



MRC Cognition
and Brain
Sciences Unit



UNIVERSITY OF
CAMBRIDGE

Functional MRI

 **GitHub** https://github.com/MRC-CBU/COGNESTIC/tree/main/05_fMRI

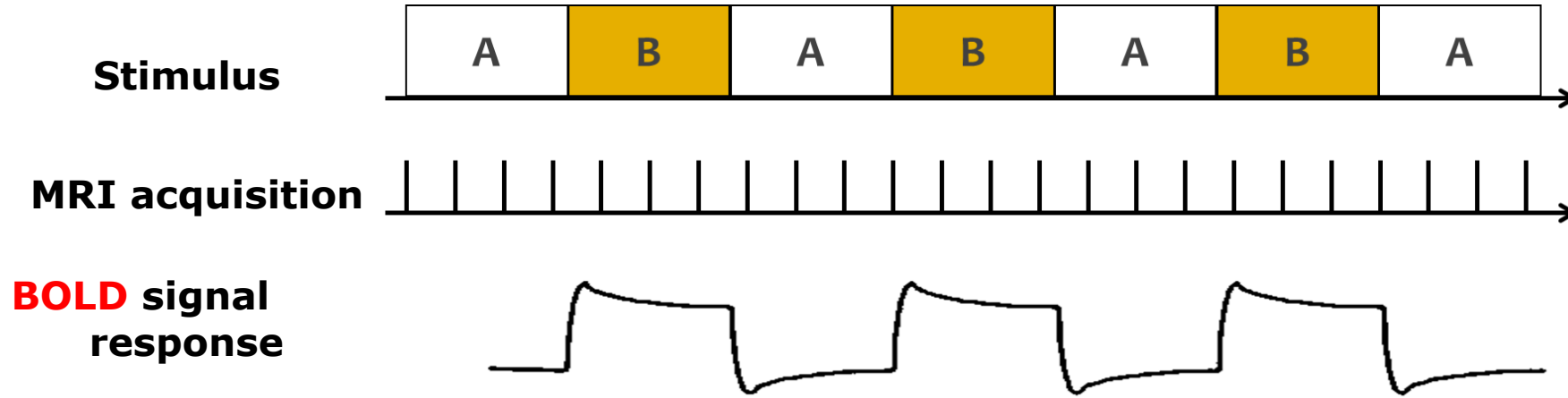
Dace Apšvalka
[Datza]



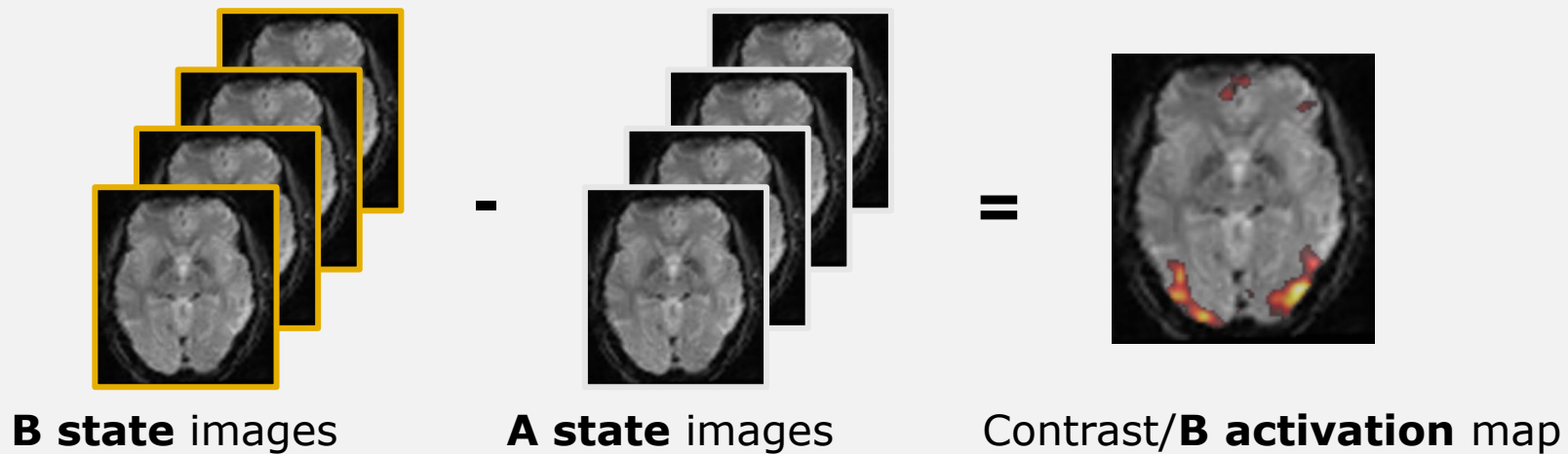
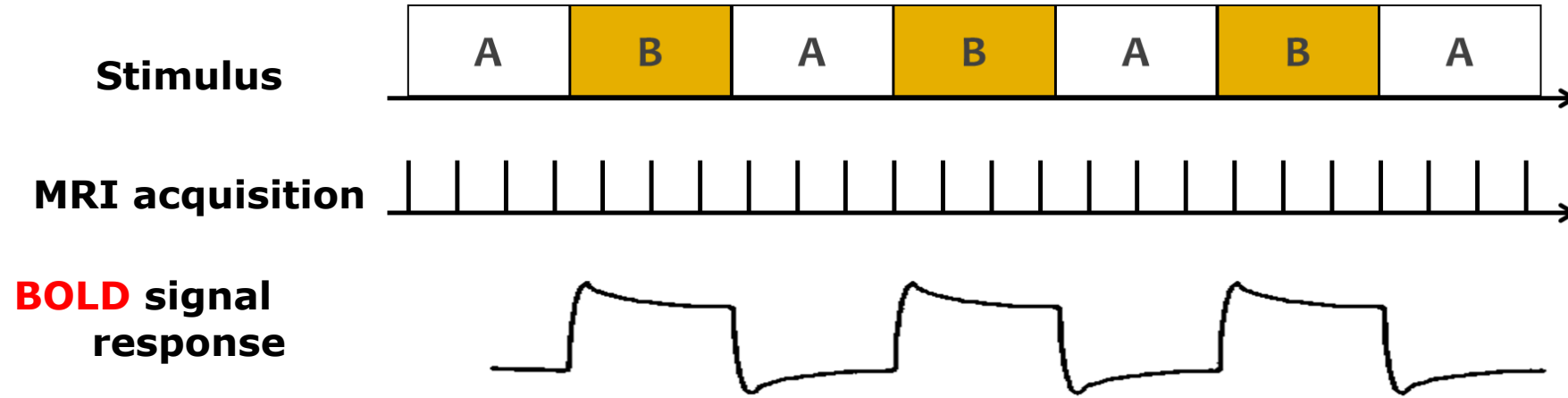
<http://www.dcdace.net>

