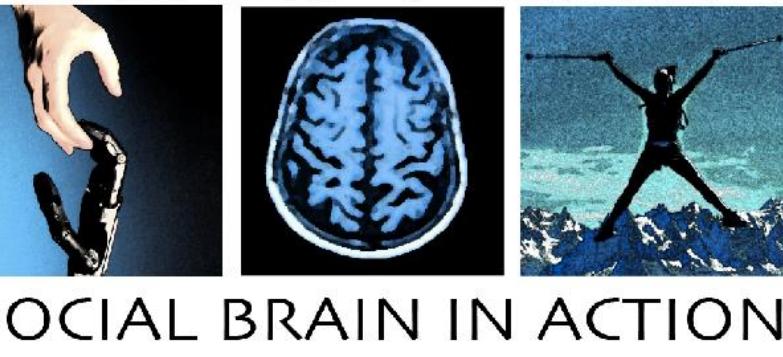




University
of Glasgow



SOBALab
SOCIAL BRAIN IN ACTION

Tools for reproducible fMRI analysis

Methods & Meta-science 19.02.20

Ruud Hortensius

✉ ruud.hortensius@glasgow.ac.uk

🐦 @ruudhortensius

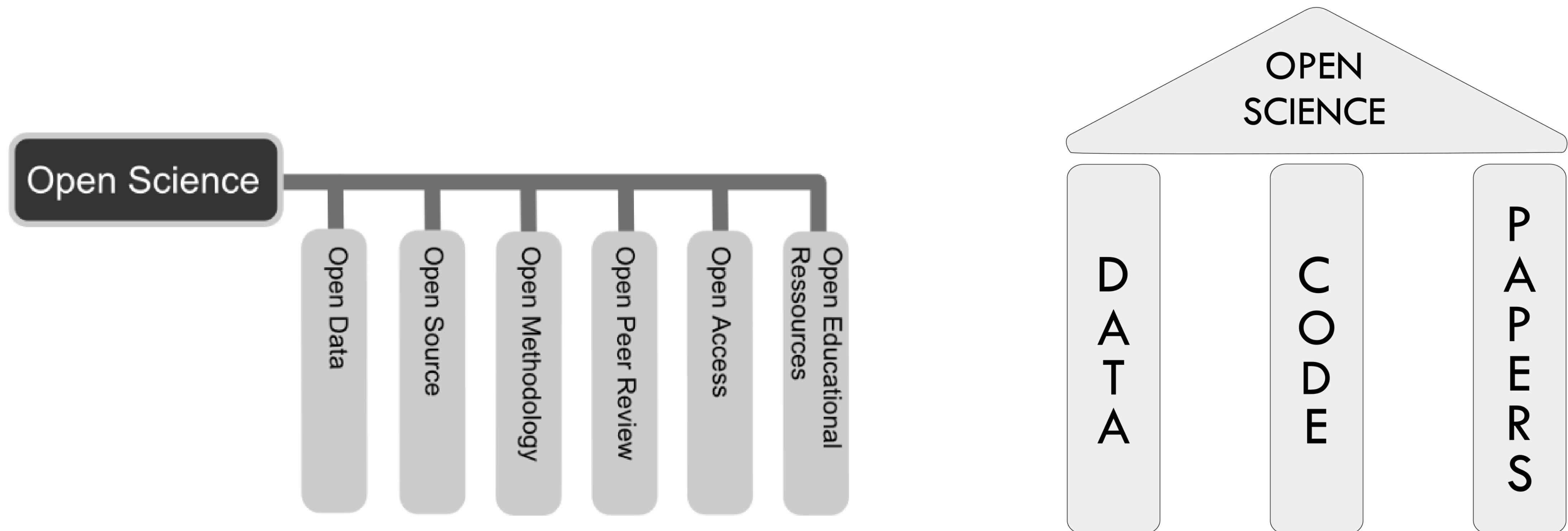
📢 www.ruudhortensius.nl

🌐 Slides and material:

🌐 <https://osf.io/c28jq/>



How to foster transparency and reproducibility



Neuroimaging and the climate emergency



How can neuroscientists respond to the climate emergency?

AUTHORS
Adam Aron, Richard Ivry, Kate Jeffrey, Russell Poldrack, Robert Schmidt, Christopher Summerfield, Anne Urai

CREATED ON February 04, 2020 **LAST EDITED** February 04, 2020

MRI brain scanning

MRI brain scanning has a carbon footprint. This comes from the manufacture, transport, and installation of the scanner; its day-to-day operation - which requires electricity; and the liquid helium that cools the super-conducting elements. [This calculation](#) puts the carbon footprint of one scan at 160kg.

