



The future is now: new innovations in the field of neuroimaging

pybrain workshop - MRC Cognition & Brain Science Unit, Cambridge

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November, 2020



Disclaimer:

The things we're going to present within this presentation are only a subset of everything there is, heavily biased towards our experience/knowledge and by no means complete.

We are aware that there is much more out there and would love suggestions, additions and feedback.

Core aspects of community driven development



- open & reproducible neuroscience
- standardization
- data management
- FAIR neuroscience
- community engagement & support
- inclusive neuroscience

Thinking about the entire research workflow



- adding alternative evaluation, e.g. with altmetrics
- communicating through social media, e.g. Twitter
- sharing posters & presentations, e.g. at FigShare
- using open licenses, e.g. CC0 or CC-BY
- publishing open access, 'green' or 'gold'
- using open peer review, e.g. at journals or PubPeer
- sharing preprints, e.g. at OSF, arXiv or bioRxiv
- using actionable formats, e.g. with Jupyter or CoCalc
- open XML-drafting, e.g. at Overleaf or Authorea
- sharing protocols & workfl., e.g. at Protocols.io
- sharing notebooks, e.g. at OpenNotebookScience
- sharing code, e.g. at GitHub with GNU/MIT license
- sharing data, e.g. at Dryad, Zenodo or Dataverse
- pre-registering, e.g. at OSF or AsPredicted
- commenting openly, e.g. with Hypothes.is
- using shared reference libraries, e.g. with Zotero
- sharing (grant) proposals, e.g. at RIO



Bianca Kramer & Jeroen Bosman <https://101innovations.wordpress.com>

DOI: 10.5281/zenodo.1147025

Roadmap

BIDS

the idea converters validator extensions

BIDS Apps

mriqc mindboggle fmriprep fmridenoise qsiprep C-PAC fitlins

python packages

NiMARE brainspace tedana nobrainer nighres MNE dipy

amazing things

OBC Neurodocker Porcupine brainlife neuroscout OpenNeuro Neurovault Neurosynth
Neuroquery DataLad ReproNim Neurolibre Neurostars brainhack

BIDS - the idea

How do you manage your data?

- storage, structure, metadata, version control?

How do you share your data?

- colleagues, students, other researchers?

**The Problem with heterogeneity in data management
hard for others (and you) to understand your data and keep
track of changes**

- unnecessary metadata input
- codes / scripts have to be adapted
- huge effort to automate workflows and no way to automatically validate data sets
- sharing data becomes a hustle

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/

BIDS - the idea

* content liberally borrowed from
Chris Markiewicz's [BIDS ecosystem presentation](#)

- **BIDS** is a directory structure, based on common practices
- builds on existing standards (NIfTI, JSON, TSV)
- intended for human and machine legibility
- the BIDS Validator makes compliance easy to verify
- the specification is a searchable HTML document



<https://bids-specification.readthedocs.io/en/stable/>
<https://bids.neuroimaging.io/>

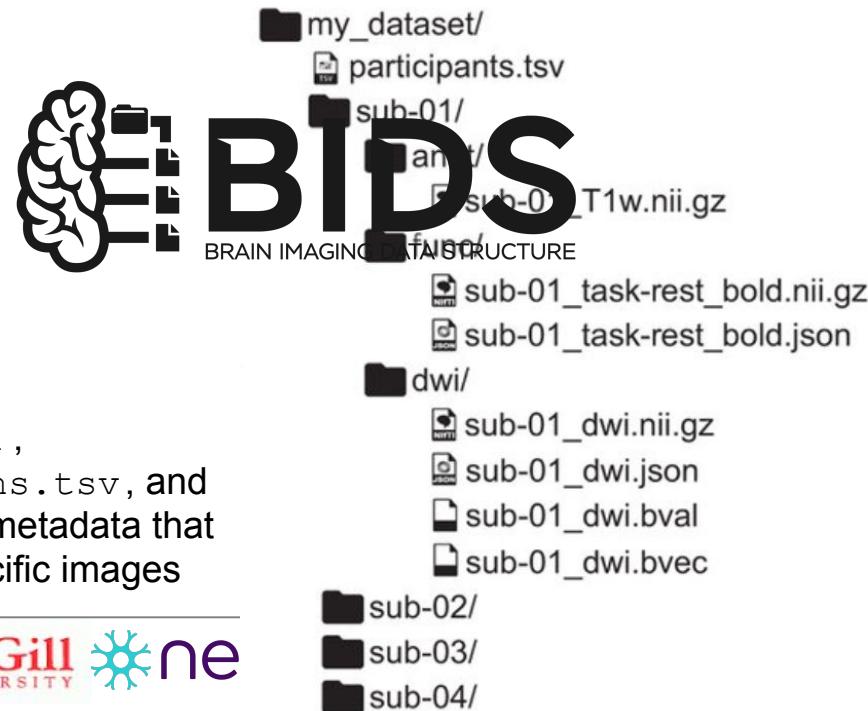
```
my_dataset/
  participants.tsv
  sub-01/
    anat/
      sub-01_T1w.nii.gz
    func/
      sub-01_task-rest_bold.nii.gz
      sub-01_task-rest_bold.json
    dwi/
      sub-01_dwi.nii.gz
      sub-01_dwi.json
      sub-01_dwi.bval
      sub-01_dwi.bvec
  sub-02/
  sub-03/
  sub-04/
```

BIDS - the idea

* content liberally borrowed from
Chris Markiewicz's [BIDS ecosystem presentation](#)

- Basic metadata in the file names
 - Subject, session, imaging modality, etc.
 - Generally just enough to assign unique names
- NIFTI headers and JSON sidecars contain detailed, image-related metadata
- `dataset_description.json`, `participants.tsv`, `sessions.tsv`, and `scans.tsv` record study-level metadata that may not be associated with specific images

<https://bids-specification.readthedocs.io/en/stable/>
<https://bids.neuroimaging.io/>

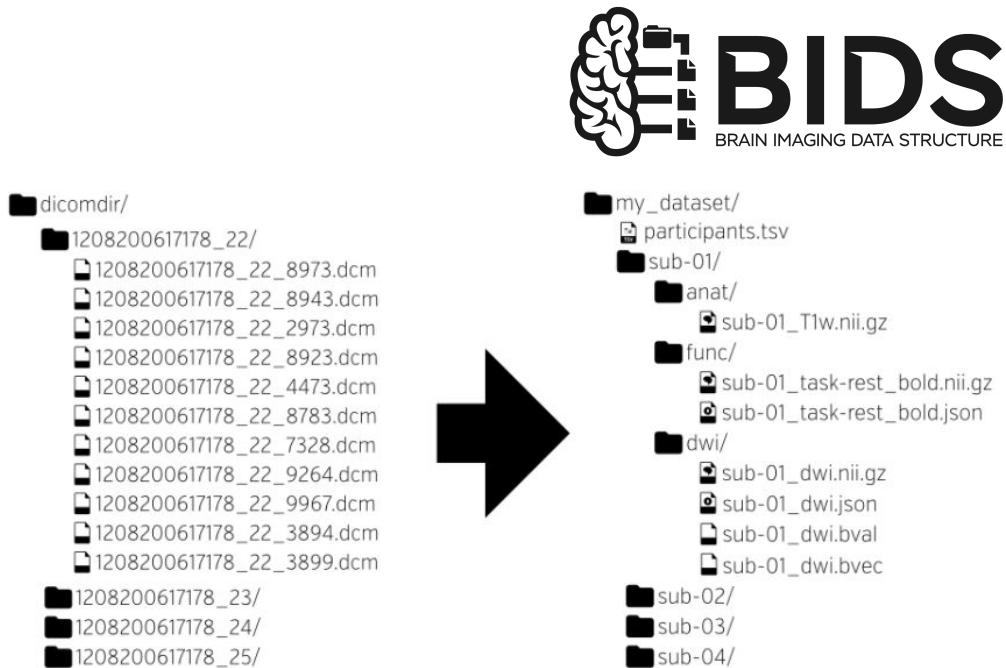


BIDS - converters

* content liberally borrowed from
Chris Markiewicz's [BIDS ecosystem presentation](#)

- three main scenarios:
 - data already converted & no access to DICOMs
 - data already converted & access to DICOMs
 - data still in DICOM
- scenario one clearly suboptimal, however there are converters for almost every situation
- AFNI BIDS-tools, BIDS2ISATab, BIDSTo3col, BIDS2NDA, bidskit, dac2bids, Dcm2bids, heudiconv, DCM2NIIx, ReproIN, XNAT2BIDS...

<https://bids-specification.readthedocs.io/en/stable/>
<https://bids.neuroimaging.io/>

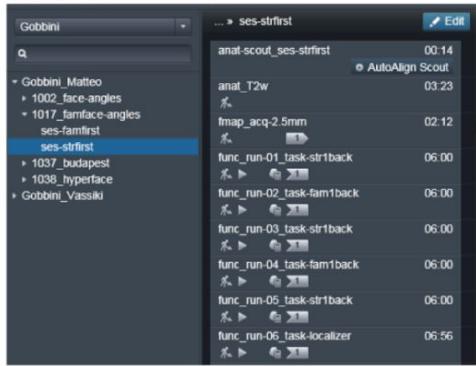


BIDS - converters

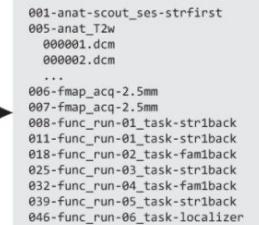
* content liberally borrowed from

Chris Markiewicz's [BIDS ecosystem presentation](#)

Scanner



DICOM



\$ heudiconv
Data
had

BIDS

```
anat
  sub-sid000005_ses-fstrfirst_T2w.json
  sub-sid000005_ses-fstrfirst_T2w.nii.gz
fmap
  sub-sid000005_ses-fstrfirst_acq-25mm_magnitude1.json
  sub-sid000005_ses-fstrfirst_acq-25mm_magnitude1.nii.gz
...
func
  sub-sid000005_ses-fstrfirst_task-famback_run-02_bold.json
  sub-sid000005_ses-fstrfirst_task-famback_run-02_bold.nii.gz
  sub-sid000005_ses-fstrfirst_task-famback_run-02_events.tsv
...
sub-sid000005_ses-fstrfirst_scans.tsv
```

From ReproIn; doi:10.5281/zenodo.3625000

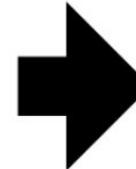
<https://bids-specification.readthedocs.io/en/stable/>
<https://bids.neuroimaging.io/>