COGNESTIC, 2024

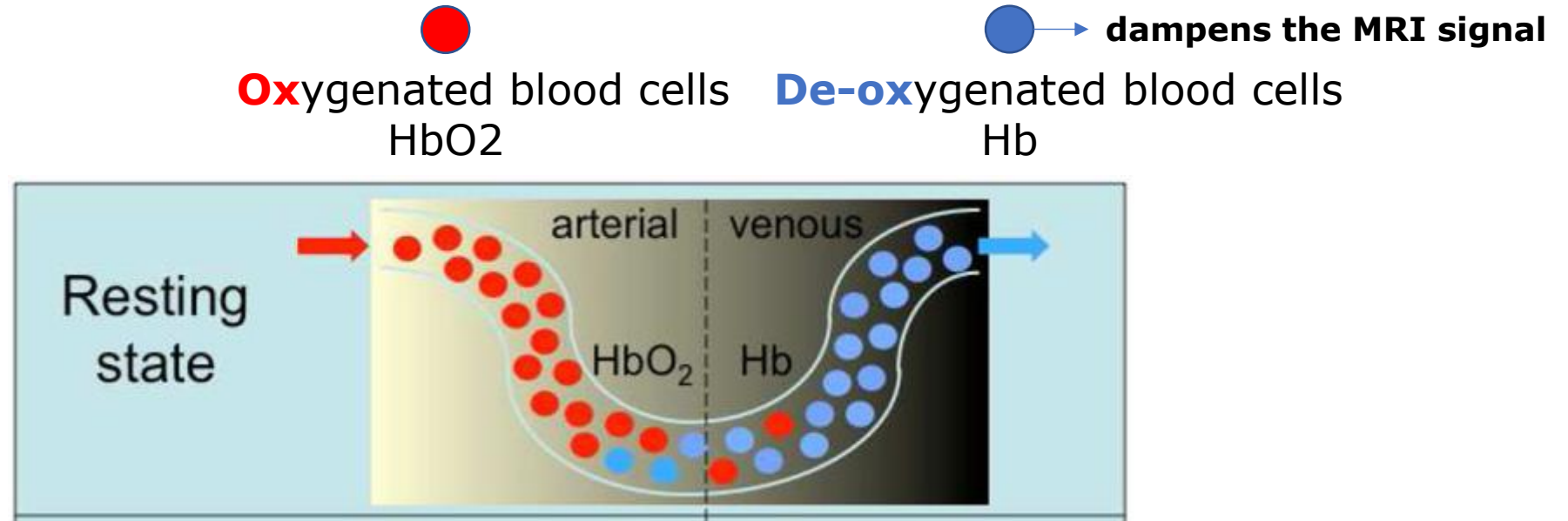
Functional MRI (fMRI)



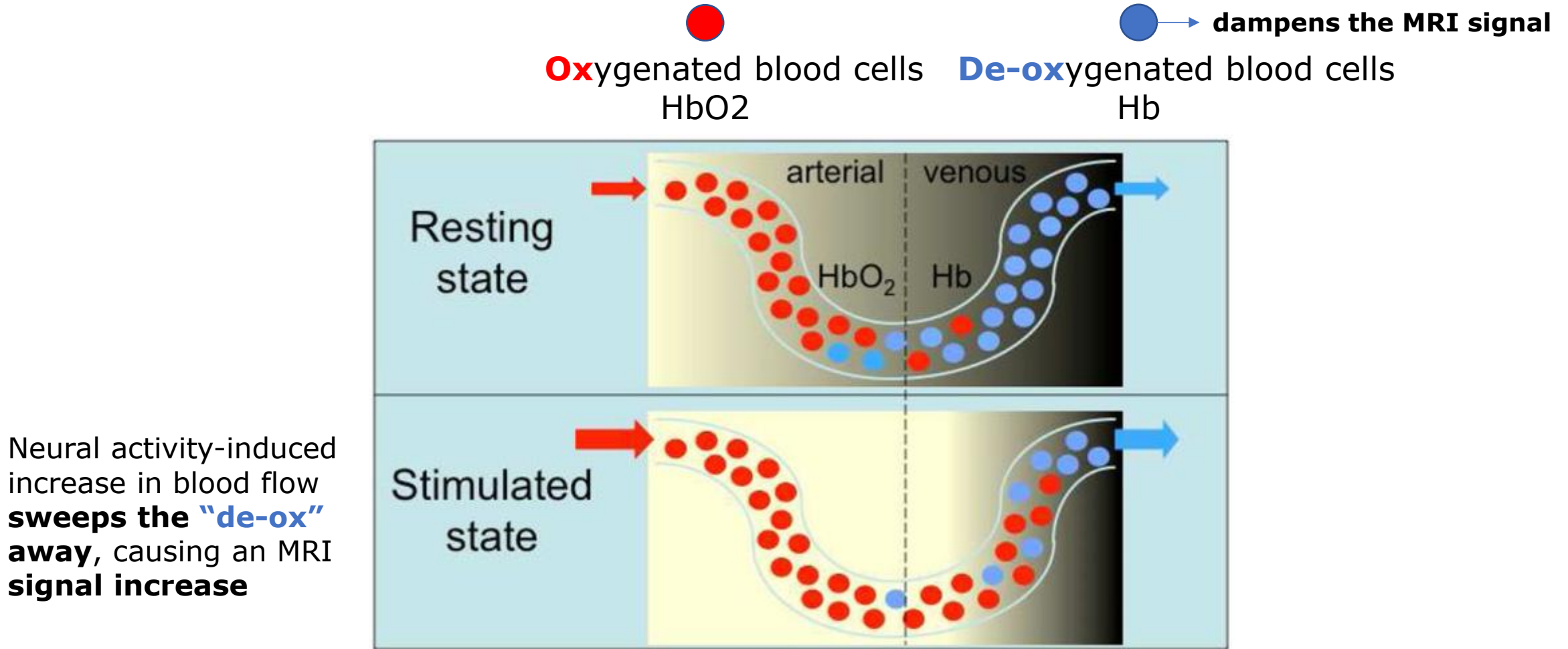
Functional MRI (fMRI)