The 2 MRI scanners we have in the [Clinical Imaging Sciences Centre](#) are Siemens models. Siemens has a large [decarbonisation program](#), and aims to be carbon neutral by 2030. For example, the energy involved in the manufacture of scanners comes from renewable sources.

The day-to-day operation of the scanner requires electricity. The University of Sussex is currently undergoing a major revamp to [replace the current systems](#) that generate energy on campus with more sustainable alternatives.

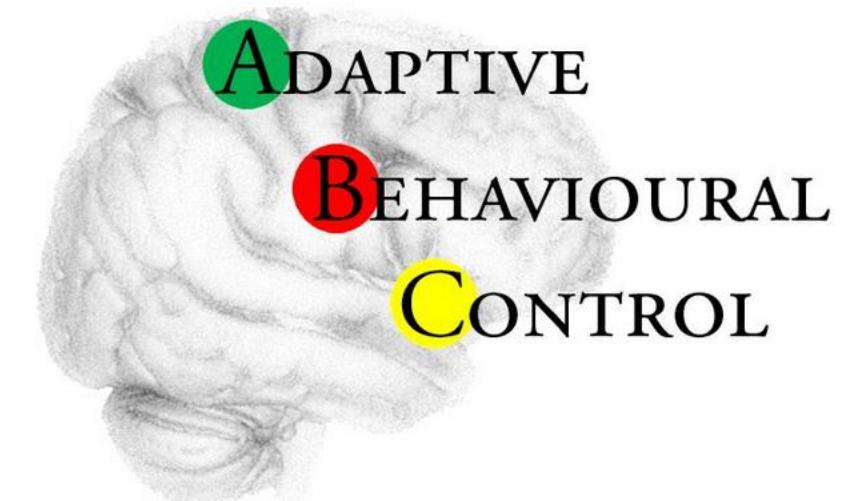
[MRI scanners require liquid helium](#) to cool the super-conducting elements. Liquid helium is a naturally-occurring substance in the geological environment. Unfortunately, [it exists almost entirely in reserves of natural gas](#). This means it is extracted as part of fossil fuel mining for natural gas - but we need to 'keep it in the ground'.

I am yet to find an answer to the climate impact of liquid helium, so I am applying the 'reduce, reuse, recycle' mantra.

Reduce: Only acquire (good quality) data that you intend to use.

Reuse: Consider if you can use data that already exist, for example from the [Human Connectome Project](#).

Recycle: Share your summary data on [Neurovault](#) so others can use it for meta-analyses.



University of Sussex

Artificial Intelligence / Machine Learning

Training a single AI model can emit as much carbon as five cars in their lifetimes