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/
```



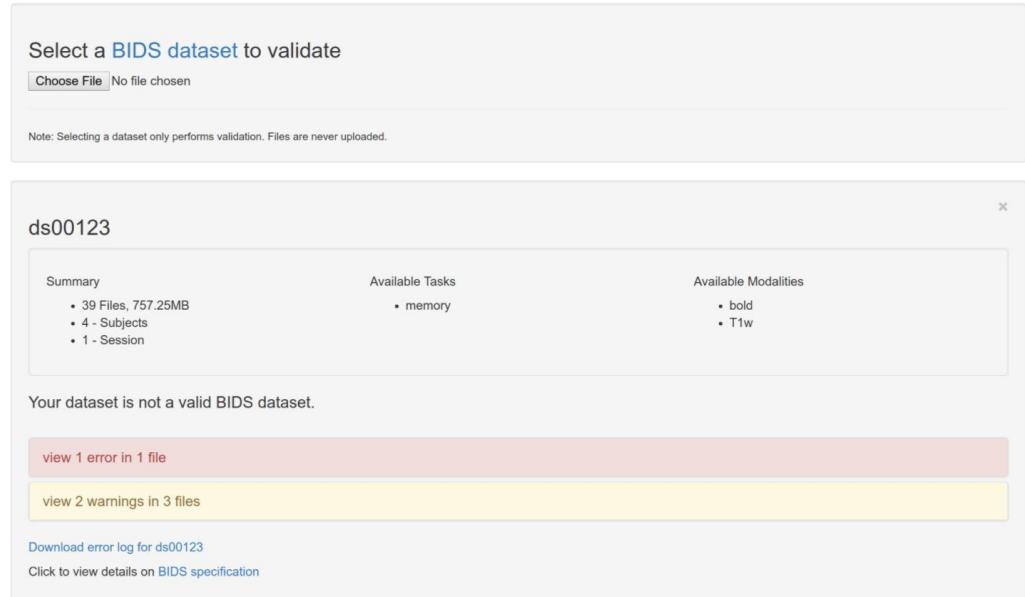
```
my_dataset/
  participants.tsv
  sub-01/
    anat/
      sub-01_T1w.nii.gz
    func/
      sub-01_task-rest_bold.nii.gz
      sub-01_task-rest_bold.json
    dwi/
      sub-01_dwi.nii.gz
      sub-01_dwi.json
      sub-01_dwi.bval
      sub-01_dwi.bvec
  sub-02/
  sub-03/
  sub-04/
```

BIDS - validator

* content liberally borrowed from
Chris Markiewicz's [BIDS ecosystem presentation](#)

- BIDS' machine readable structure makes automated validation possible and easy
- BIDS-validator does a comprehensive check
- three options to run it:
 - npm module
 - container
 - web version

<https://bids-specification.readthedocs.io/en/stable/>
<https://bids.neuroimaging.io/>
<https://bids-standard.github.io/bids-validator/>



The screenshot shows the BIDS-validator web application interface. At the top, there is a header with the text "Select a BIDS dataset to validate" and a "Choose File" button with the placeholder "No file chosen". Below this, a note states: "Note: Selecting a dataset only performs validation. Files are never uploaded." The main content area displays a dataset named "ds00123". It has three columns: "Summary", "Available Tasks", and "Available Modalities". The "Summary" column lists: "• 39 Files, 757.25MB", "• 4 - Subjects", and "• 1 - Session". The "Available Tasks" column lists: "• memory". The "Available Modalities" column lists: "• bold" and "• T1w". Below the summary, a message says "Your dataset is not a valid BIDS dataset." A red button labeled "view 1 error in 1 file" is visible. A yellow button labeled "view 2 warnings in 3 files" is also visible. At the bottom, there are links: "Download error log for ds00123" and "Click to view details on BIDS specification".

BIDS - validator

* content liberally borrowed from
Chris Markiewicz's [BIDS ecosystem presentation](#)

ds00123

Summary	Available Tasks	Available Modalities
<ul style="list-style-type: none">• 39 Files, 757.25MB• 4 - Subjects• 1 - Session	<ul style="list-style-type: none">• memory	<ul style="list-style-type: none">• bold• T1w

Your dataset is not a valid BIDS dataset.

[view 1 error in 1 file](#)

Error: 1 1 file

Repetition time did not match between the scan's header and the associated JSON metadata file.

sub-04_ses-01_task-memory_run-03_bold.nii.gz 55354.461 KB | application/gzip

Location: ds00123/sub-04/ses-01/func/sub-04_ses-01_task-memory_run-03_bold.nii.gz

Reason: Repetition time defined in the JSON (2.007 sec.) did not match the one defined in the NIFTI header (1.99 sec.)

[view 2 warnings in 3 files](#)

<https://bids-specification.readthedocs.io/en/stable/>
<https://bids.neuroimaging.io/>
<https://bids-standard.github.io/bids-validator/>

ds00123

Summary	Available Tasks	Available Modalities
<ul style="list-style-type: none">• 39 Files, 757.25MB• 4 - Subjects• 1 - Session	<ul style="list-style-type: none">• memory	<ul style="list-style-type: none">• bold• T1w

Your dataset is not a valid BIDS dataset.

[view 1 error in 1 file](#)

[view 2 warnings in 3 files](#)

Warning: 1 1 file

Not all subjects contain the same files. Each subject should contain the same number of files with the same naming unless some files are known to be missing.

sub-02_ses-01_T1w.nii.gz NaN KB |

Location: /sub-02/ses-01/anat/sub-02_ses-01_T1w.nii.gz

Reason: This file is missing for subject sub-02, but is present for at least one other subject.

Warning: 2 2 files

Not all subjects/sessions/runs have the same scanning parameters.

BIDS - extensions

* content liberally borrowed from
Chris Markiewicz's [BIDS ecosystem presentation](#)

- BIDS is constantly expanded & updated through community driven development

- Positron Emission Tomography (PET)
- Common Derivatives
- Models Specification
- Magnetoencephalography (MEG)
- Electroencephalography (EEG)
- intracranial Electroencephalography (iEEG)
- Eye Tracking including Gaze Position and Pupil Size
- Susceptibility Weighted Imaging (SWI)
- Genetic information
- Microelectrode Recordings (MER)

<https://bids-specification.readthedocs.io/en/stable/>
<https://bids.neuroimaging.io/>

Extension label	Title	Moderators/leads	Test name
BEP003	Common Derivatives	Chris Markiewicz	
BEP005	Electromyography (EMG)	Cyril Perinet, Stefan Appelhoff, Robert Condorelli	
BEP007	Hierarchical Event Descriptor (HED) Tags	Chris Gorgolewski	
BEP008	Magnetoencephalography(MEG)	Guoming Nao	
BEP010	intracranial Electroencephalography (iEEG)	Chris Holstig, Dora Hernes	
BEP018	Genetic Information	Cyril R Perinet, Clémie Moreau, Thomas Nichols	
Some proposals that set out to extend the BIDS specification have instead become tools for handling BIDS. See the table below.			
Extension label	Title	Moderators/leads	Test name
BEP015	Mapping file	Eric Earl, Camille Maumet, and Vassilios Ragouam	file mapper

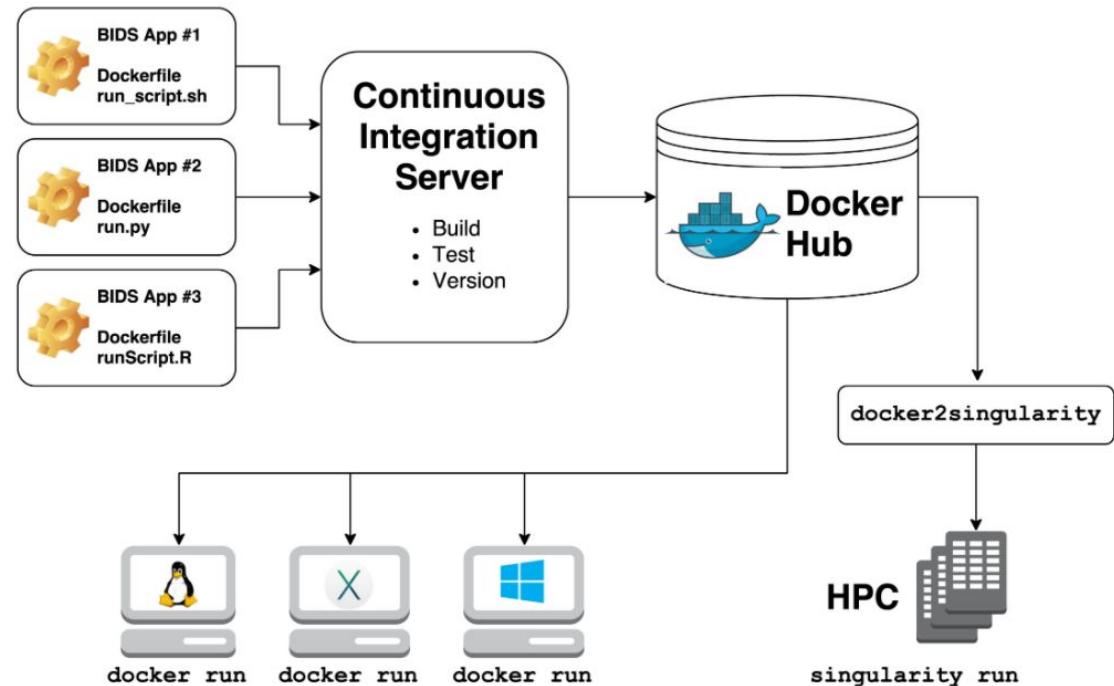
Extension label	Title	Moderators/leads	Summary	Testing priority
BEP001	Structural derivatives that contain multiple subjects (e.g., multi-subject brain activation maps)	Oliver Giedd, and Kristin Weller	BIDS has been submitted as a pull request.	None
BEP041	The BIDS Model Specification	Tat Yarkoni	Recently went through several iterations, and is being used in several papers.	Reviewing and testing
BEP044	Susceptibility Weighted Imaging (SWI)	Available	Looking for a new maintainer.	Searching for a new maintainer
BEP053	Atrial Spin Lesions (ASL)	Mark J. Szaflarski, Jennifer L. Pae, Marco J. Caramella	BIDS is close to being merged with BIDS, and is accompanied with a pull request.	None
BEP055	Positron Emission Tomography (PET)	Madeline Gure	BIDS is close to being merged with BIDS, and is accompanied with a pull request.	None
BEP057	The structural preparation extension	Viktor Blasie	Upcoming. Need to incorporate the current version of the GitHub repository.	None
BEP058	The functional imaging derivatives extension	Gentle Maitland and Diane Gholson	Upcoming. Need to incorporate the current version of the GitHub repository.	None
BEP059	The resting-state fMRI derivatives extension	Daniel Giedd	Upcoming to BIDS.	None
BEP064	The active derivatives and nonlinear field maps extension	Eric Markiewicz	A proposal to add an active spatial registration extension, and a pull request has been submitted. This is the first step towards the usage of the BIDS framework for active spatial registration, and is currently in progress.	In progress