Blood oxygen level-dependent (BOLD) signal



Blood oxygen level-dependent (BOLD) signal



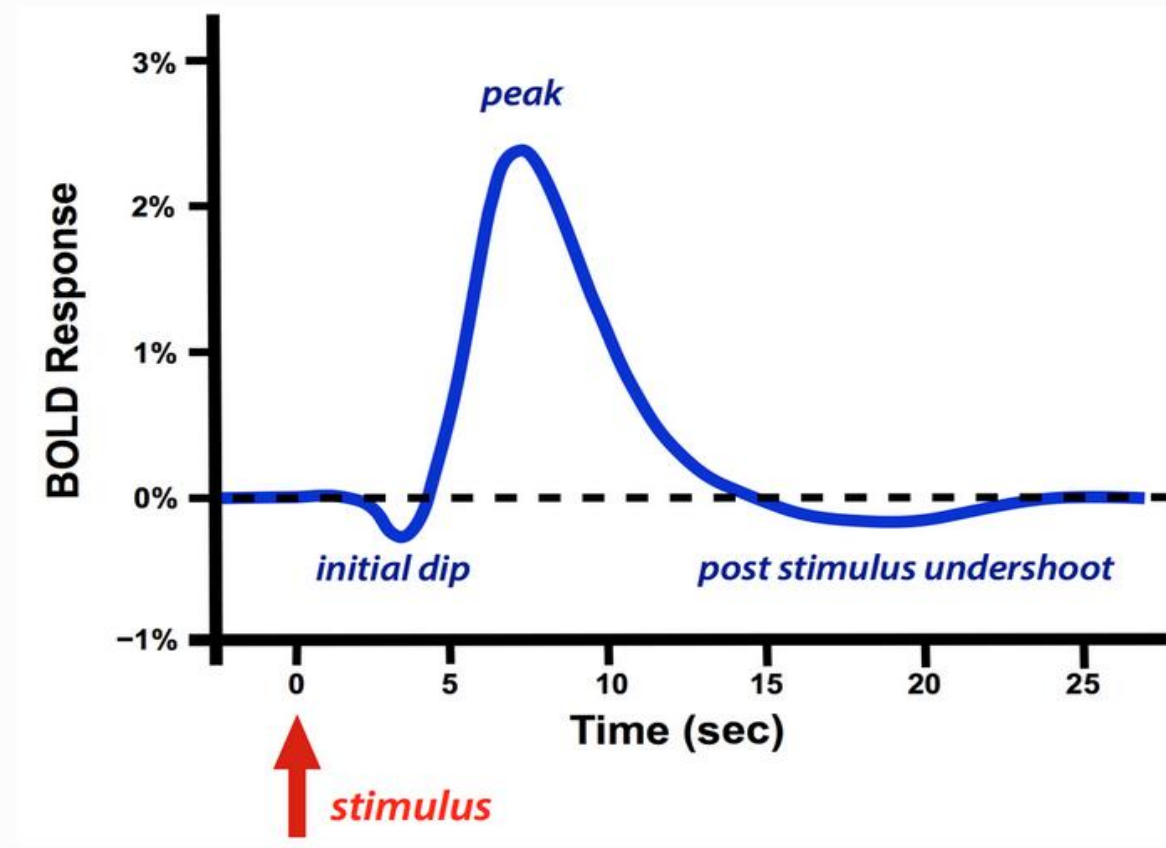
This difference in the magnetic properties of de-oxygenated and oxygenated Hb is used in BOLD fMRI to create contrast in images – BOLD contrast

By controlling for all other factors, any observed differences in the BOLD signal are inferred to be due to differences in neuronal activity

BOLD response

Hemodynamic response function (HRF)

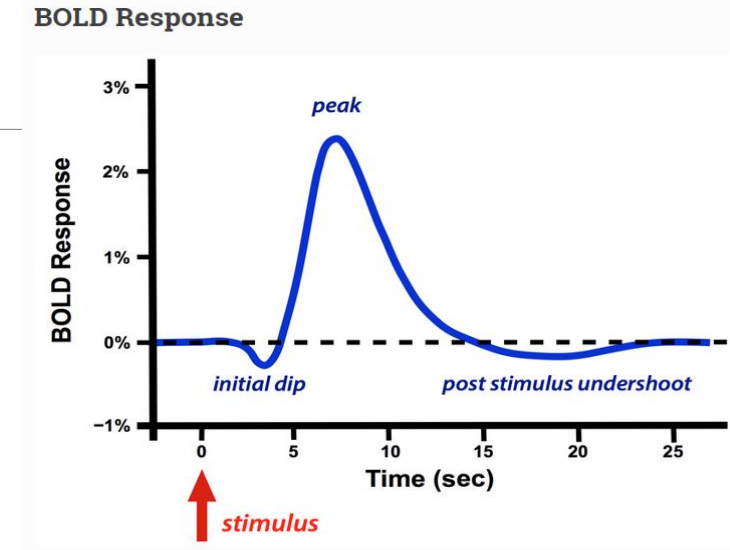
BOLD Response



©Andy Jahn

Hemodynamic response function (HRF)

- Depends on stimulus intensity and duration
- Varies across individuals
- Varies with healthy ageing and development
- Varies with common stimulants such as caffeine
- Varies across the brain, both at a distant and local scale
- The most common solution to HRF variability is to pretend it doesn't exist and use a generic model for all participants