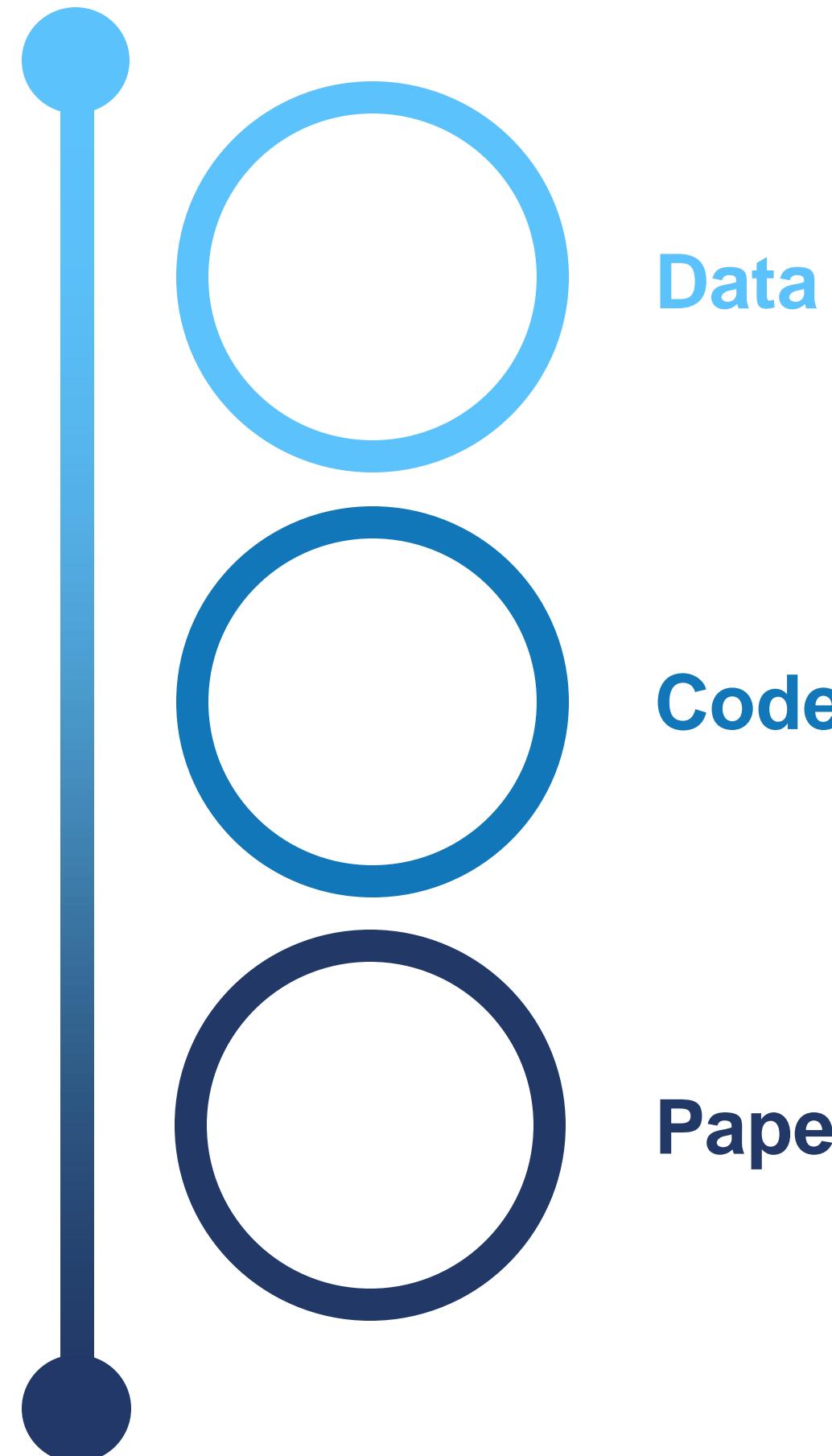
Deep learning has a terrible carbon footprint.

by Karen Hao

MIT
Technology
Review

Jun 6, 2019

How to foster transparency and reproducibility



How to foster transparency and reproducibility

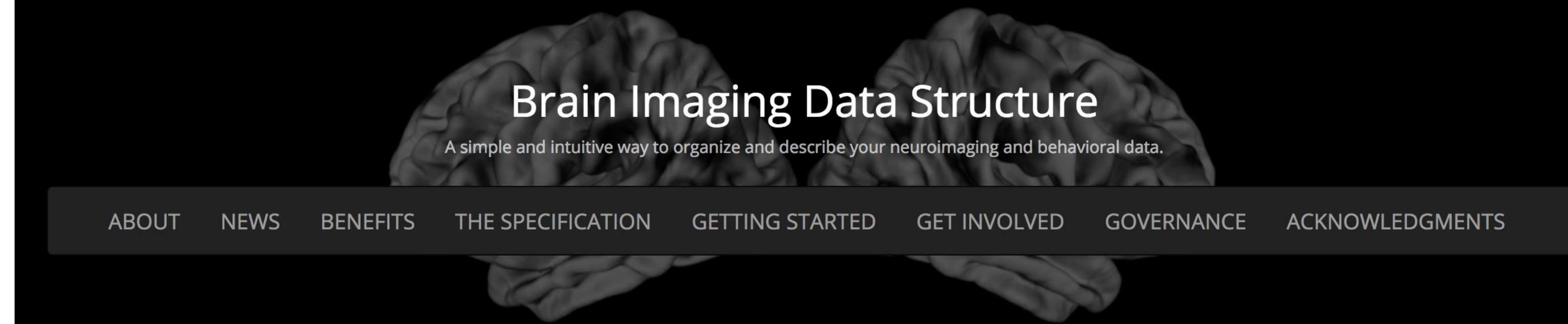


Data: BIDS

Code: BIDS apps [MRIQC, MRIQCception, fMRIprep]

Paper: NeuroVault, OpenNeuro

Data: BIDS



Brain Imaging Data Structure: <http://bids.neuroimaging.io/>

What?