BEP065	The diffusion susceptibility derivatives extension	Ricardo Henriquez and Daniel Gholson	Being discussed in GitHub repository.	None
BEP071	Genetic BIDS uncertainty data storage	Eugenie Huff and Paul MacCaffery	This BIDS is now using BIDS specific storage, and is no longer maintained by the original project.	None
BEP073	DCIM Metadata	Nicolas Gobet	No active, perhaps this is an old BIDS extension, and is no longer maintained by the original project, rather than in BIDS.	None
BEP075	Eye tracking including Gaze Position and Pupil Size	Ben Hinkin	BIDS is close to being merged with BIDS, and is accompanied with a pull request.	None
BEP077	Connectome Derivatives	Matthew J. Haggar, Michael A. Arghamani, and Michael A. Giedd	Currently under development. The maintainers are the ones that are maintaining this extension. It is a derivative of the Connectome BIDS extension.	None
BEP078	Magnetic Resonance Spectroscopy (MRS)	Mark J. Szaflarski and William J. Pae	Group discussion underway.	None
BEP083	PET Processing derivatives extension	Matthew Mairagam, Daniel Sznajder, Madeline Gure	A looking for a maintainer for this extension, which is currently maintained by the PET project.	None
BEP094	Urinary Derivatives extension	Jean Michael	Last meeting quite a few months ago, and is no longer maintained.	None
BEP095	Medical Imaging Data Structures (MIMIC)	John M. Pauly, Tomas, Mario, and Michael	Preparing to submit, this extension is currently in the process of becoming a pull request.	None
BEP097	Microworlds Derivatives	Stephen Gómez	Focusing on: microworlds, and how to make them more useful for research.	None
BEP097	BIDS Evaluation	Chris Gorgolewski and Geoff Neal	Chris Gorgolewski and Geoff Neal are currently working on this extension, and are looking for future maintainers.	None
BEP104	Powerline	Sylvia Martinelli and Camille Maumet	New BIDS activity continues, and is currently in the process of becoming a pull request.	None
BEP106	Virtual and physical motion data	Sam Joring and Michael Weller	New BIDS activity continues, and is currently in the process of becoming a pull request.	None
BEP107	New Infrared Motion Capture	Robert Luke and Michael Weller	New BIDS activity continues, and is currently in the process of becoming a pull request.	None
BEP107	Microscopy	Marko Matijevic, John Colton, and Michael Weller	New BIDS activity continues, and is currently in the process of becoming a pull request.	None

BIDS Apps

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

* content liberally borrowed from
Chris Markiewicz's [BIDS ecosystem presentation](#)

- containerized pipelines/workflow that understand BIDS datasets
- set of core command line arguments
- should not depend on software outside the container
- hosted on docker/singularity hub and includes version tags
- targeting automated and standardized analyses that are reproducible



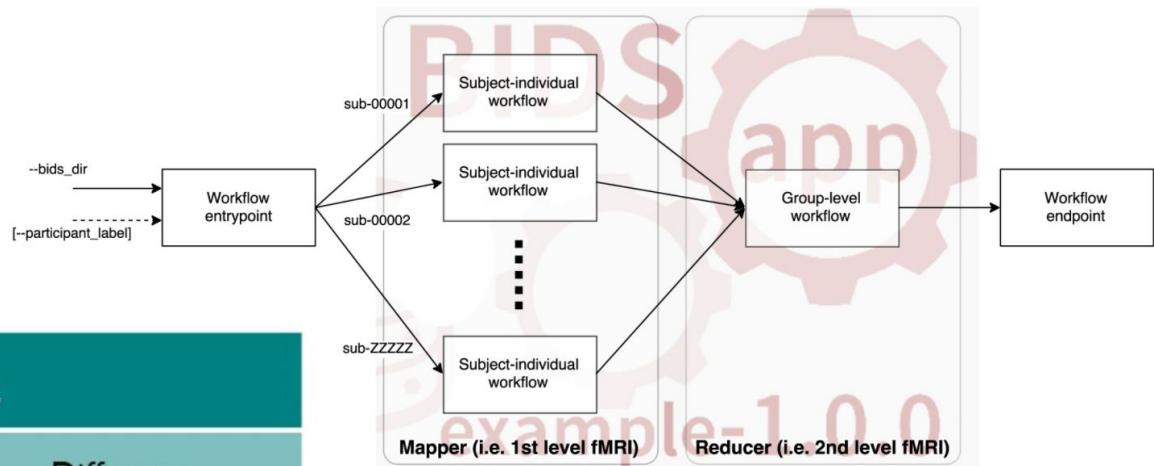
From doi:10.1371/journal.pcbi.1005209.g001

BIDS Apps

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

* content liberally borrowed from
Chris Markiewicz's [BIDS ecosystem presentation](#)

- a lot of sources of analyses/results variability (OS, dependencies, etc.)

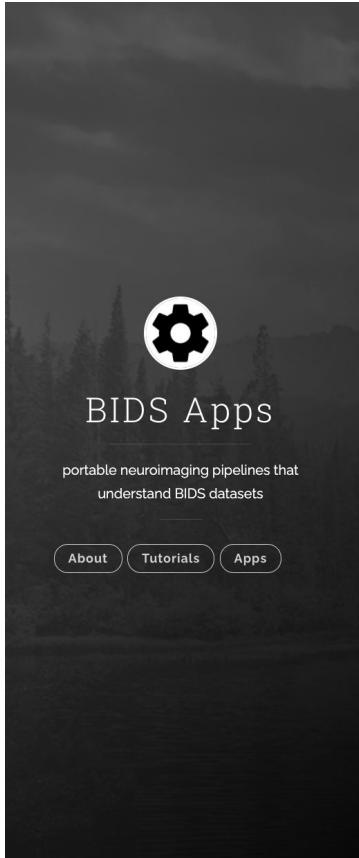


From doi:10.1371/journal.pcbi.1005209.g002

		Data	
		Same	Different
Analysis	Same	Reproducible	Replicable
	Different	Robust	Generalisable

From The Turing Way, Ch. 2; doi:10.5281/zenodo.3233853

- BIDS Apps aims to address aspects of this problem via a common interface, container technologies and standardization
- open analyses on (open) data



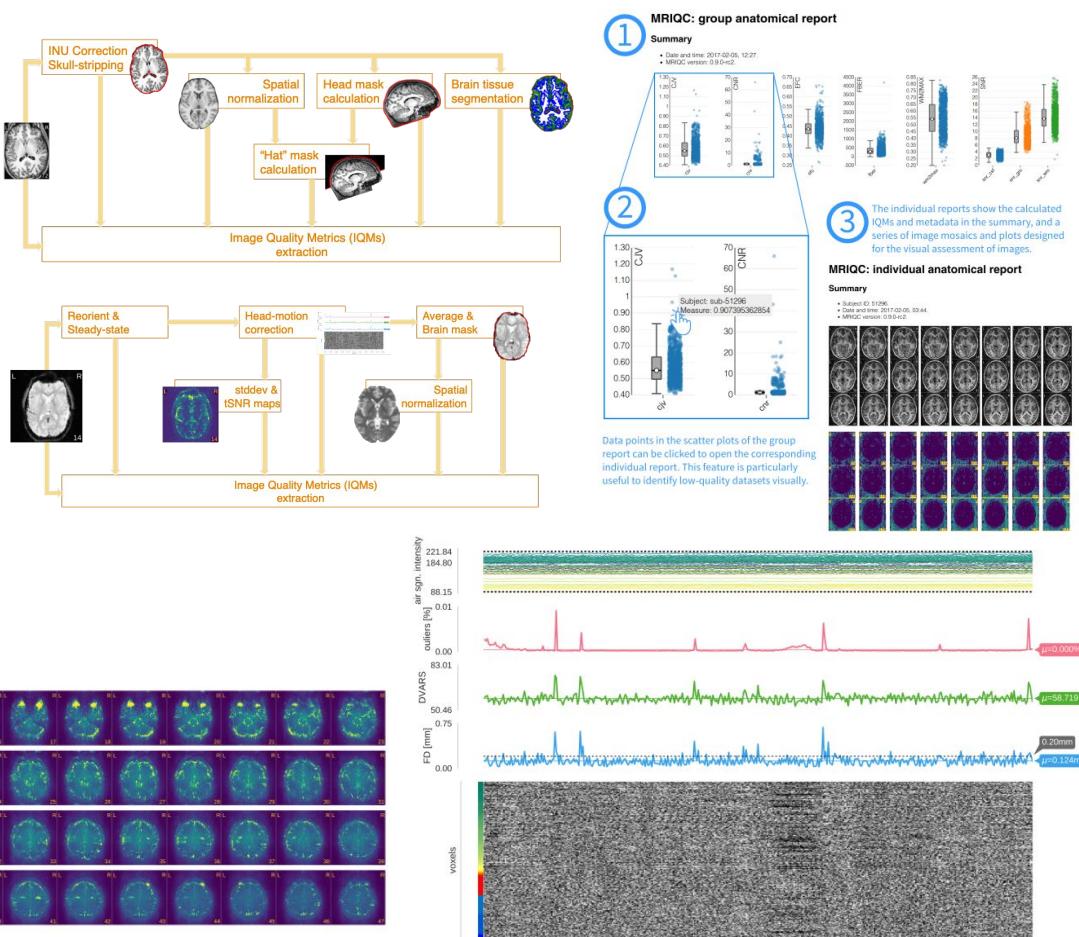
Available BIDS Apps

BIDS-Apps/example	version v0.0.7	open issues 5	circled passing	open bug pull requests 0	docker pulls 14k	439.5MB 23 layers
BIDS-Apps/freesurfer	version v6.0.1-6.1	open issues 13	circled passing	open bug pull requests 0	docker pulls 11k	2.6GB 52 layers
BIDS-Apps/ndmg	version v0.1.0	open issues 1	circled passing	open bug pull requests 0	docker pulls 8k	920.9MB 31 layers
BIDS-Apps/BROCCOLI	version v1.0.1	open issues 6	circled passing	open bug pull requests 0	docker pulls 522	3GB 21 layers
BIDS-Apps/FibreDensityAndCrosssection	version v0.0.1	open issues 17	circled passing	open bug pull requests 0	docker pulls 259	576.8MB 31 layers
BIDS-Apps/SPM	version v0.0.20	open issues 3	circled passing	open bug pull requests 0	docker pulls 1.5k	2GB 24 layers
poldracklab/mriqc	version v0.15.3	open issues 125	circled passing	open bug pull requests 0	docker pulls 68k	3GB 41 layers
BIDS-Apps/QAP	version v0.0.1	open issues 5	circled passing	open bug pull requests 0	docker pulls 7	Image not found
BIDS-Apps/CPAC	version v1.0.1a_22	open issues 10	circled passing	open bug pull requests 0	docker pulls 3.2k	1.6GB 45 layers
BIDS-Apps/hyperalignment	version v0.0.9	open issues 0	circled passing	open bug pull requests 0	docker pulls 169	Image not found
BIDS-Apps/mindboggle	version v0.0.4-1	open issues 8	circled passing	open bug pull requests 0	docker pulls 752	1.9GB 81 layers
BIDS-Apps/MRtrix3_connectome	version v0.4.2	open issues 31	circled passing	open bug pull requests 0	docker pulls 1.4k	7.3GB 56 layers
BIDS-Apps/rs_signal_extract	version v0.1	open issues 9	circled passing	open bug pull requests 0	docker pulls 238	240MB 17 layers
BIDS-Apps/aa	version v0.2.0	open issues 2	circled passing	open bug pull requests 0	docker pulls 272	6.3GB 30 layers
BIDS-Apps/niak	version v1.0	open issues 3	circled passing	open bug pull requests 0	docker pulls 279	2.7GB 103 layers
BIDS-Apps/oppni	version v0.7.0-1	open issues 5	circled passing	open bug pull requests 0	docker pulls 315	2.9GB 41 layers
poldracklab/fmriprep	version v20.2.0	open issues 192	circled passing	open bug pull requests 0	docker pulls 376k	5GB 49 layers
BIDS-Apps/brainiak-srm	version v0.0.1	open issues 0	circled failing	open bug pull requests 0	docker pulls 207	559.3MB 11 layers
BIDS-Apps/nipypipelines	version v0.3.0	open issues 9	circled passing	open bug pull requests 0	docker pulls 381	478.1MB 20 layers
BIDS-Apps/HCPPipelines	version v4.1.3	open issues 7	circled passing	open bug pull requests 0	docker pulls 1.9k	4GB 31 layers