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^{1,2} & Richard N. Henson²

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

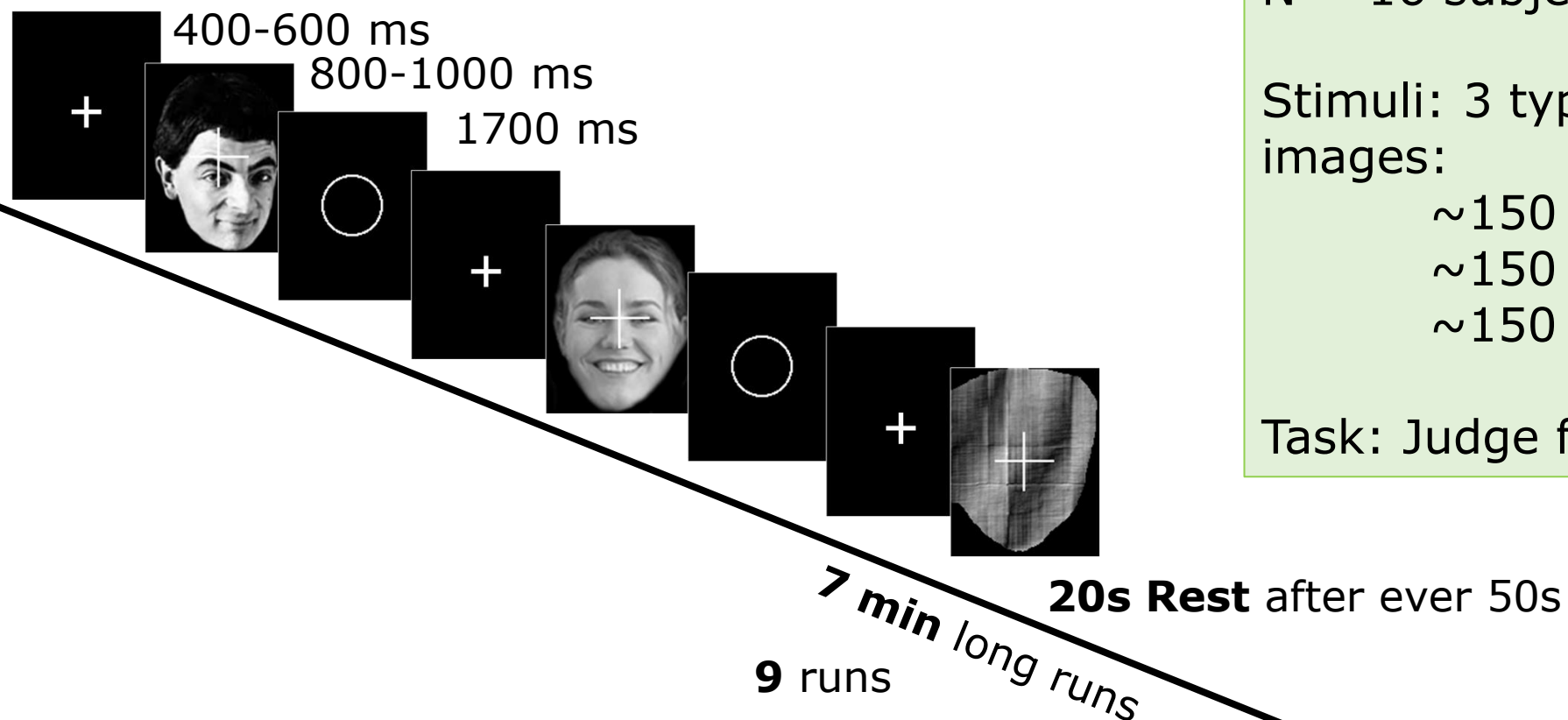
Example Experiment: Face Recognition

N = 16 subjects

Stimuli: 3 types of greyscale face images:

- ~150 x Familiar
- ~150 x Unfamiliar
- ~150 x Scrambled

Task: Judge face symmetry



Each image was presented twice, with the second presentation occurring either immediately after (Immediate Repeats), or after 5–15 intervening stimuli (Delayed Repeats), with 50% of each type of repeat.

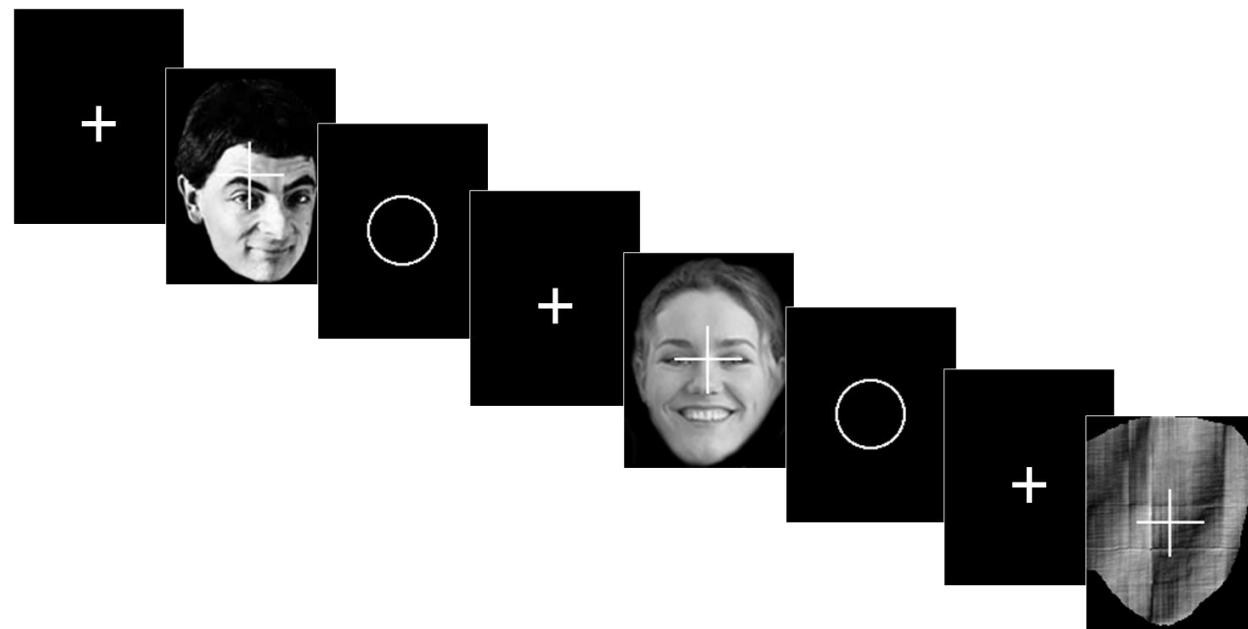
Example Experiment: Face Recognition

- Conditions

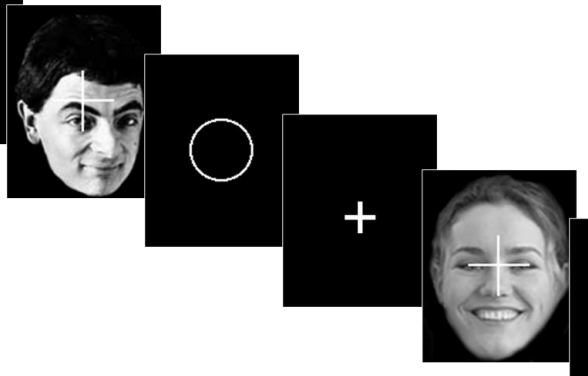
- Familiar faces
- Unfamiliar faces
- Scrambled faces
- Initial presentation
- Immediate repeat
- Delayed repeat

- Possible questions to investigate

- Brain areas for Faces
- Brain areas for Face Familiarity
- Response to Initial vs Repeated presentations
- Response to the Repetition of Familiar vs Repetition of Unfamiliar
- ...



Design an experiment



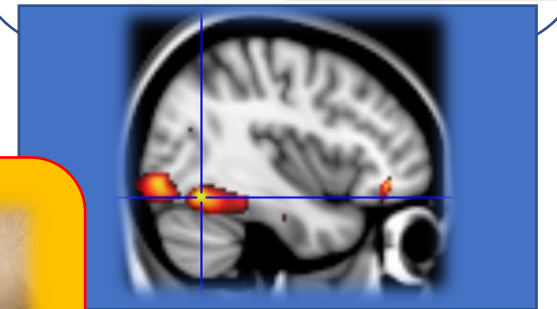
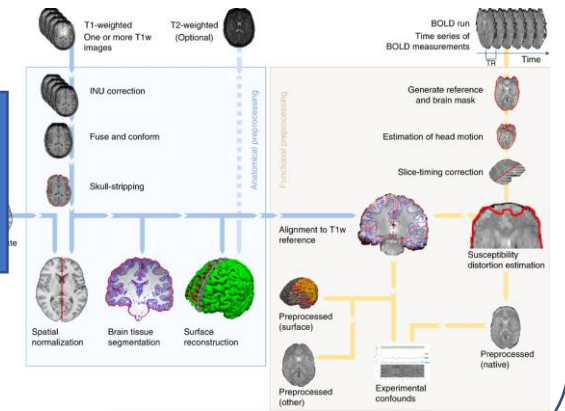
Collect the MRI data