- Standard for organisation and description
- Fully compatible with existing software
- Unites existing practices in the field
- Contains metadata as input for processing

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^{20,23}, John Pellman⁶, Jean-Baptiste Poline²⁴, Ariel Rokem²⁵, Gunnar Schaefer^{1,26}, Vanessa Sochat²⁷, William Triplett¹, Jessica A. Turner^{3,28}, Gaël Varoquaux²⁹ & Russell A. Poldrack¹

Received: 18 December 2015

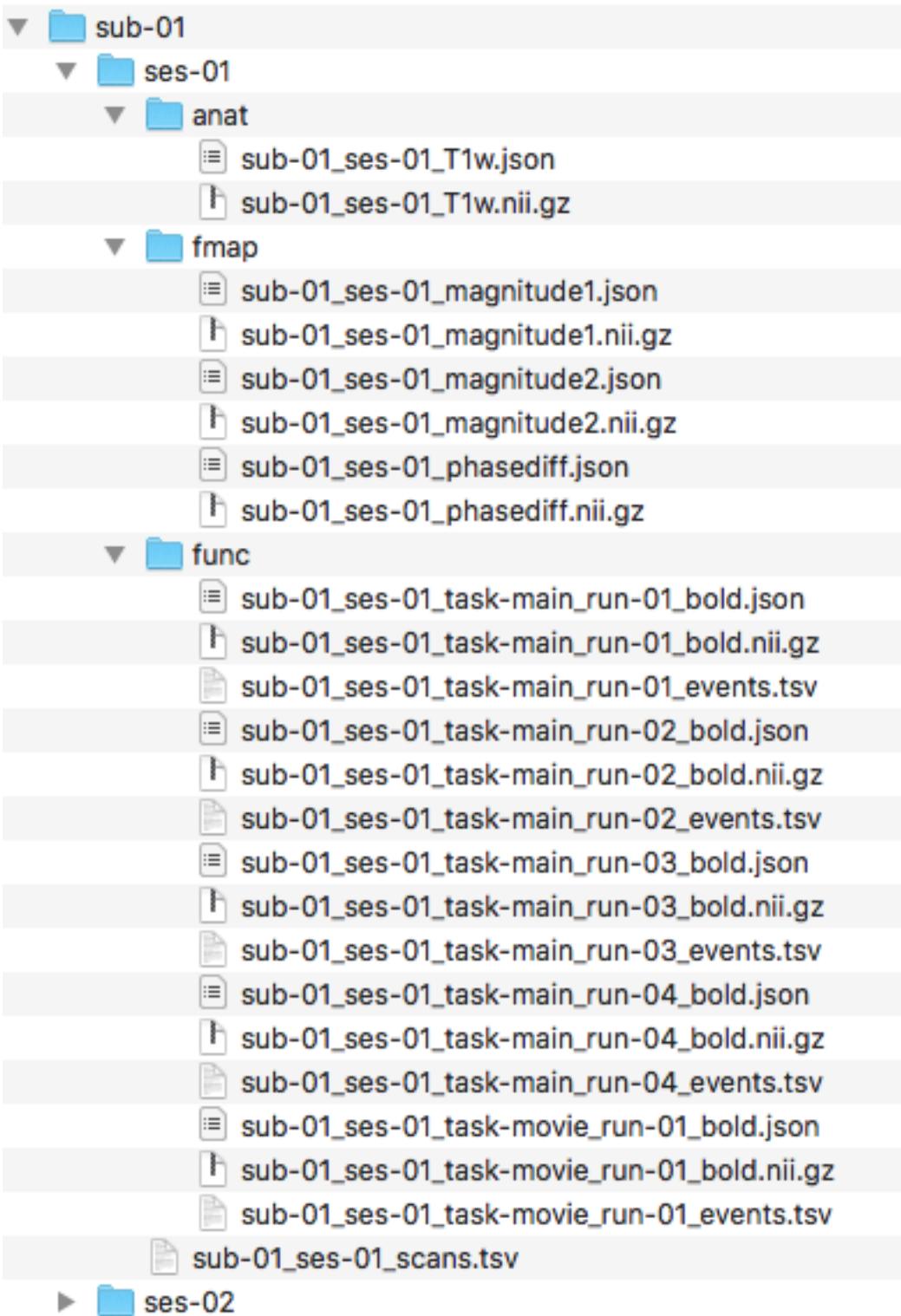
Accepted: 19 May 2016

Published: 21 June 2016

Data: BIDS

Why?