BIDS-Apps/MAGEtbrain	version v0.3.1	open issues 2	circled passing	open bug pull requests 0	docker pulls 466	Image not found
BIDS-Apps/tracula	version v6.0.0-5	open issues 0	circled passing	open bug pull requests 0	docker pulls 689	3.4GB 57 layers
BIDS-Apps/baracus	version v1.1.4	open issues 2	circled passing	open bug pull requests 0	docker pulls 1.2k	Image not found
BIDS-Apps/antsCorticalThickness	version v2.2.0-1	open issues 0	circled passing	open bug pull requests 0	docker pulls 207	351.9MB 21 layers

BIDS Apps - MRIQC

- QC is hard and cumbersome, additionally almost no one trained to do it
- extensive & comprehensive QC for structural & functional images
- versatile range of image quality metric (IQMs)
- intuitive output reports and summary statistics (example [structural](#), example [functional](#))
- pre-trained classifier to predict pass/fail
- docker pull poldracklab/mriqc

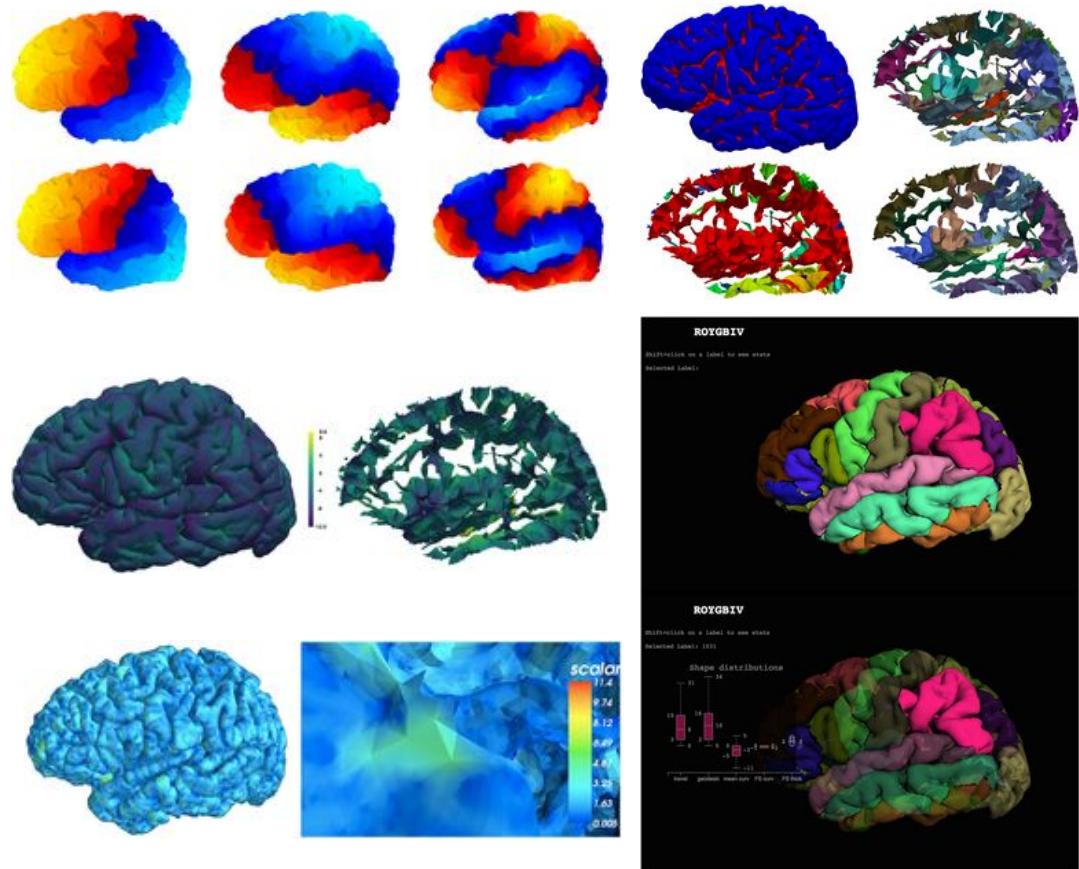
[Esteban et al. \(2017\)](#),
<https://mriqc.readthedocs.io/en/stable/index.html>



BIDS Apps - mindboggle

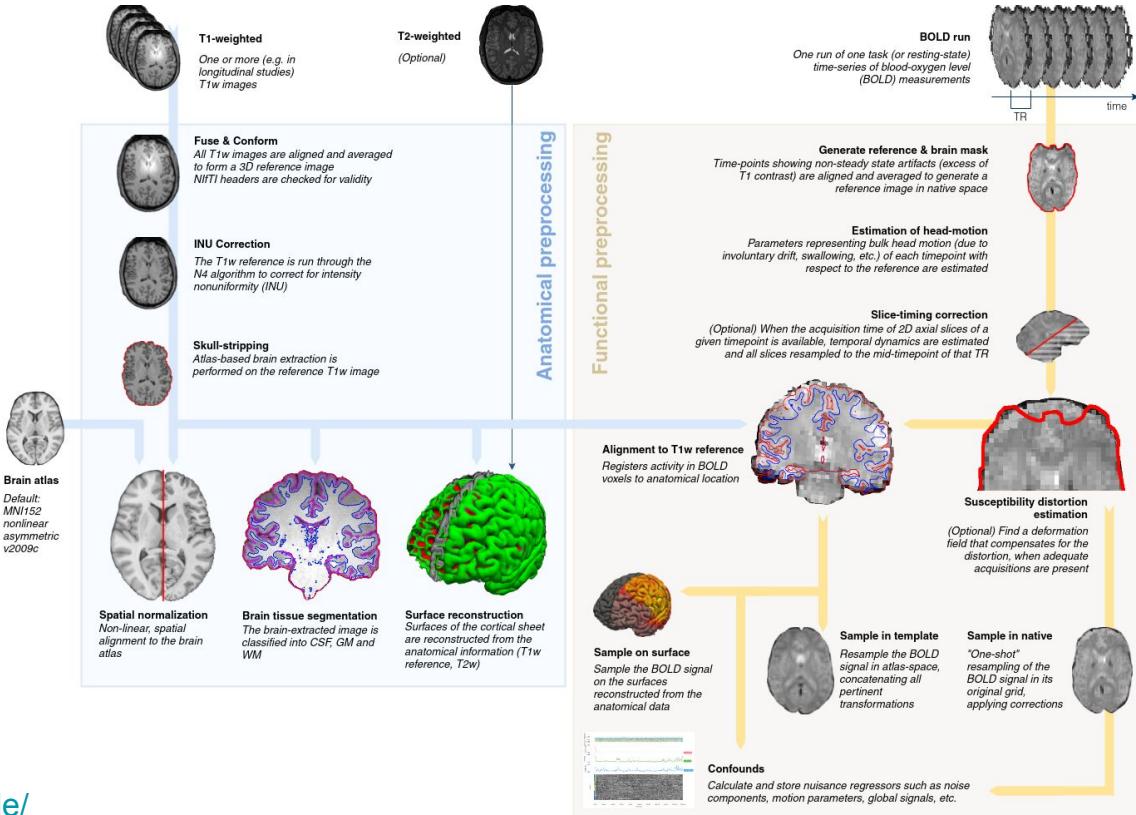
- structural features central to a lot of research questions
- extensive & comprehensive processing pipeline for structural shape features
- volume & surface based measures
- intuitive summary statistics
- docker pull bids/mindboggle

Klein et al. (2017),
<https://mindboggle.info/>



BIDS Apps - fMRIPrep

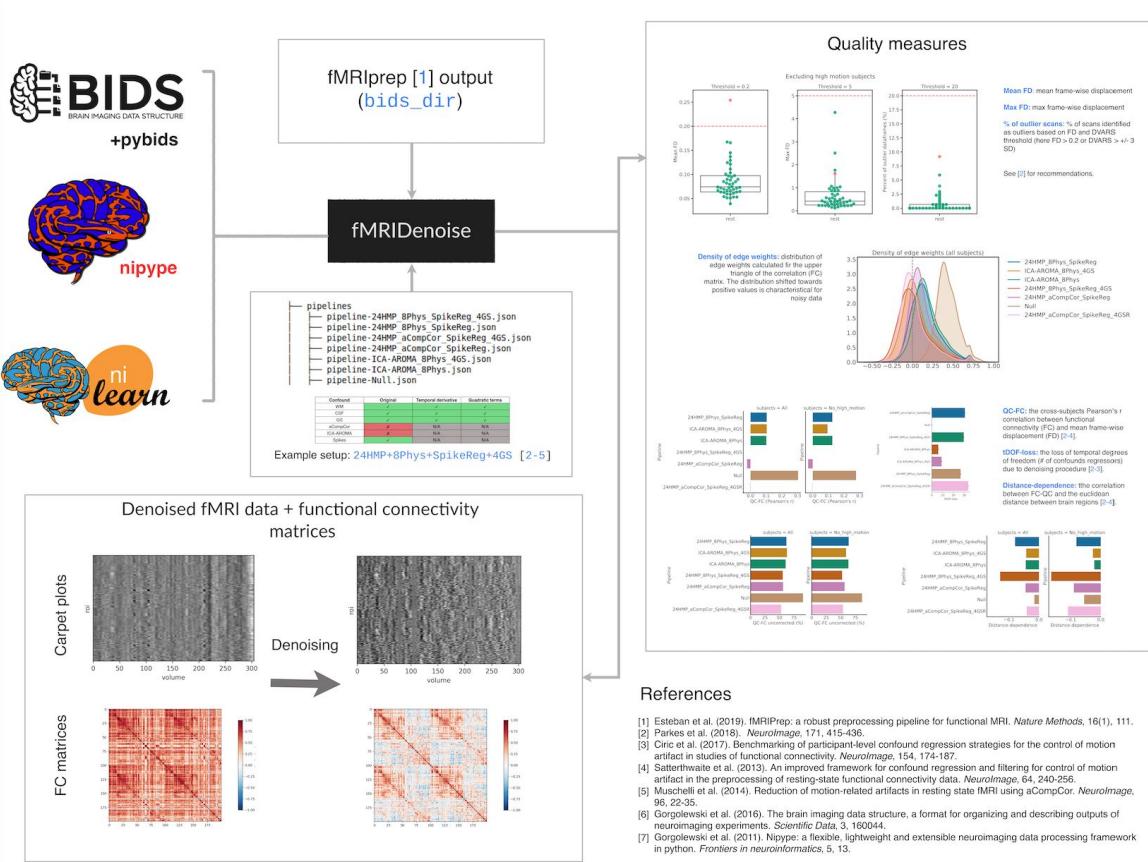
- a lot of variation and problems in preprocessing of s/fMRI data
- extensive & comprehensive preprocessing pipeline for structural & functional data
- versatile range of workflow specifications
- intuitive output reports and summary statistics (example report)
- volume/surface, output spaces, regressors
- docker pull poldracklab/fmriprep



BIDS Apps - fMRIdenoise

- a lot of options re denoising your data
- extensive & comprehensive pipeline for automatic denoising and strategy comparison
- functional connectivity QC
- intuitive output reports and summary
- docker pull (yet to come, but Dockerfile is there)

<https://github.com/compneuro-ncl/fmridenoise>



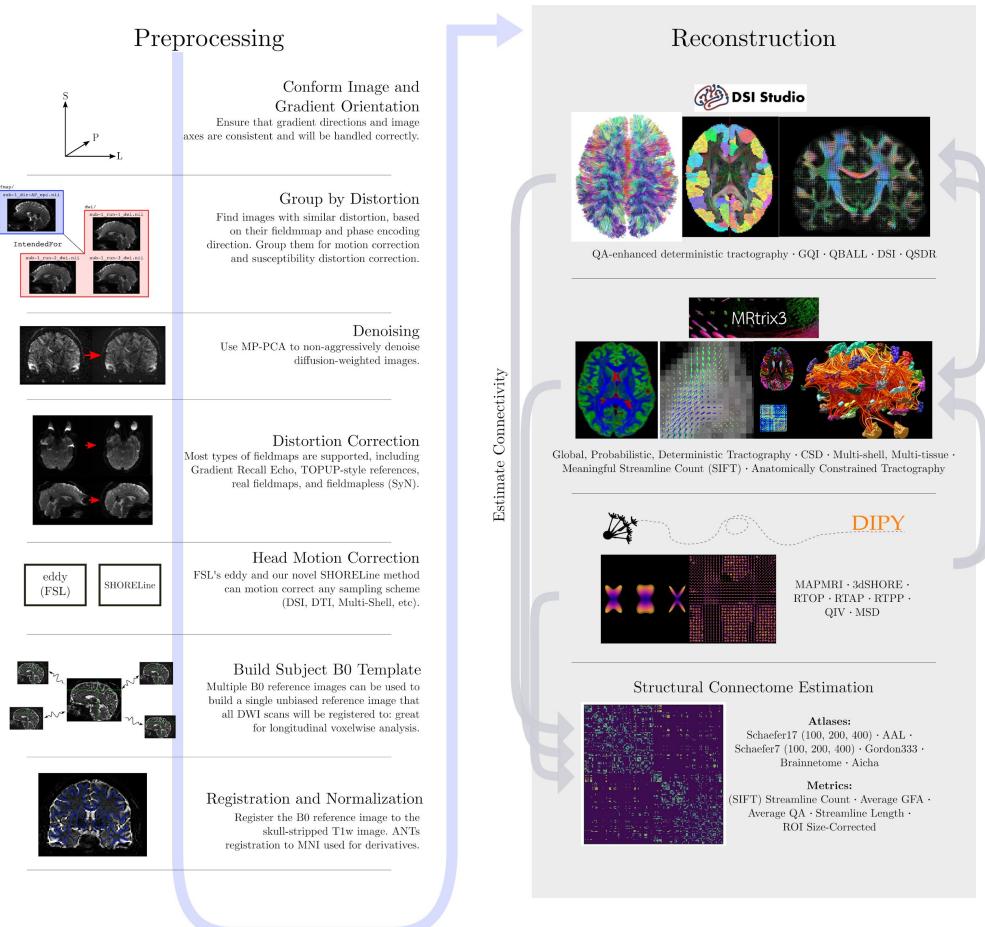
References

- [1] Esteban et al. (2019). MRIPrep: a robust preprocessing pipeline for functional MRI. *Nature Methods*, 16(1), 111.
- [2] Parkes et al. (2018). *NeuroImage*, 171, 415-436.
- [3] Ciric et al. (2017). Benchmarking of participant-level confound regression strategies for the control of motion artifact in studies of functional connectivity. *Neuroimage*, 154, 174-187.
- [4] Satterthwaite et al. (2013). An improved framework for confound regression and filtering for control of motion artifact in the preprocessing of resting-state functional connectivity data. *NeuroImage*, 64, 240-256.
- [5] Marmugi et al. (2014). Reduction of motion-related artifacts in resting state fMRI using aCompCor. *NeuroImage*, 96, 22-33.
- [6] Gorgolewski et al. (2016). The brain imaging data structure, a format for organizing and describing outputs of neuroimaging experiments. *Scientific Data*, 3, 160044.
- [7] Gorgolewski et al. (2011). Nipype: a flexible, lightweight and extensible neuroimaging data processing framework in python. *Frontiers in neuroinformatics*, 5, 13.

BIDS Apps - qsiprep

- a lot of variation and problems in preprocessing of dMRI data
- extensive & comprehensive pipeline for preprocessing, reconstruction, connectome
- provides QC & confounds
- intuitive output reports and summary statistics
- docker pull pennbbl/qsiprep

<https://qsiprep.readthedocs.io/en/latest/>



BIDS Apps - C-PAC

- a lot of variation and problems in processing of rs-fMRI data
- extensive & comprehensive pipeline for structural and functional preprocessing, seed-based analyses, ALFF, mirrored homotopic connectivity, regional homogeneity, scrubbing, bootstrap of stable clusters, connectome
- provides QC & confounds
- intuitive output reports and summary statistics
- docker pull fcpindi/c-pac

<https://fcp-indi.github.io/>

The screenshot shows the C-PAC web application interface. At the top, there is a header with the Child Mind Institute logo and the text "C-PAC". Below the header, a navigation bar includes a home icon and the word "HOME". The main content area has a teal header titled "Pipelines". Under this header, there is a list of pipeline types: "Default C-PAC 1.6.0", "Anatomical", "Functional", and "6 derivatives". There is also a "..." button. To the right of the pipelines section is a large, mostly empty teal box with a small speech bubble icon in the top right corner. Below the pipelines section is another teal header titled "About C-PAC". The text in this section describes C-PAC as an open-source pipeline for automated preprocessing and analysis of resting-state fMRI data, mentioning its build upon AFNI, FSL, and ANTS, and its user-friendly nature for both novices and experts. It also explains how users define analysis pipelines and compare results across groups.

Child Mind®
INSTITUTE
big data analytics

C-PAC

HOME

Pipelines

- Default
C-PAC 1.6.0
- Anatomical
- Functional
- 6 derivatives
- ...

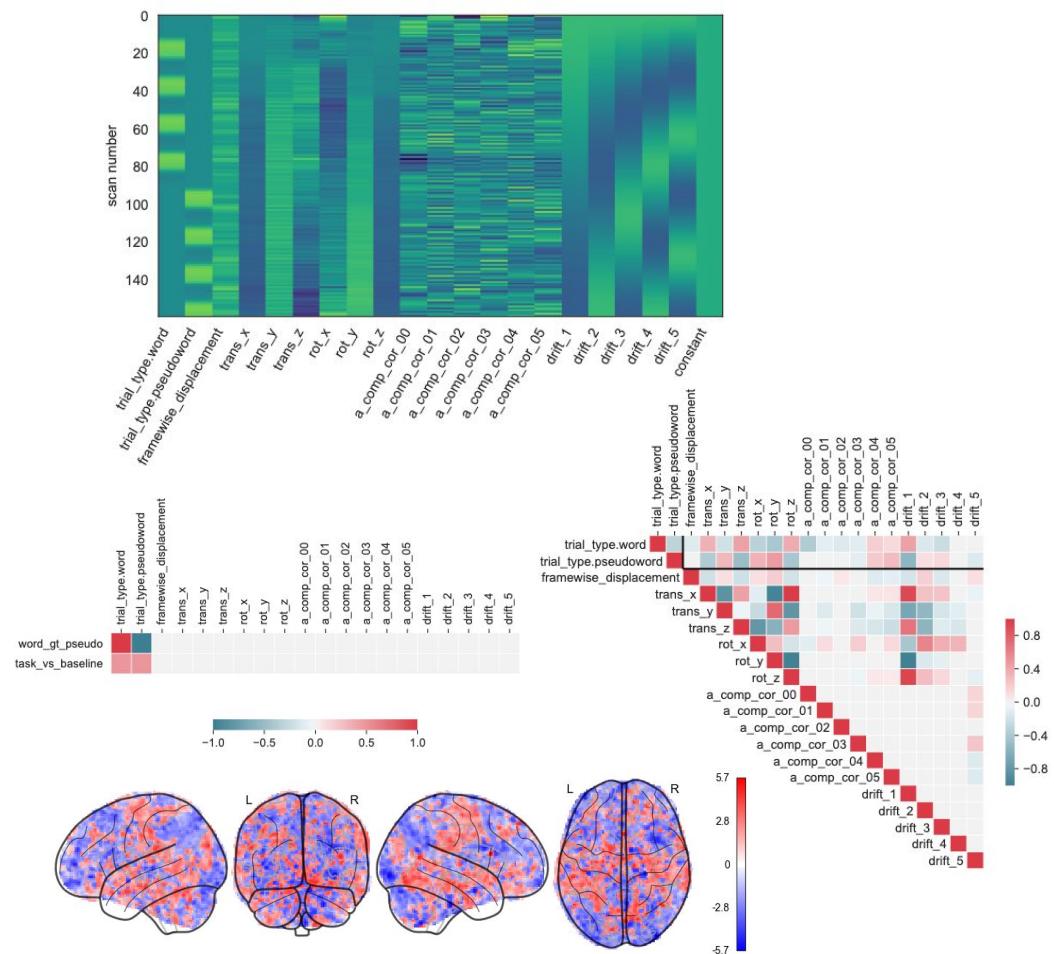
About C-PAC

The Configurable Pipeline for the Analysis of Connectomes (C-PAC) is an open-source software pipeline for automated preprocessing and analysis of resting-state fMRI data. C-PAC builds upon a robust set of existing software packages including AFNI, FSL, and ANTS, and makes it easy for both novice users and experts to explore their data using a wide array of analytic tools. Users define analysis pipelines by specifying a combination of preprocessing options and analyses to be run on an arbitrary number of subjects. Results can then be compared across groups using the integrated group statistics feature.

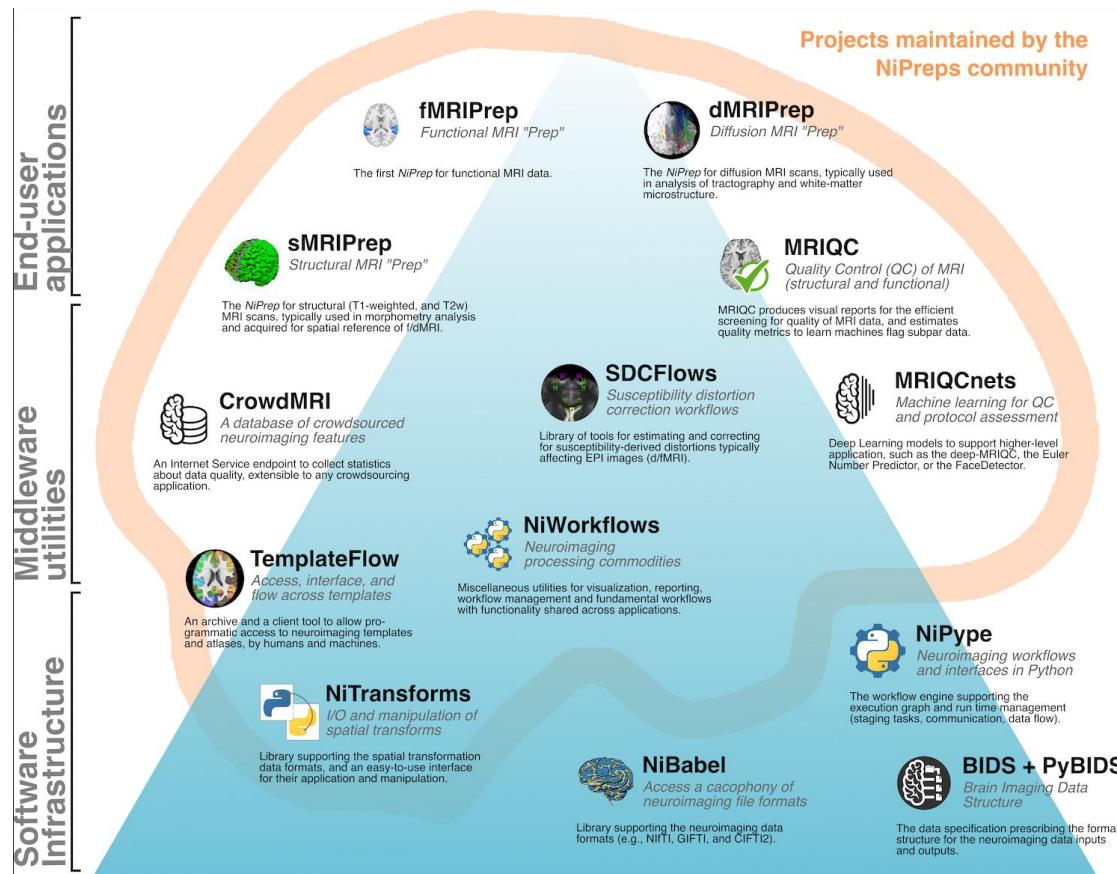
BIDS Apps - fitlins

- a lot of variation and problems in statistical analyses of task fMRI
- pipeline for linear models building upon BIDS derivatives and BIDS Stats Models
- provides QC & confounds
- intuitive output reports and summary statistics
- docker pull poldracklab/fitlins

<https://fitlins.readthedocs.io/en/latest/index.html>



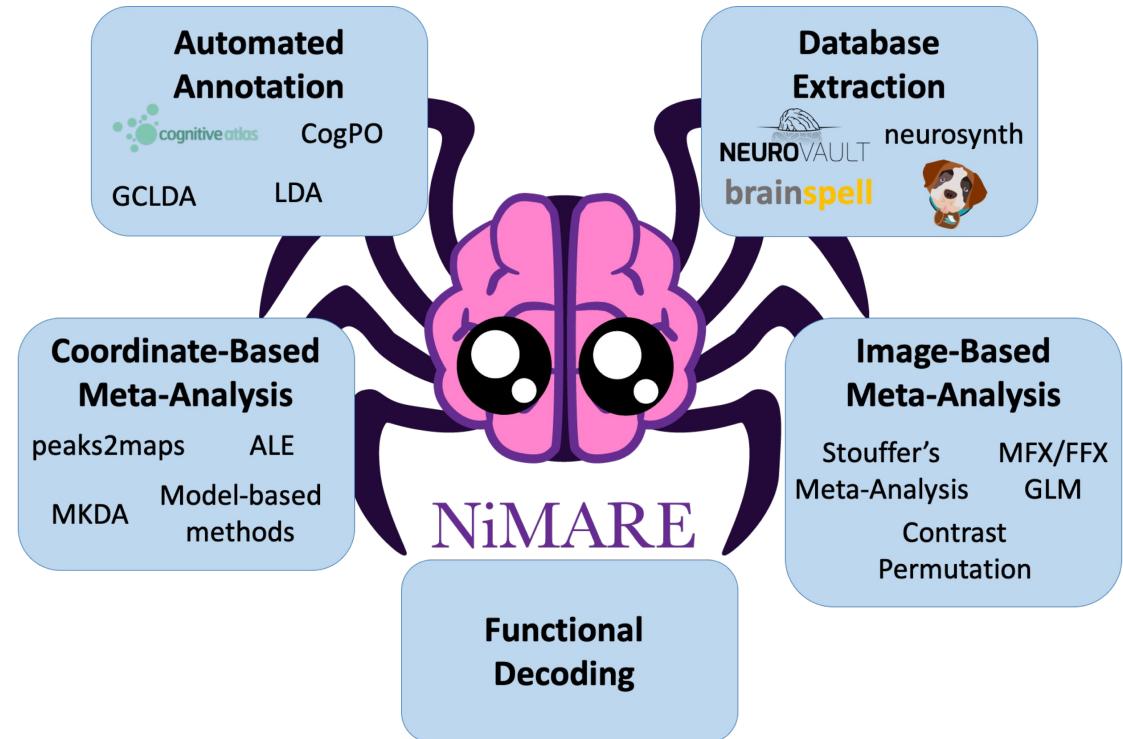
BIDS Apps - python modules - bonus round



<https://www.nipreps.org/>

python modules - NiMARE

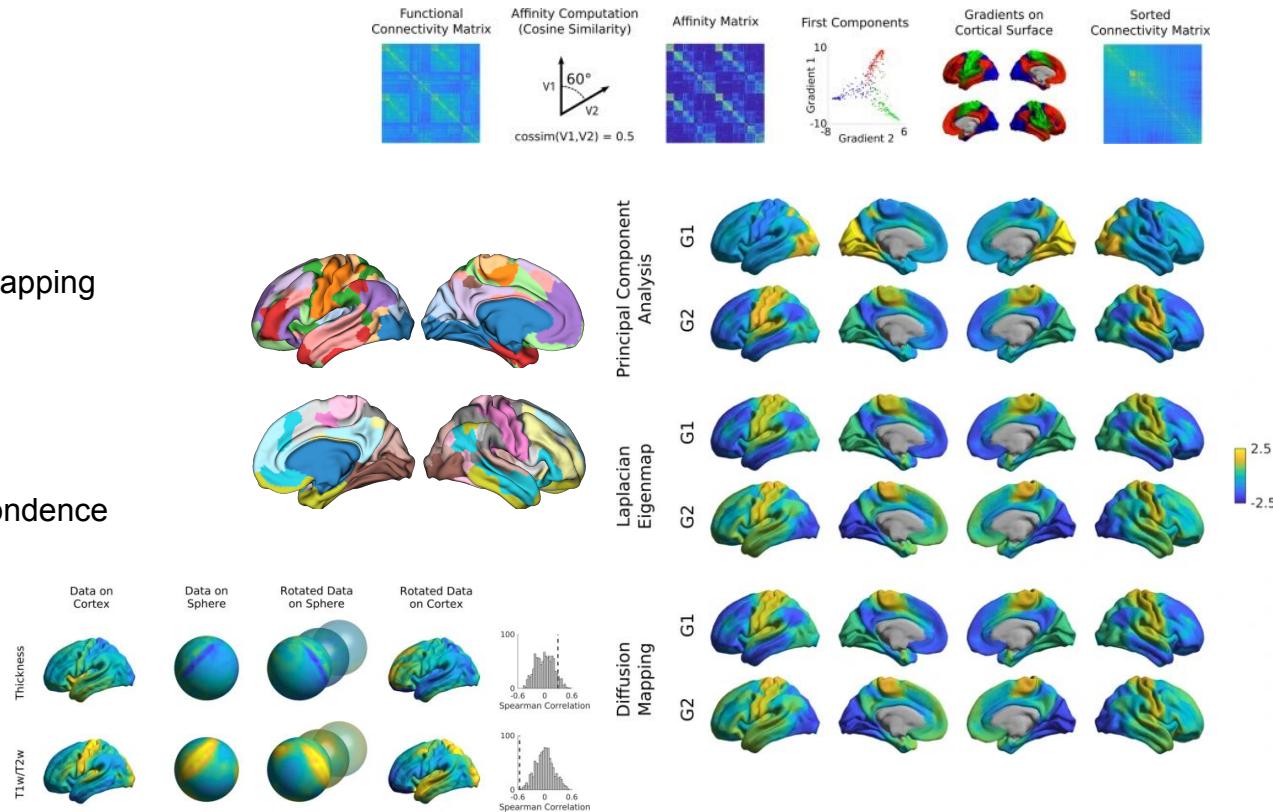
- everything meta-analyses