Data

Anatomical image
Functional images
Event details

Pre-process & Analyse



Design an experiment



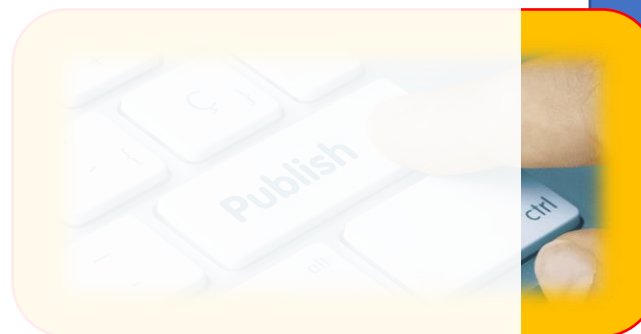
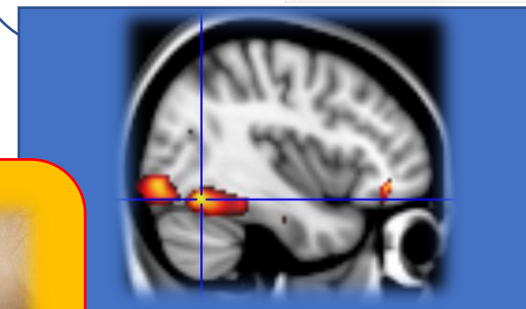
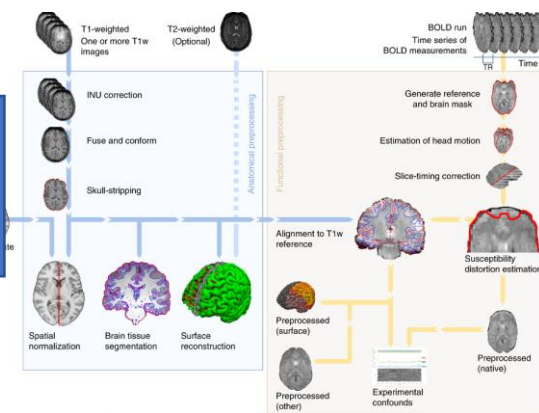
Collect the MRI data



Data

Anatomical image
Functional images
Event details

Pre-process & Analyse



Environment



```
graph TD; Environment[Environment] -- contains --> Data[Data Organise & Manage]; Data -- contains --> PreProcess[Pre-process]; Data -- contains --> Analyse[Analyse]; Data -- contains --> Report[Report];
```

Data
Organise & Manage

Pre-process

Analyse

Report

Environment

PROGRAMMING LANGUAGES



BASH
&
Shell Scripts

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.



MATLAB®

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

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

main 1 Branch 0 Tags

dcdace fix: typo

01_Primer_on_Python

02_Statistics

03_Structural_MRI

04_DWI

05_fmRI

06_Connectivity

07_Networks

08_EEG_MEG

09_MVPA_MRI

10_MVPA_EEG_MEG

.gitignore

README.md

mri_environment.yml

stats_environment.yml

Environment

G LANGUAGES

ASH

&

ll Scripts

thon™

ATLAB®

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 **MRI analysis environment** that includes packages needed for your analysis work.


```

1  name: mri
2  channels:
3    - conda-forge
4    - defaults
5  dependencies:
6    - pip=24.2
7    - python=3.11 # dipy v1.9.0 dependency >=3.9, <3.12
8    - pytest=8.3.2
9    - seaborn=0.13.2
10   - pip:
11     - antspyx==0.5.3
12     - atlasreader==0.3.2
13     - dcm2niix==1.0.20220715
14     - dipy==1.9.0
15     - fury==0.11.0 # dipy v1.9.0 visualisation didn't work with fury 0.10.0
16     - heudiconv==1.1.6
17     - ipykernel==6.29.3
18     - ipython==8.22.1
19     - jupyter==1.0.0
20     - matplotlib==3.8.3
21     - nibabel==5.2.1
22     - niflow-nipype1-workflows==0.0.5
23     - nilearn==0.10.4
24     - nipy==0.6.0
25     - nipype==1.8.6
26     - numpy==1.26.4 # dipy v1.9.0 dependency >=1.21.6, <1.27.0
27     - nxviz==0.7.4
28     - pandas==2.2.2
29     - plotly==5.23.0
30     - pybids==0.16.4
31     - python-louvain==0.16
32     - requests==2.31.0
33     - rsatoolbox==0.1.5
34     - scikit-image==0.24.0
35     - scikit-learn==1.5.1
36     - scipy==1.14.0

```

Environment

PACKAGE MANAGER



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Environment

PROGRAMMING LANGUAGES



BASH
&
Shell Scripts



PACKAGE MANAGER



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

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

<https://conda.io/projects/conda/en/latest/user-guide/tasks/manage-environments.html>

Creating an environment from a .yaml file

```
conda env create -f mri_environment.yaml
```

