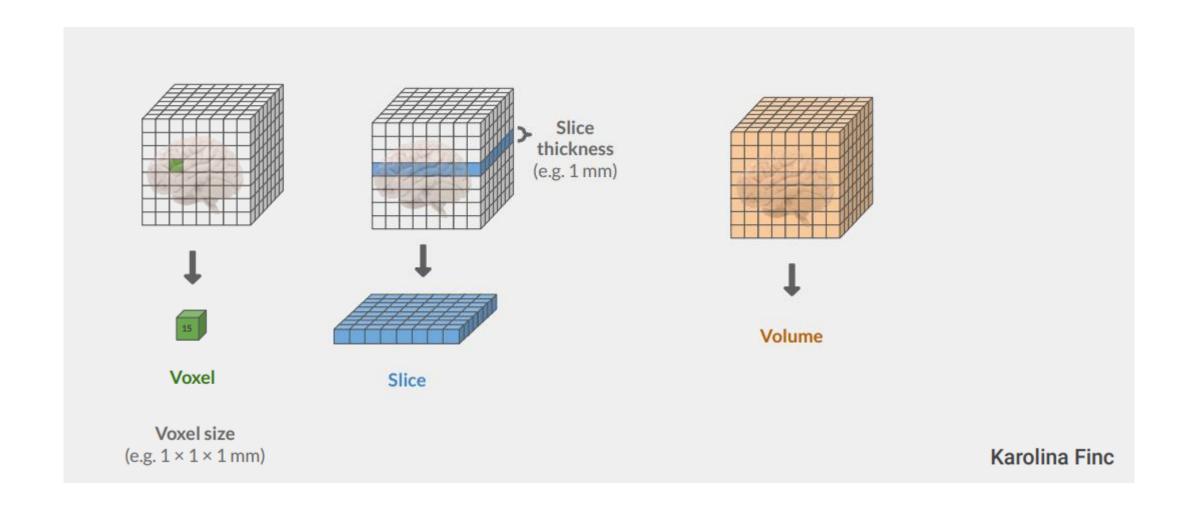


Image from Poldrack et al., 2011



# MRI data

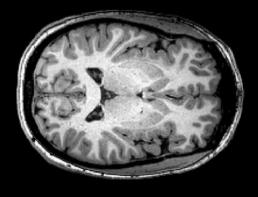


## MRI data

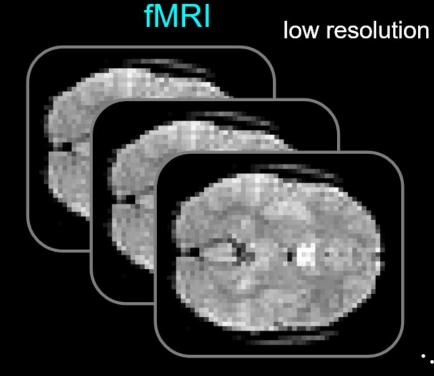
What determines the resolution?

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

# high resolution MRI



One 3D volume

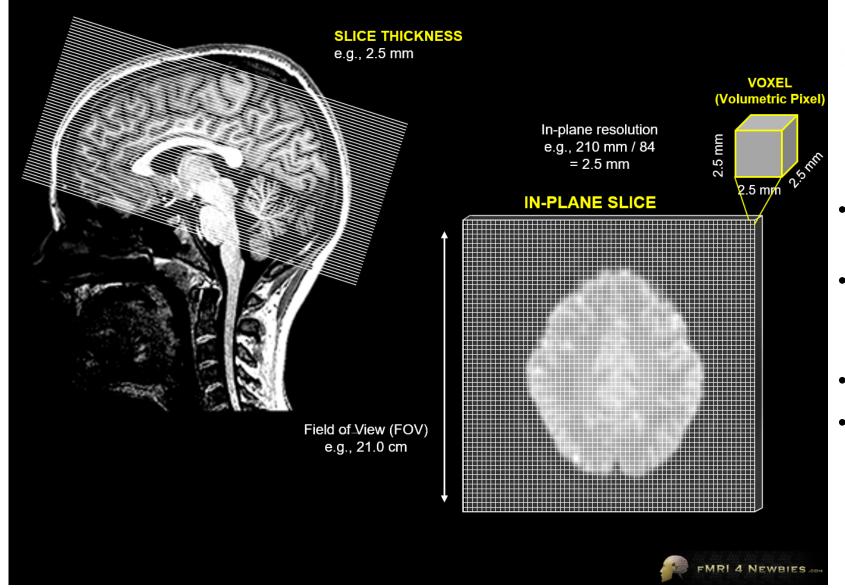


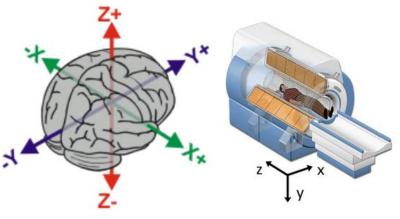
series of 3D volumes (i.e., 4D data) (e.g., every 2 sec for 5 mins)



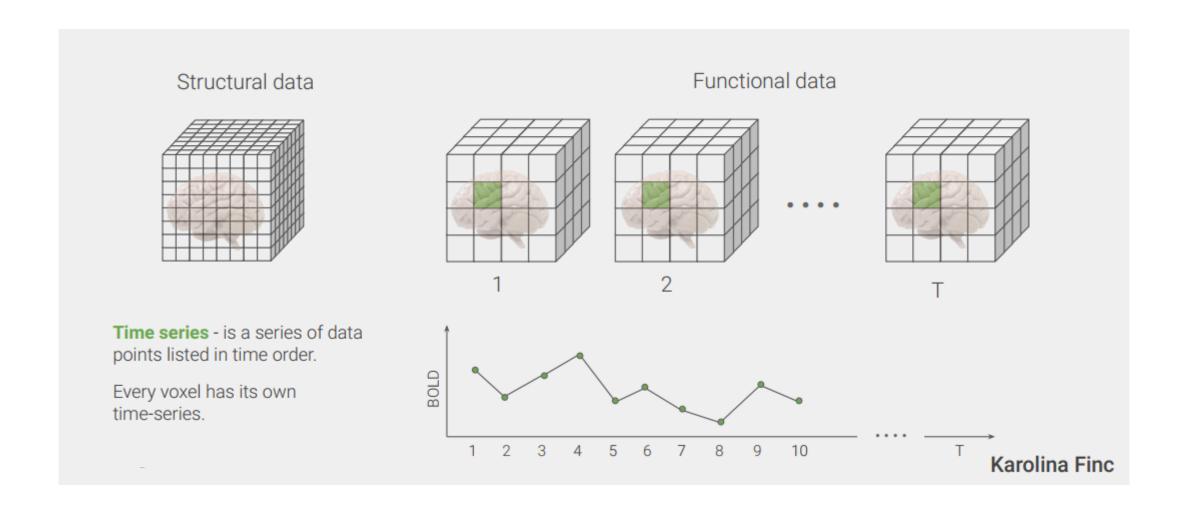
## fMRI data

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



# Environment

# **Data**Organise & Manage

Let's see the nbo3\_Neuroimaging\_data\_manipulation.ipynb notebook







Pre-process

Analyse

Report