- CBMA & IBMA
- multiple databases
- annotations
- functional decoding, coactivation
- pip install nimare



<https://nimare.readthedocs.io/en/latest/index.html>

python modules - brainspace

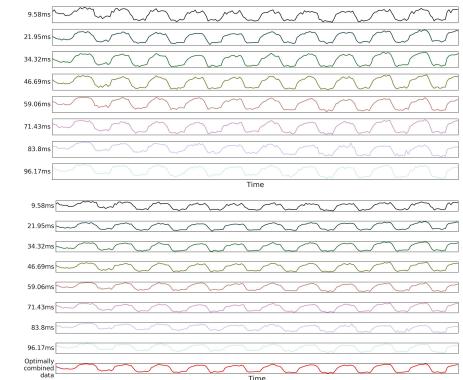
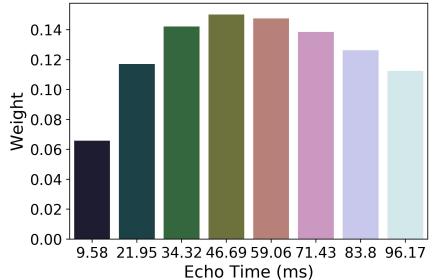
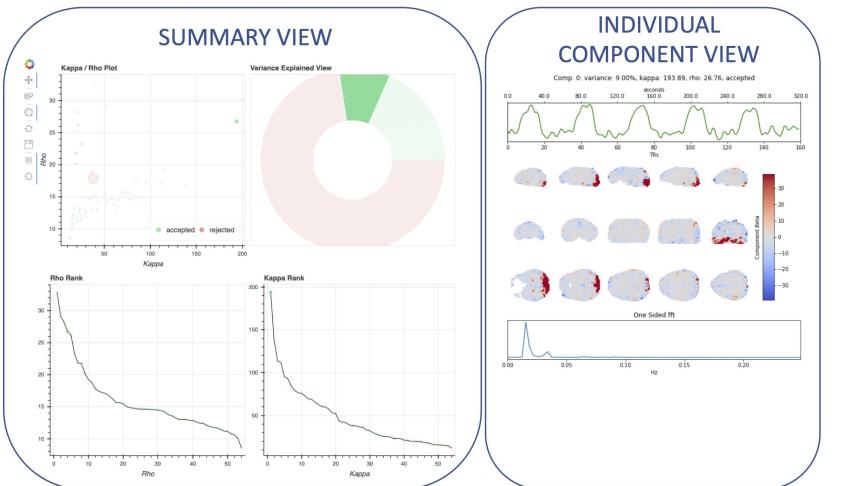
- everything macroscale gradient mapping
- creation & alignment of gradients
- various null models
- multimodal data gradient correspondence
- all the plotting functions
- pip install brainspace



<https://brainspace.readthedocs.io/en/latest/>

python modules - tedana

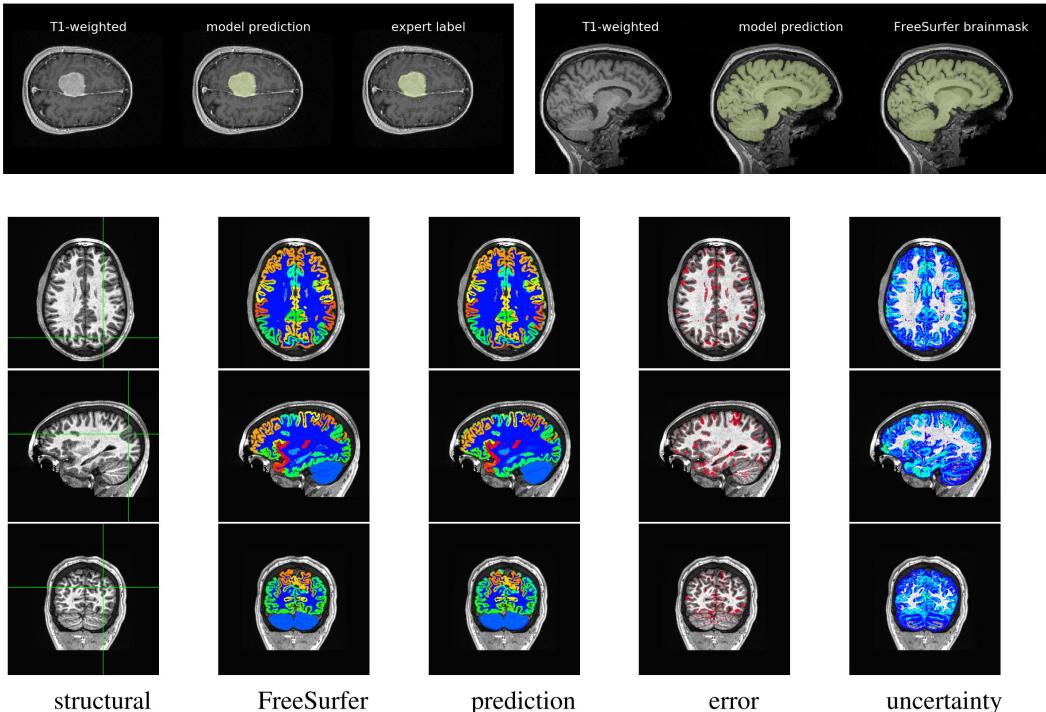
- multi-echo fMRI is giving you a hard time?
no worries, tedana's got your back
- adaptive mask generation, monoexponential decay model fit, optimal combination, denoising, TEDPCA, TEDICA, removal of spatially diffuse noise
- provides QC & confounds
- intuitive output reports and summary statistics
- pip install tedana



<https://tedana.readthedocs.io/en/latest/index.html>

python modules - nobrainer

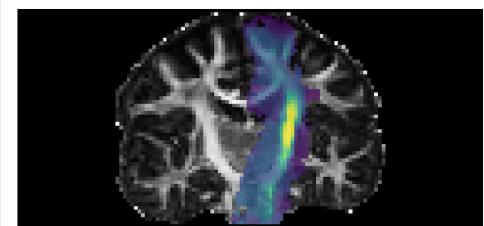
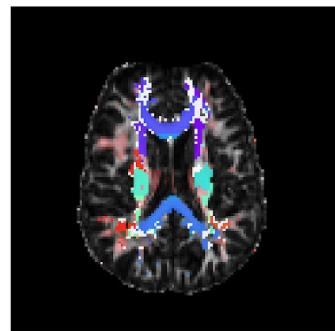
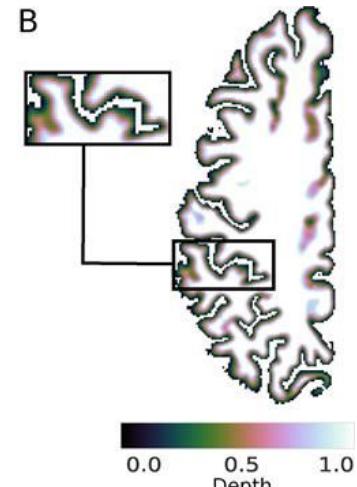
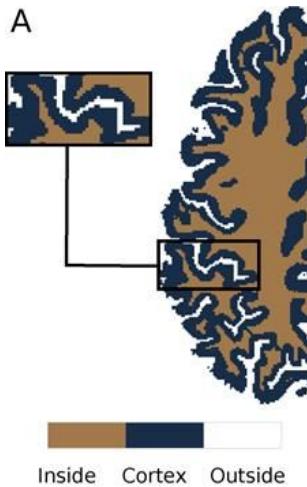
- deep learning framework for 3D image processing
- multiple 3D convolutional models from current literature
- TensorFlow or Keras implementation
- pre-trained models for brain extraction, segmentation, etc.
- pip install nobrainer



<https://github.com/neuronets/nobrainer>

python modules - nighres

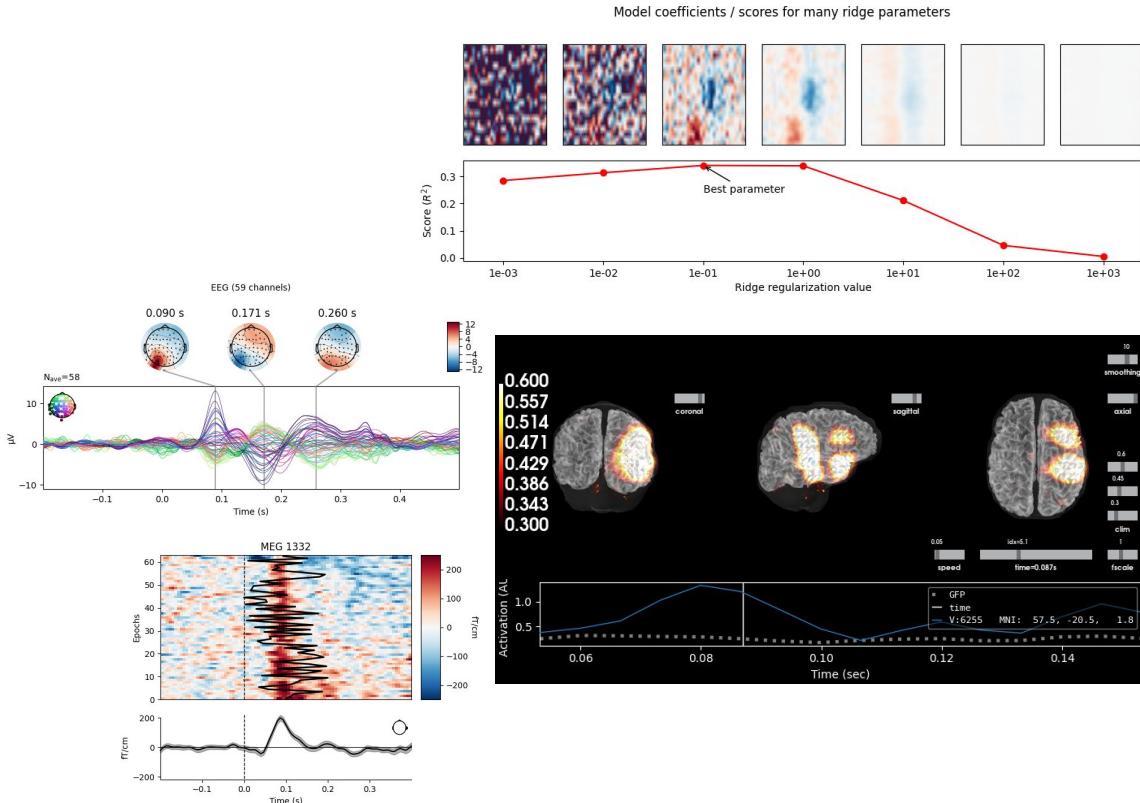
- python package for everything high resolution MRI
- vascular reconstruction, tissue classification, parcellations, co-registration, cortical depth estimation, laminar, surface
- build upon CBS tools
- due to some dependencies, unfortunately no pip install, but installation still doable
- make sure to also check [LAYNII](#)



<https://nighres.readthedocs.io/en/latest/index.html>

python modules - MNE

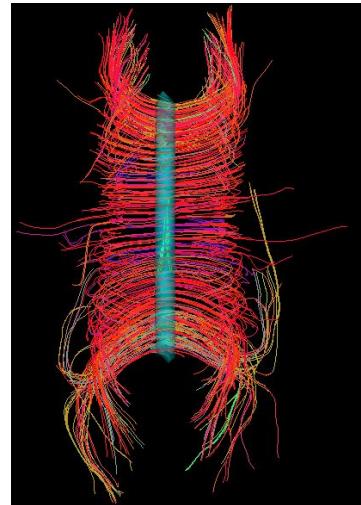
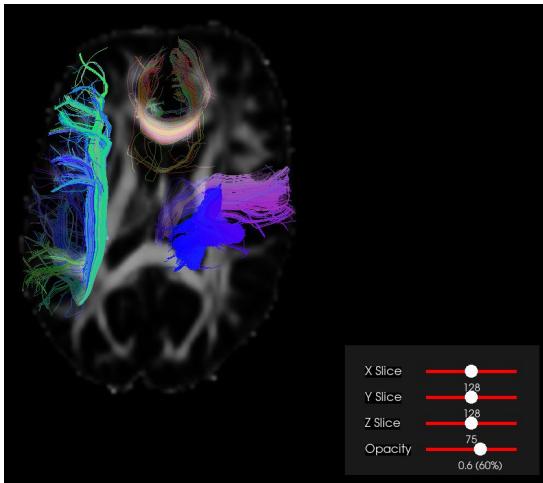
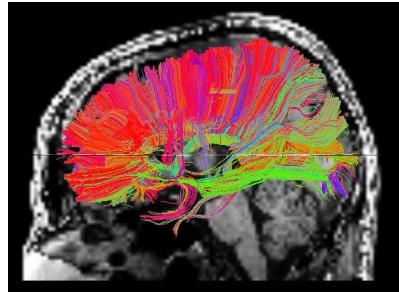
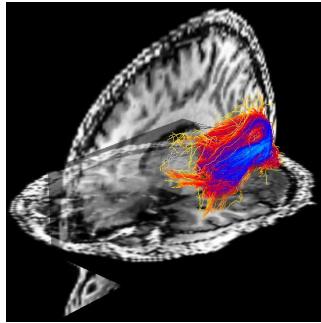
- everything you ever wanted for your human neurophysiological data: MEG, EEG, sEEG, ECoG, NIRS, etc.
- preprocessing, uni-/multivariate analyses, encoding/decoding, source estimates, connectivity, time frequency
- ALL the graphics
- works nicely with BIDS and includes informative output reports
- pip install mne



<https://mne.tools/stable/index.html>

python modules - dipy

- you have diffusion MRI data? -> check dipy and all its possibilities
- preprocessing, reconstruction, fiber tracking, streamline analysis, registration, segmentation, connectivity, etc.
- great (interactive) visualizations
- pip install dipy



<https://www.dipy.org/>

Make open data sharing a no-brainer for ethics committees.

Ultimate consent form

The following consent form has been put together, by merging best parts of existing consent forms and consulting with experts in research ethics.

English

Single access type version (all data shared publicly, recommended)

Version: OBC-ULT 1.0.0

The data and samples from this study might be used for other, future research projects in addition to the study you are currently participating in. Those future projects can focus on any topic that might be unrelated to the goals of this study. We will give access to the data we are collecting, including the imaging data, to the general public via the Internet and a fully open database.

The data we share with the general public will not have your name on it, only a code number, so people will not know your name or which data are yours. In addition, we will not share any other information that we think might help people who know you guess which data are yours.

If you change your mind and withdraw your consent to participate in this study (you can call <PI name> at <phone number> to do this), we will not collect any additional data about you. We will delete your data if you withdraw before it was deposited in the database. However, any data and research results already shared with other investigators or the general public cannot be destroyed, withdrawn or recalled.

By agreeing to participate, you will be making a free and generous gift for research that might help others. It is possible that some of the research conducted using your information eventually could lead to the development of new methods for studying brain, new diagnostic tests, new drugs or other commercial products. Should this occur, there is no plan to provide you with any part of the profits generated from such products and you will not have any ownership rights in the products.

To the best of our knowledge, the data we release to the general public will not contain information that can directly identify you. The data will not have your name on it, only a code number, so people will not know your name or which data are yours. In addition, the data will not include data that we think might help people who know you guess which data are yours, such as your facial features or the date that you participated. If we write a report or article about this study or share the study data set with others, we will do so in such a way that you cannot be directly identified. However, by using additional data linked to your name (for example brain scans obtained from your medical records) one could potentially associate your imaging or other information in our database back to you. In addition a security breach (break-in or cyber attack) might lead to someone being able to link you to your data. This risk is very low because your data are stored in a secure database, and the information about your identity is stored separately from the data themselves, linked only through a code.

GDPR edition

Context