✓ Environment

Data

Organise & Manage

Pre-process

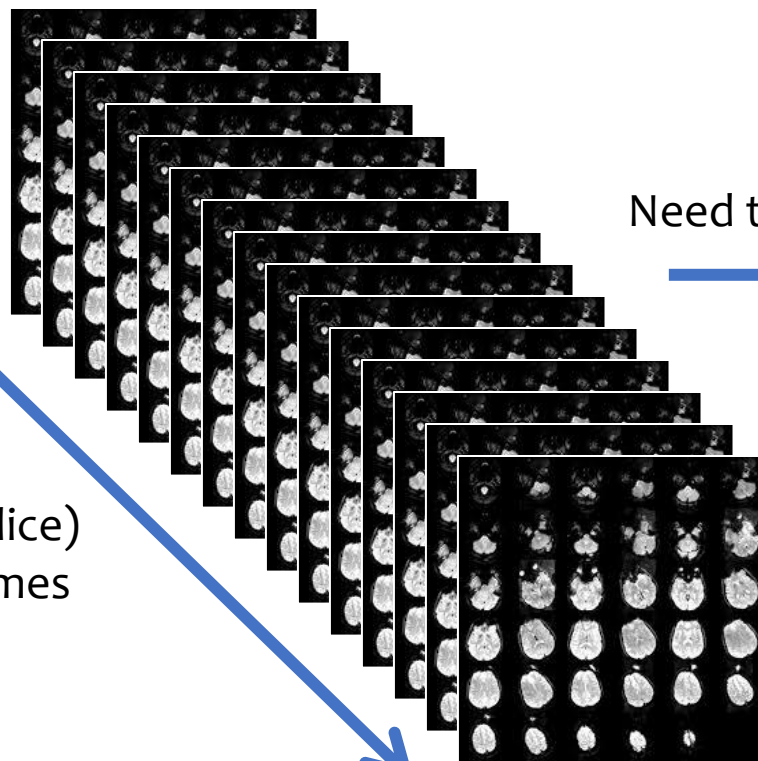
Analyse

Report

Collect the data



DICOM format

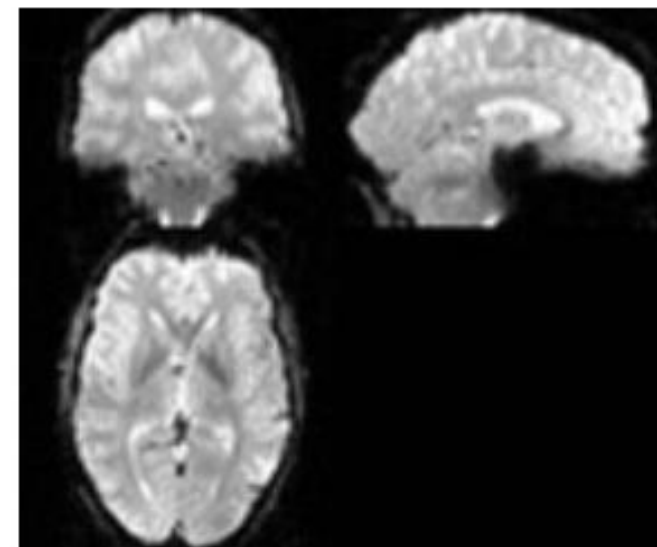
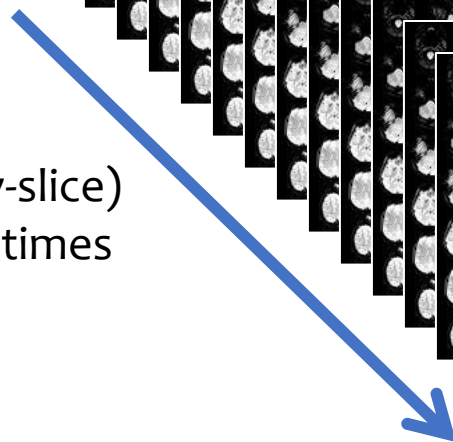


Need to convert to NIfTI



functional scan

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



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

How should we
name and
organise our files?

- and even more files (more sessions and tasks)

fMRI data organisation



- **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 organisation

- 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. Gorgolewski¹, Tibor Auer², Vince D. Calhoun^{3,4}, R. Cameron Craddock^{5,6}, Samir Das⁷, Eugene P. Duff⁸, Guillaume Flandin⁹, Satrajit S. Ghosh^{10,11}, Tristan Glatard^{7,12}, Yaroslav O. Halchenko¹³, Daniel A. Handwerker¹⁴, Michael Hanke^{15,16}, David Keator¹⁷, Xiangrui Li¹⁸, Zachary Michael¹⁹, Camille Maumet²⁰, B. Nolan Nichols^{21,22}, Thomas E. Nichols^{23,24}, John Pellmar⁵, Jean-Baptiste Poline²⁴, Ariel Rokem²⁵, Gunnar Schaefer^{1,26}, Vanessa Sochat²⁷, William Triplett¹, Jessica A. Turner^{3,28}, Gaël Varoquaux²⁹ & Russell A. Poldrack¹

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Published: 21 June 2016

RESEARCH ARTICLE

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

Krzysztof J. Gorgolewski^{1*}, Fidel Alfaro-Almagro², Tibor Auer³, Pierre Bellec^{4,5}, Mihai Capota⁶, M. Mallar Chakravarty^{7,8}, Nathan W. Churchill⁹, Alexander Li Cohen¹⁰, R. Cameron Craddock^{11,12}, Gabriel A. Devenyi^{7,8}, Anders Eklund^{13,14,15}, Oscar Esteban¹, Guillaume Flandin¹⁶, Satrajit S. Ghosh^{17,18}, J. Swaroop Guntupalli¹⁹, Mark Jenkinson², Anisha Keshavan²⁰, Gregory Kiar^{21,22}, Franziskus Liem²³, Pradeep Reddy Raamana^{24,25}, David Raffelt²⁶, Christopher J. Steele^{7,8}, Pierre-Olivier Quirion¹⁵, Robert E. Smith²⁶, Stephen C. Strother^{24,25}, Gaël Varoquaux²⁷, Yida Wang⁶, Tal Yarkoni²⁸, Russell A. Poldrack¹



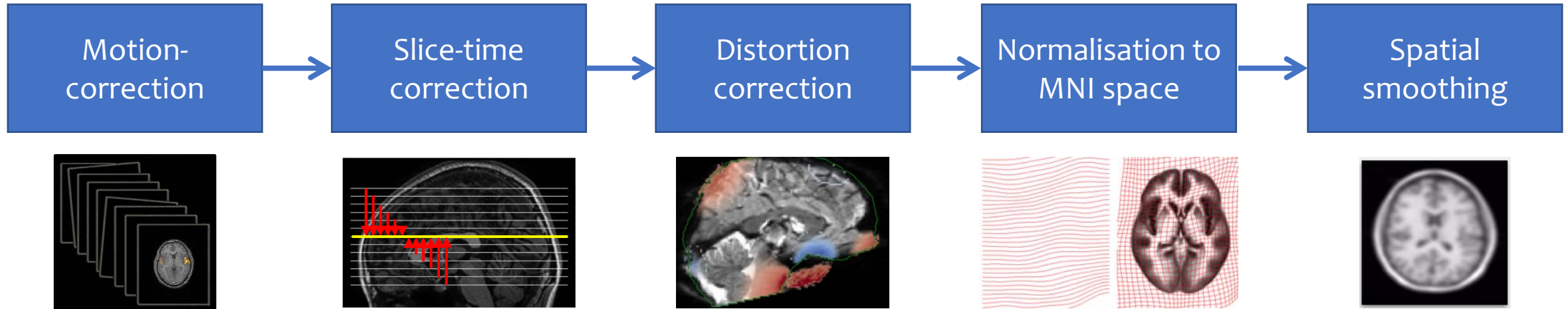
✓ Environment



Data
Organise & Manage

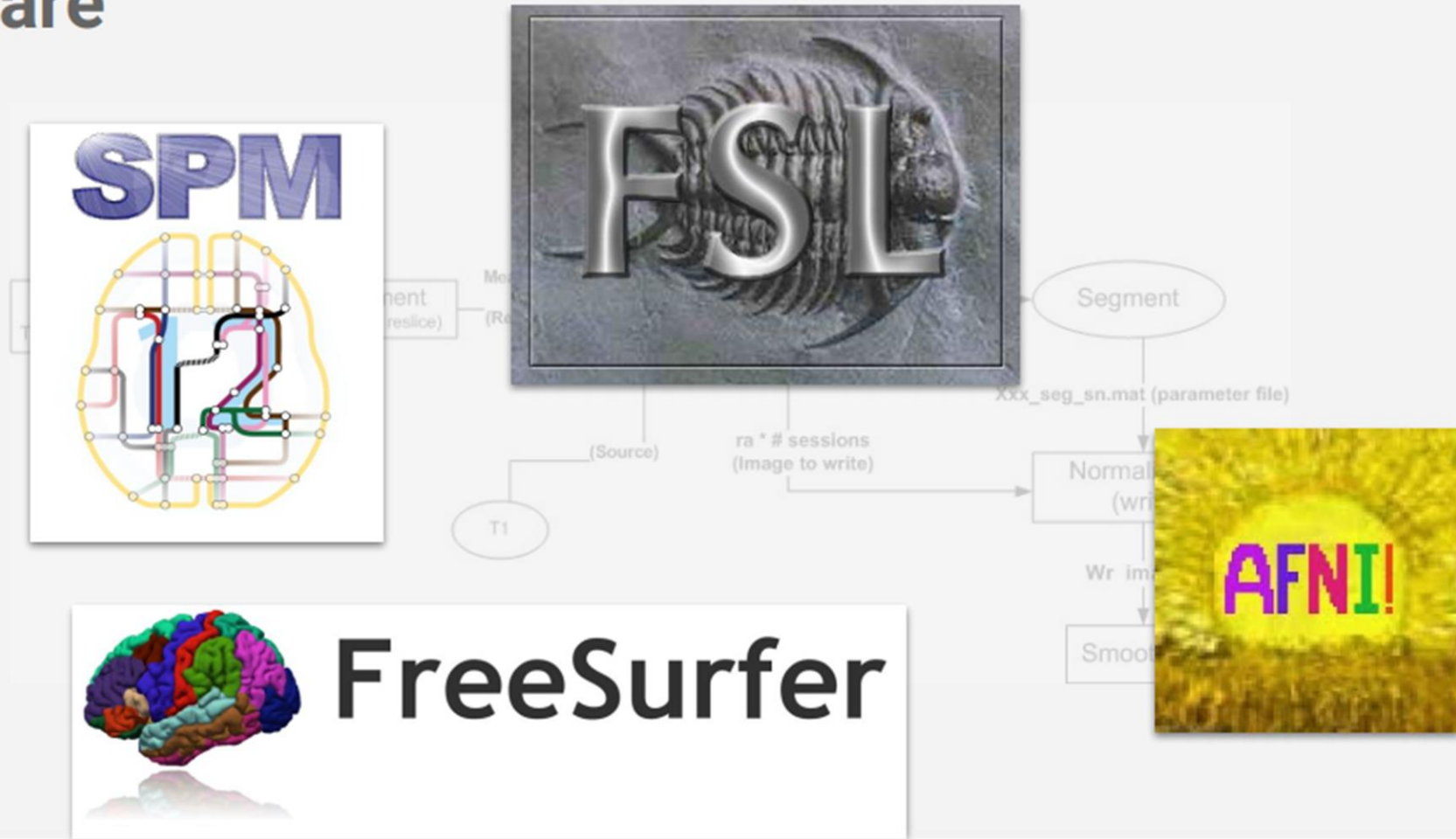
Pre-process

Typical fMRI pre-processing pipeline

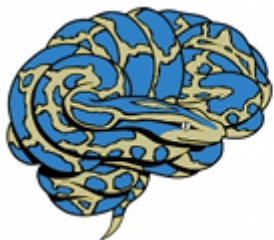


Pre-processing tools

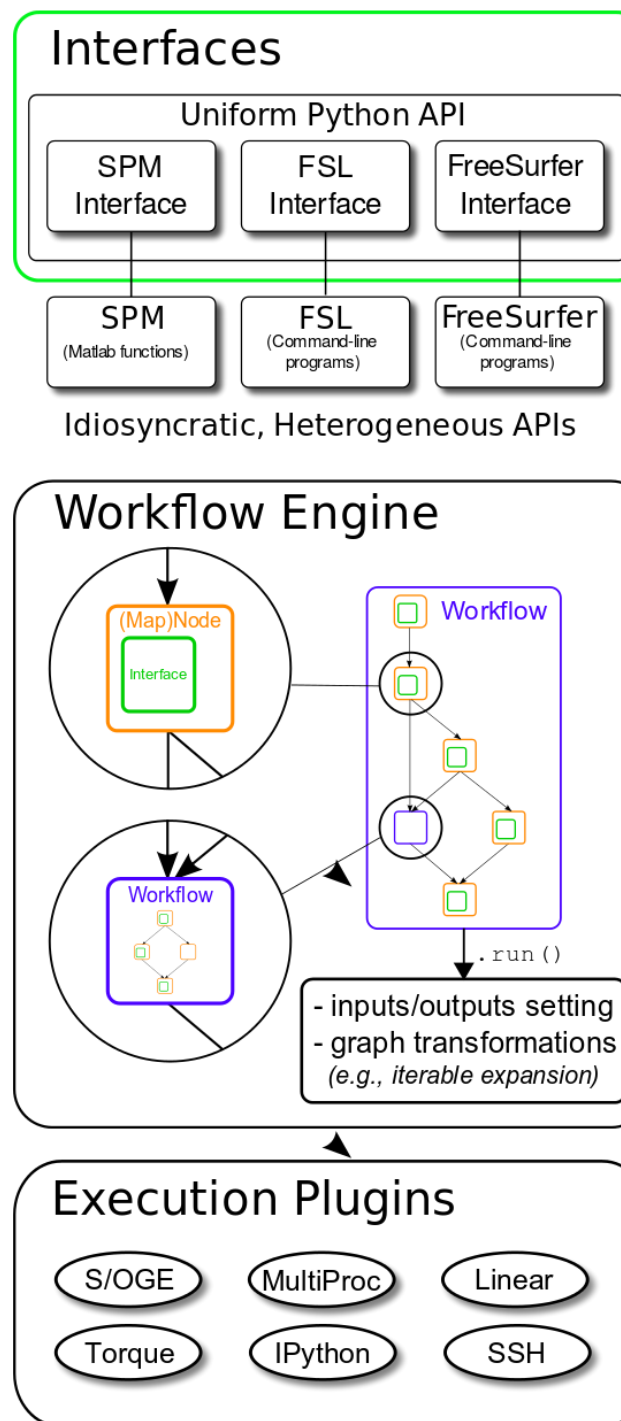
Software



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 is designed to provide the best software implementation for each state of pre-processing.
 - **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.