Responsible and ethical sharing of data and code that underlie the results of scientific work is an important step towards improving research transparency, fostering inclusivity and building public trust in science. At the same time, privacy of sensitive personal data, including neuroimaging data, is highly important. Ethical review boards at research institutions are responsible for reviewing a study protocol and deciding whether it can continue based on its adherence to the relevant ethical and research integrity principles, which typically include regulations on personal data privacy. In the European Union, such data privacy requirements are subject to the [General Data Protection Regulation \(GDPR\)](#) as implemented by its member countries. Despite the increased importance that funders and institutions are currently placing on open science practices, no clear, thorough and openly available guides exist for publicly sharing neuroimaging data under the GDPR. Our goal is to share community-contributed templates for consent forms and other documentation required for ethical approval of brain research data processing and sharing under the GDPR.

History and links

Several people and groups have contributed to this project over the past years. Below are some links pointing to events/initiatives where work was done on the templates.

- Initial [GitHub issue](#) suggesting that GDPR should be added to the Open Brain Consent templates
- [OHBM Hackathon 2019 project](#) aiming to create GDPR compatible templates and educational content
- [Work-in-progress Google document](#) attempting to distill the core concepts of the GDPR as they relate to brain imaging research data
- [COST workshop](#) to update templates to include clinical research and a data user agreement

The final push to make the GDPR version of the open brain consent took place during a GLIMR workshop ([COST action CA18206](#)) the 27th November 2019, COST Association, 149 Avenue Louise, Brussels. See [GDPR/credit](#) document for more information.

Anonymization tools

Sanitization of headers/filenames

- see http://www.researchgate.net/post/Best_free_tool_for_DICOM_data_anonymization discussion on sanitization of DICOM headers
- [DelID](#) (see paper), which provides an interactive tool for inspection and sanitization of Analyze and NIfTI images
- [PyDICOM's delid](#), the "best effort anonymization for medical images using python" assists in filtering out DICOM fields and also masking out actual image data

Elimination of facial (and dental) features

Skull stripping

One of the approaches is perform complete skull stripping, e.g. using

- [BET of FSL](#)
- [3dSkullStrip of AFNI](#)
- [FreeSurfer](#)

Some dedicated anonymization tools work on this principle, e.g. [DelID](#)

Faces/dental stripping

More "gentle" approach is to strip out only the areas of face/mouth leaving skull, which might be important for some types of analysis. Usually achieved through alignment of pre-crafted mask to the research participants anatomy and removing of the masked out regions.

- [BIDSonym](#) - a BIDS app interfacing a number of methods ([pydeface](#), [quickshear](#), [mri_deface](#)) listed below
- [mri_deface](#) from FreeSurfer (paper from 2007 with overview)
- [pydeface](#) (and former [deface](#) pipeline)
- https://github.com/hanke/gumpdata/blob/master/scripts/conversion/convert_dicoms_anatomy#L26
- [quickshear](#)

Rendering faces unrecognizable

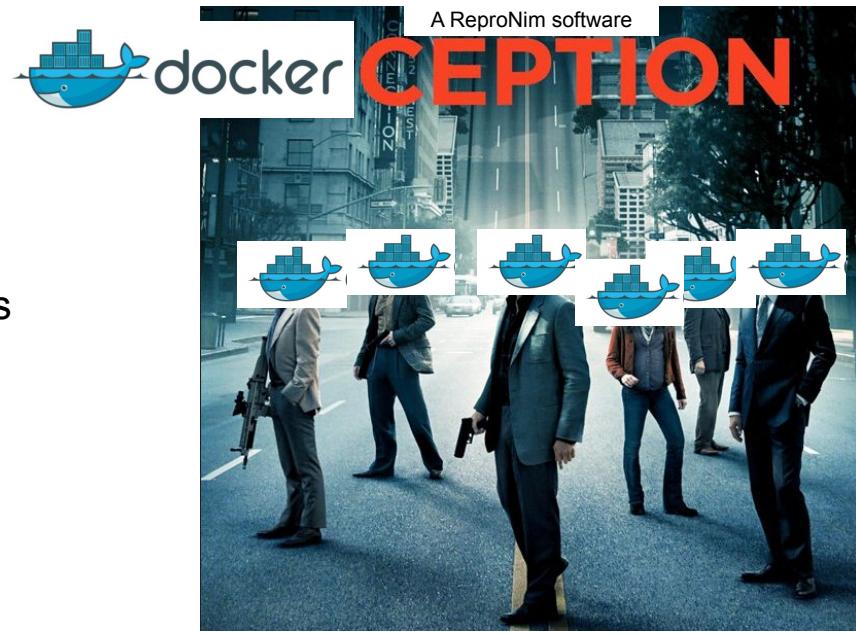
Even more data/information preserving approach is to just obscure facial features in the anatomical images:

- [Obscuring Surface Anatomy in Volumetric Imaging Data Used for HCP data](#)

amazing things - Neurodocker

<https://github.com/ReproNim/neurodocker>

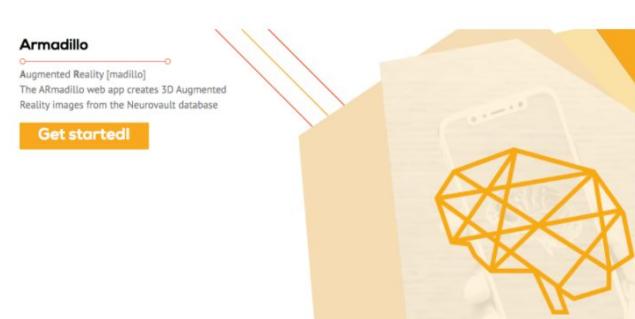
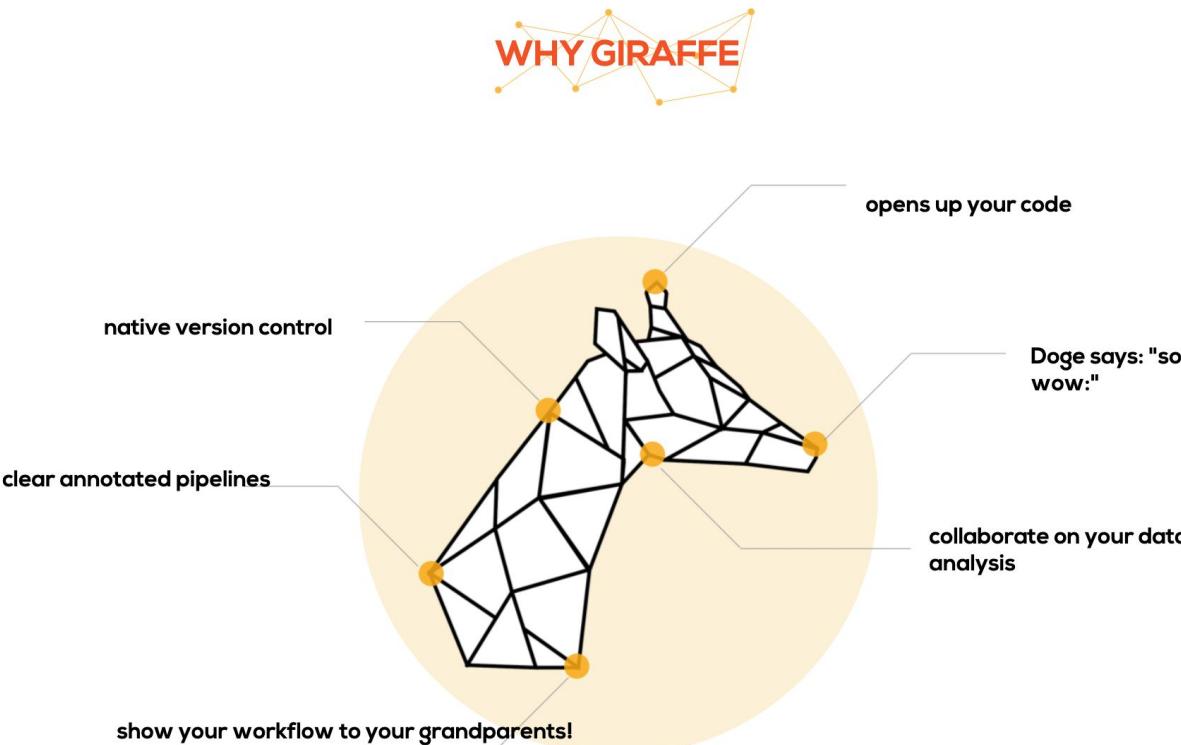
- Neurodocker, a docker image that targets the creation of docker/singularity images.
-> Yes, it's Dockerception!
- allows to quickly and reproducibly create containers targeted at neuroimaging analyses, including AFNI, ANTs, FreeSurfer, FSL, MCR, MINC, Miniconda (everything python you want), SPM, etc.
- same holds true for operating systems, etc.



<https://www.flickr.com/photos/methodshop/5245100040>

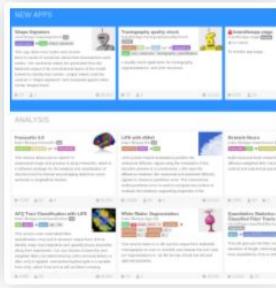
amazing things - Porcupine/Giraffe

<https://giraffe.tools/>



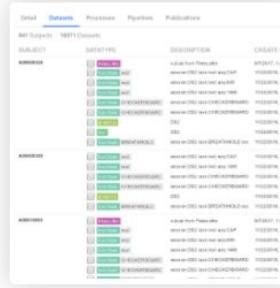
amazing things - brainlife

<https://brainlife.io/>



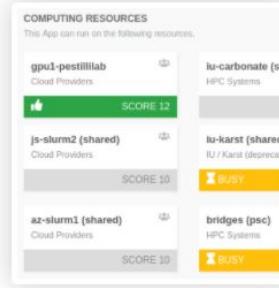
Code

Share your analyses by registering a GitHub repository as an App. Apps can be publicly shared and executed on the several cloud computing platforms.



Data

Share your neuroimaging data publicly or privately. Data on brainlife.io is organized as Datatypes to allow interoperability between Apps.



Computing

Share your computing resources on brainlife.io to accelerate scientific discovery and increase resources utilization.





Neuroscout

A platform for fast and flexible re-analysis of (naturalistic) fMRI studies

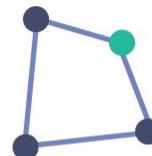
Browse public analyses

Re-use public data



Select from openly available naturalistic fMRI datasets, from sources such as [OpenNeuro](#) and [DataLad](#).

Design your analysis



Browse hundreds of annotations automatically extracted from stimuli using **state-of-the-art machine learning** algorithms, such as Google Cloud Vision, IBM Watson, and more.

Execute and share



Portable BIDS pipelines enable execution with no configuration. Results are automatically uploaded to [NeuroVault](#) for easy sharing.

Learn more



OpenNEURO

A free and open platform for sharing MRI,
MEG, EEG, iEEG, and ECoG data

Browse All Public Datasets

436

Public Datasets

14277

Participants



Get Data

Browse and download datasets from
contributors all over the world.



Share Data

Upload your data to an NIH Brain Initiative
approved repository.



Use Data

Use our affiliated website to process applicable
data.

<https://openneuro.org/>

NeuroVault Collections Metaanalyses About herholz.peer Search Search



NEUROVAULT

A public repository of unthresholded statistical maps, parcellations, and atlases of the brain.

What is it?

A place where researchers can publicly store and share unthresholded statistical maps, parcellations, and atlases produced by MRI and PET studies.

Why use it?

- Interactive visualization
- A permanent URL
- Publicly shareable
- Improves meta-analyses

Get started and upload an image!

NeuroVault Collections Metaanalyses About herholz.peer Search Search

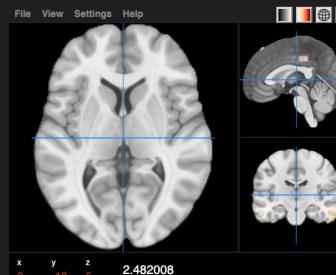
Improvising at rest: Differentiating jazz and classical music training with resting state functional connectivity

Description: Improvisationally trained musicians, Classically trained musicians, and the Minimally Musically Trained (MMT) in seed-based functional connectivity and network analyses in resting state functional MRI.

Related article: Belden, A., Zeng, T., Przybinda, E., Anteraper, S. A., Whitfield-Gabrieli, S., & Loui, P. (2020). Improvising at rest: Differentiating jazz and classical music training with resting state functional connectivity. *NeuroImage*, 207, 116384. doi:10.1016/j.neuroimage.2019.116384

Source data:

3D View Download



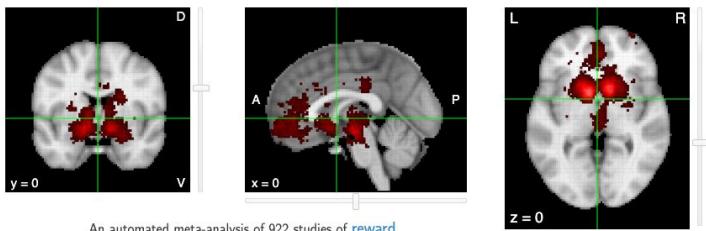
Group	Metadata
Show	7 entries
View	ID ↑ Name Type
133730	Class LECN spmT 0001 T map
133731	Class Precun spmT 0001 T map
133732	Class RECN spmT 0001 T map
133733	Class Vis spmT 0001 T map
133734	Class pSalience spmT 0001 T map
133735	Class vDMN spmT 0001 T map
133736	Imp LECN spmT 0001 T map

Showing 1 to 7 of 76 entries First Previous Next Last

neurosynth.org

Neurosynth is a platform for large-scale, automated synthesis of functional magnetic resonance imaging (fMRI) data.

It takes thousands of published articles reporting the results of fMRI studies, chews on them for a bit, and then spits out images that look like this:



Database Status

507891 activations reported in [14371 studies](#)

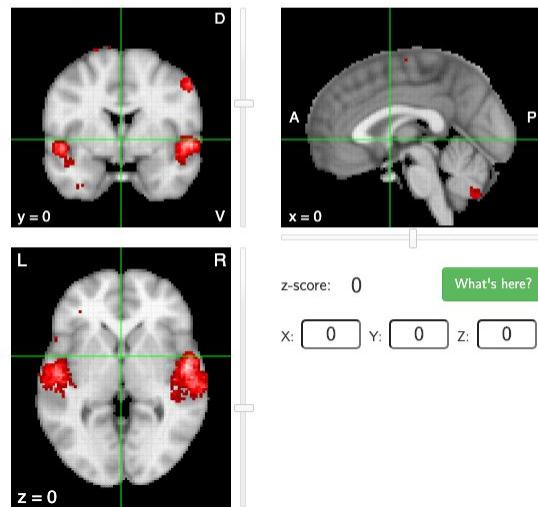
Interactive, downloadable meta-analyses of [1335 terms](#)

Functional connectivity and coactivation maps for over [150,000 brain locations](#)

music

An automated meta-analysis of 163 studies

Maps Studies FAQs



<input checked="" type="checkbox"/> music: association test	<input type="button" value="Delete"/>	<input type="button" value="Download"/>
<input checked="" type="checkbox"/> music: uniformity test	<input type="button" value="Delete"/>	<input type="button" value="Download"/>
<input checked="" type="checkbox"/> anatomical	<input type="button" value="Delete"/>	<input type="button" value="Download"/>

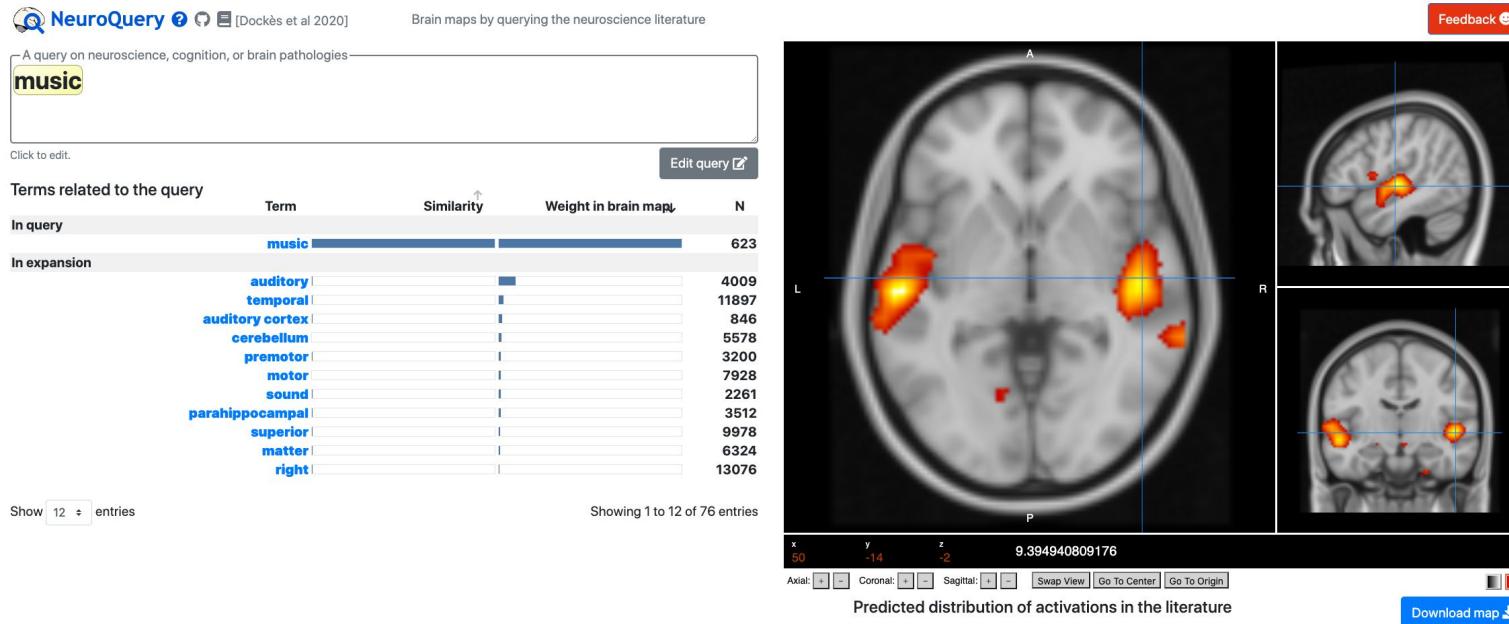
Color palette:	<input type="button" value="red"/>	<input checked="" type="checkbox"/> Crosshairs
Positive/Negative:	<input type="checkbox"/> Pan/zoom	<input checked="" type="checkbox"/> Labels

z-score:	0	<input type="button" value="What's here?"/>
x:	<input type="button" value="0"/>	<input type="button" value="0"/>
y:	<input type="button" value="0"/>	<input type="button" value="0"/>

Thresholds:	0	0
Opacity:	<input type="button" value="1"/>	<input type="button" value="0"/>

amazing things - neuroquery

<https://neuroquery.org/>



Publications related to the query

[Separate cortical networks involved in music perception: preliminary functional MRI evidence for modularity of music processing](#)

[Music and Emotions in the Brain: Familiarity Matters](#)

[It don't mean a thing...](#)

[A Functional MRI Study of Happy and Sad Emotions in Music with and without Lyrics](#)

[The rewards of music listening: Response and physiological connectivity of the mesolimbic system](#)

[Moving to Music: Effects of Heard and Imagined Musical Cues on Movement-Related Brain Activity](#)

amazing things - DataLad

Discover Data
DataLad has built-in support for metadata extraction and search. With only a few steps, you can search through a large collection of readily available datasets and immediately download them. [See more...](#)

Consume Data
DataLad offers direct access to individual files — great when you only need a few files from some large datasets for an analysis. Files in a dataset can be distributed across multiple download sources with tailored permissions to match your data privacy needs. [See more...](#)

Publish Data
DataLad supports sharing datasets with the public or just some colleagues on platforms that you are using already — no need for a central service. You have complete freedom to share your work in multiple platforms simultaneously (your own server, DropBox, GitHub, etc.) without losing track. [See more...](#)

Reproducibility
DataLad provides joint management of analysis code and data. This enables you to comprehensively track the exact state of any analysis inputs that produced your results — across the entire lifetime of a project, and across multiple datasets. [See more...](#)

Data Portal
The DataLad project operates a crawler that regularly indexes datasets from scientific data portals such as [OpenFMRI](#) and [CRCNS](#), making them trivial to acquire and work with using DataLad. Take a look at the [available datasets](#).

Community
Have a question? The primary support forum for [DataLad is on Neurostars](#). If you're having a problem with DataLad, you can use this [pre-filled form](#) to help you report your problem. Just wanna chat? We are hanging out in our [matrix chatroom](#). Come join us.



Star

53

The DataLad handbook will supply you with everything you need to get started and break new grounds with DataLad.



Contributors

This guide is the result of the collaboration of many people, and your contributions are welcome!

Useful Links

[DataLad Website](#)
[Developer Docs](#)
[DataLad@GitHub](#)
[Handbook@GitHub](#)
[Frequently Asked Questions](#)
[Handbook Index](#)
[DataLad cheat sheet](#)



Feedback

We highly appreciate your feedback on the handbook and on DataLad

<https://www.datalad.org>
<http://handbook.datalad.org>

DataLad

The Handbook

Welcome!

This handbook is a living resource about why and – more importantly – *how* to use DataLad. It aims to provide novices and advanced users of all backgrounds with both the basics of DataLad and start-to-end use cases of specific applications. If you want to get hands-on experience and learn DataLad, the *Basics* part of this book will teach you. If you want to know what is possible, the *use cases* will show you. And if you want to help others to get started with DataLad, the *companion repository* provides free and open source teaching material tailored to the handbook.

Before you read on, please note that the handbook is based on **DataLad version 0.12**, but the section [Installation and configuration](#) will set you up with what you need if you currently do not have DataLad 0.12 or higher installed.

If you're new here, please start the handbook [here](#). Alternatively, try to identify with one of several user-types in this [user specific guide to the handbook](#).

Important:

The handbook is currently in beta stage. If you would be willing to provide feedback on its contents, please [get in touch](#).