Environment



Data
Organise & Manage



Pre-process

Analyse

GLM: $Y = X\beta + \varepsilon$

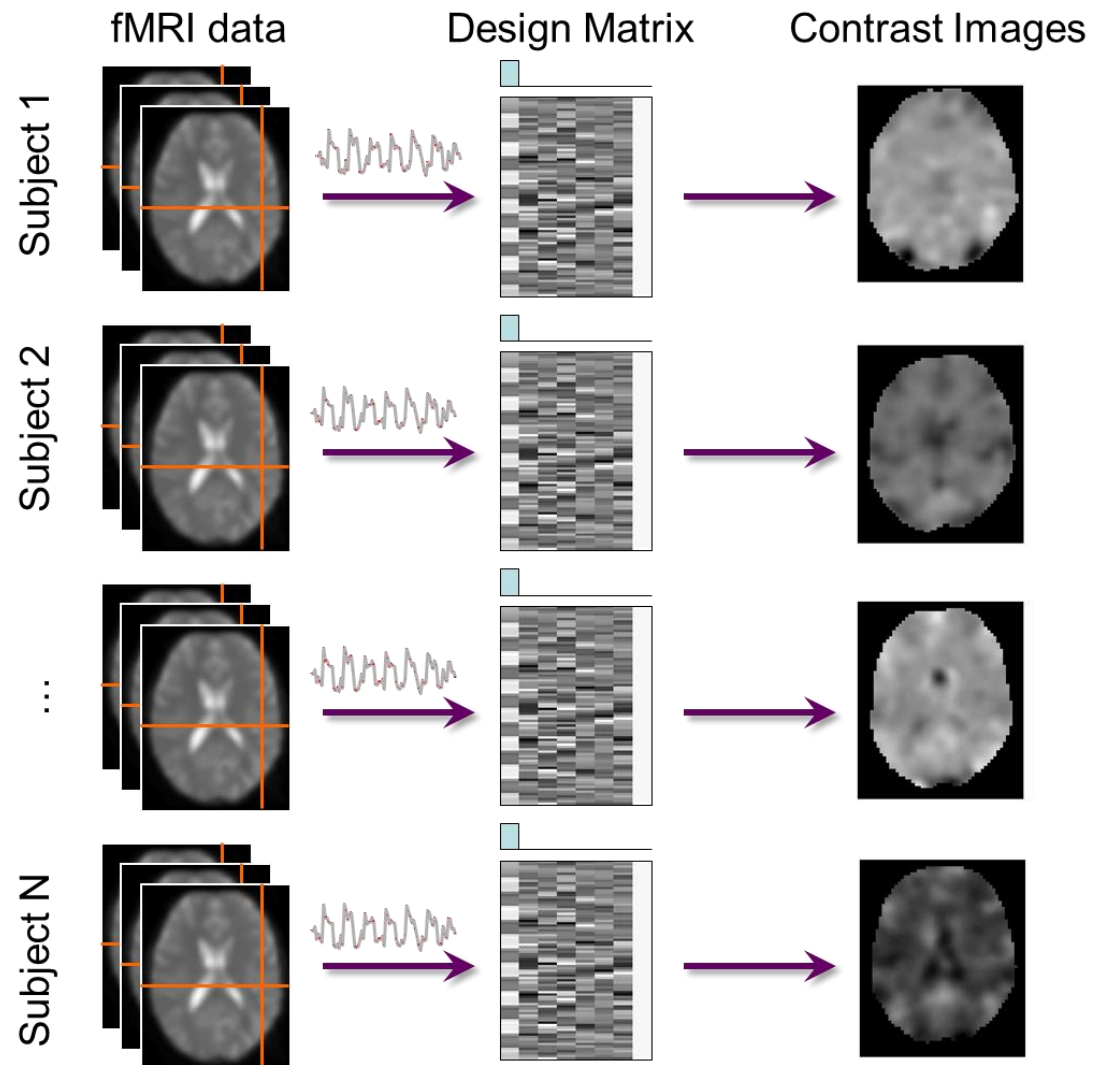
$$\text{BOLD signal} = \underbrace{X * b}_{\substack{\text{explained variation} \\ \text{task-related activity changes}}} + \underbrace{\text{errors}}_{\substack{\text{unexplained variation} \\ \text{noise (other changes)}}}$$

- **What we know?**
 - **BOLD signal**: we collect this from the brain (functional data)
 - **X**: the design matrix (each column is a predictor that we build ourselves)
- **What we want to find?**
 - **b**: vector of beta-weights (one weight for predictor in X) that give the best approximation of the BOLD signal
- **How we find it?**
 - By **minimising the sum of squared errors**. In practice, the **GLM** has a formula, which guarantees to find these beta-weights

1. **Extract the signal time-series** from a given voxel
2. **Run GLM** (the signal and the design matrix are the inputs) to **find beta-weights** that best approximate the true signal
3. Define your **contrast** and test it
4. Repeat for **all voxels**
 - Produces an image file with contrast values for each voxel: **contrast-maps**

First-level analysis

- Run the GLM for each subject



Group level (2nd level) analysis is across subjects

- Which voxels are showing significant activation differences between our conditions consistently **within a group**
- Importantly, all subject brains need to be in a common space, e.g. MNI, to perform voxel-wise group analyses



Environment



Data Organise & Manage



Pre-process



Analyse

Report

Sharing & Reporting



- Share your **code** and notebooks on GitHub



- Make it **citable** with Zenodo
 - <https://docs.github.com/en/repositories/archiving-a-github-repository/referencing-and-citing-content>



- If you have consent from participants, share the **BIDS data** on OpenNeuro.



- Add your **contrast maps** to NeuroVault

The Plan

1

Data
Organisation



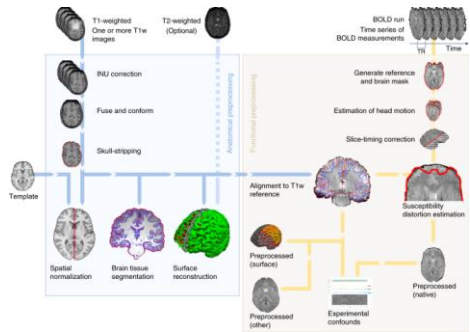
2

MRI Data
Manipulation

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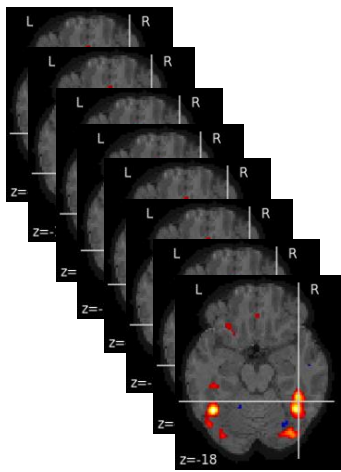
3

Quality Control &
Pre-processing



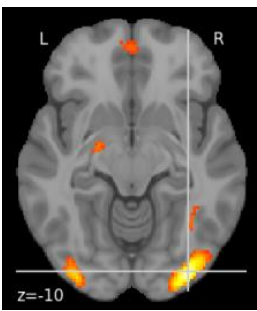
4

Subject-Level
Analysis



5

Group-Level
Analysis



6

ROI
Analysis