Introduction





ReproNim: A Center for Reproducible Neuroimaging Computation

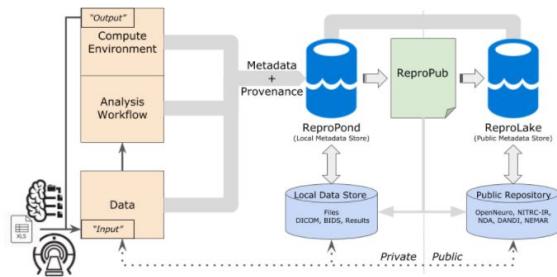
Welcome to ReproNim!

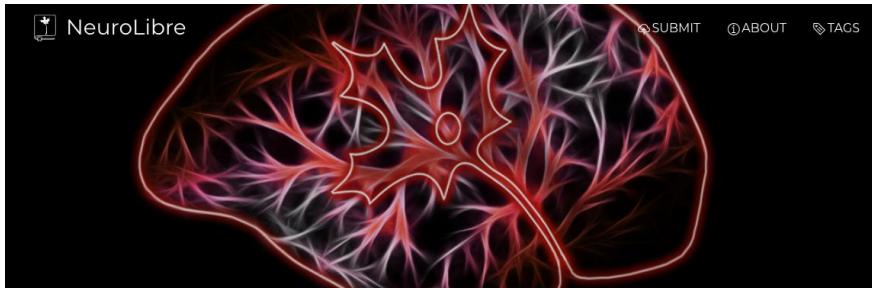
ReproNim's goal is to improve the reproducibility of neuroimaging science and extend the value of our national investment in neuroimaging research, while making the process easier and more efficient for investigators.

ReproNim delivers a reproducible analysis framework comprised of components that include:

- data and software discovery
- implementation of standardized description of data, results and workflows
- development of execution options that facilitates operation in all computational environments
- provide training and education to the community

All components of the framework are intended to foster continued use and development of the reproducible and generalizable framework in neuroimaging research. See our [Blog Post](#) for more discussion of ReproLake and ReproPond.





Supported by the [Canadian Open Neuroscience Platform \(CONP\)](#).

NeuroLibre is a curated repository of interactive neuroscience notebooks. Committed to publishing curated Jupyter notebooks with zero article processing charges or subscription fees.

[Submit a paper to NeuroLibre](#)

[Explore Papers](#)

[Documentation](#)

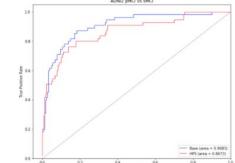
[Learn More](#)

The screenshot displays the NeuroLibre website's homepage. It features a large, light gray header bar with the CONP logo and a "View Left" button. Below the header, there is a main content area with a white background. The text describes NeuroLibre as a curated repository of interactive neuroscience notebooks, emphasizing its commitment to zero article processing charges and subscription fees. It includes a prominent "Submit a paper to NeuroLibre" button. Below this, there are four main navigation links: "Explore Papers", "Documentation", and "Learn More", each accompanied by a small icon. The overall design is clean and modern, using a combination of white, red, and gray colors.

A highly predictive signature (HPS) of Alzheimer's disease dementia from cognitive and structural brain features

A Jupyter notebook containing analyses that give a highly predictive signature (HPS) of Alzheimer's disease dementia from cognitive and structural features using simulated data.

[NeuroLibre](#) [Book](#) [GitHub](#) [Code](#)



Introduction to machine learning with Nilearn

An introductory tutorial for using the popular Nilearn software package to perform machine learning analyses with neuroimaging data. This material is adapted from the Montreal AI and Neuroscience (MAIN) 2018 workshops.

[NeuroLibre](#) [Book](#) [GitHub](#) [Code](#)



Image processing with Spinal Cord Toolbox (SCT)

This notebook presents an example analysis pipeline using the Spinal Cord Toolbox (SCT), a suite of tools specialized for analysis of spinal cord MRI images of the spinal. Topics covered include: segmentation, masking, registration, warping, and quantitative metric computation. This tutorial was generated in a Jupyter Notebook and coded in Python.

[NeuroLibre](#) [Book](#) [GitHub](#) [Code](#)



amazing things - Neurostars

<https://neurostars.org/>

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Welcome to INCF Neurostars.

A question and answer forum for neuroscience researchers, infrastructure providers and software developers.

How to start
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Important links

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Category	Topics
Neuro Questions This is a place to ask any and all questions about Neuroscience.	2898 3 new
Announcements Announcements is the place to post some general information that is of interest to the community. It can be a new project, a software release, a job posting, or any information you want to share that's not a "question".	162 2 new
Community Chat A place for friendly conversation, ideas, discussion, and otherwise un-categorizable things in the NeuroStars community.	10 1 unread
Institutions Category for institutions that are partnered with INCF to discuss the institution-specific topics. OCNS	37 3 new
ABCD ReproNim The ABCD-ReproNim Course provides training for reproducible analyses of the Adolescent Brain Cognitive Development (ABCD) Study® data. Course starts October 16, 2020. Course website: https://www.abcd-repronim.org	13 3 new

Latest

 Datalad on github + cluster storage	2	42m
 BIDS and cookiecutter? bids	0	1h
 OCNS Infrastructure/software/tools SIG: meet and greet, initial discussions	64	4h
 Seed map - HELP from a newbie	0	6h
 Deadline extended to Nov. 15th Postdoctoral position for the development of acquisition, storage and processing pipelines for reproducible science building on the BIDS standard.	0	20h

The homepage features a large green brain logo composed of a grid of smaller squares. Below the logo are several navigation links: SEARCH PROJECTS, +SUBMIT PROJECT, EVENTS, PROCEEDINGS, LEARN MORE, JOIN MATTERMOST CHANNEL, and CODE OF CONDUCT.

<http://brainhack.org/>

<https://brainhack.org/global2020/>

Brainhack Global 2020 is happening!

November 30th - December 13th



Host your own local Brainhack

What is Brainhack?

Brainhack is a unique event format that convenes researchers from across the globe and a myriad of disciplines to work together on innovative projects related to neuroscience.

Year after year, global Brainhack events have brought researchers together to participate in **open collaboration**, and regional Brainhack events keep the momentum going throughout the year.

2020 being 2020, this year's Brainhack Global will unite several **virtual** regional Brainhack events throughout the world.

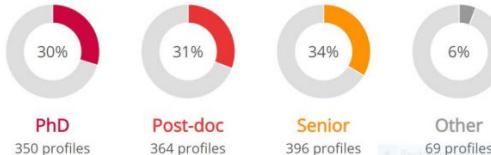


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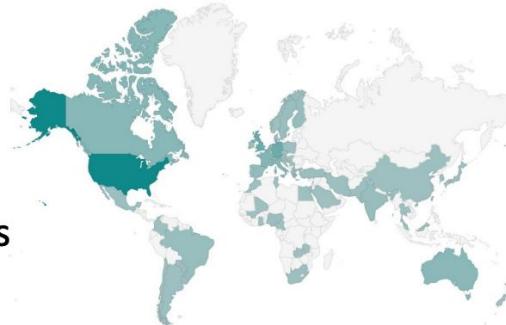
Repository for Women in Neuroscience

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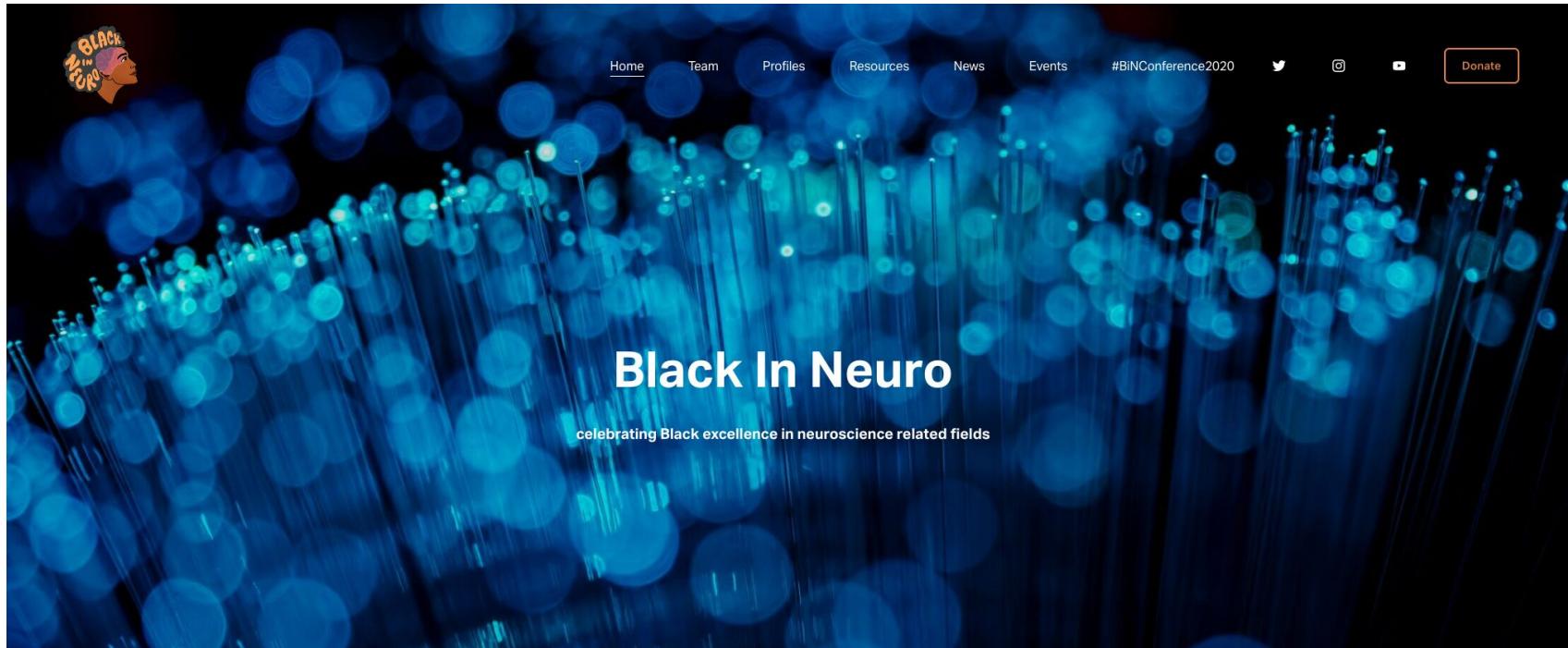
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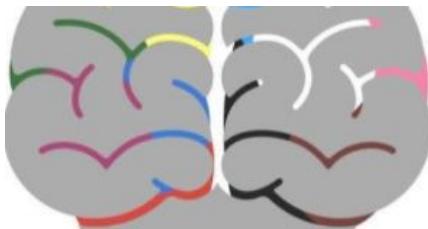


Black In Neuro

celebrating Black excellence in neuroscience related fields

<https://www.blackinneuro.com/>

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