- Increase collaborative possibilities with minimal curation: future you, students, lab, and community
- Allow for automated tools (MRIQC, fMRIprep and other BIDS app)
- Metadata standardised and machine-readable: perfect for data analysis software
- Improves reproducibility
- Error reduction: validation tool
- Data sharing



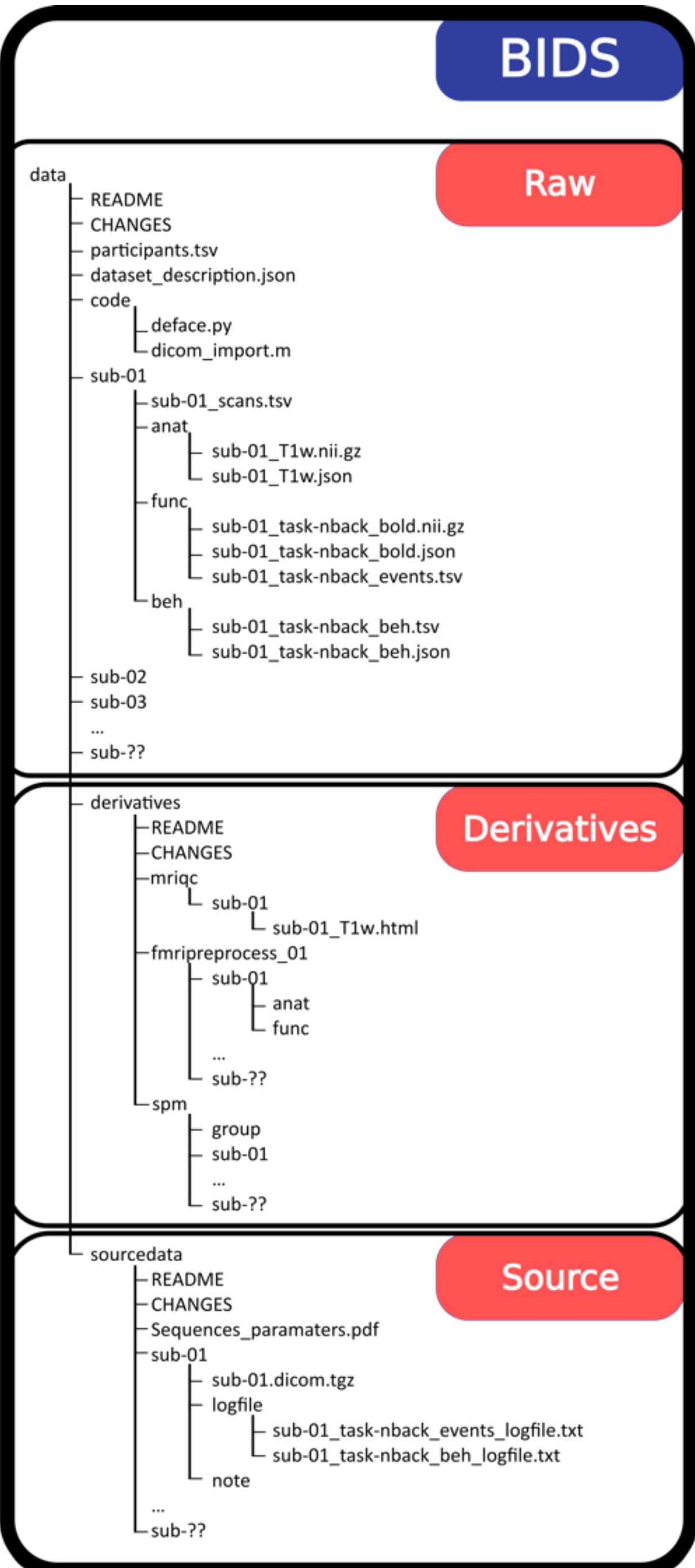
Gorgolewski, K. J., Auer, T., Calhoun, V. D., Craddock, R. C., Das, S., Duff, E. P., et al. (2016). The brain imaging data structure, a format for organizing and describing outputs of neuroimaging experiments. *Scientific Data*, 3, 160044.
<http://doi.org/10.1038/sdata.2016.44>

BIDS

Data: BIDS

- /data ←the raw folder: BIDS conform
- /data/derivatives ←no standard yet (but same logic)
- /data/sourcedata ←raw dicoms and other data (sequence pdf)

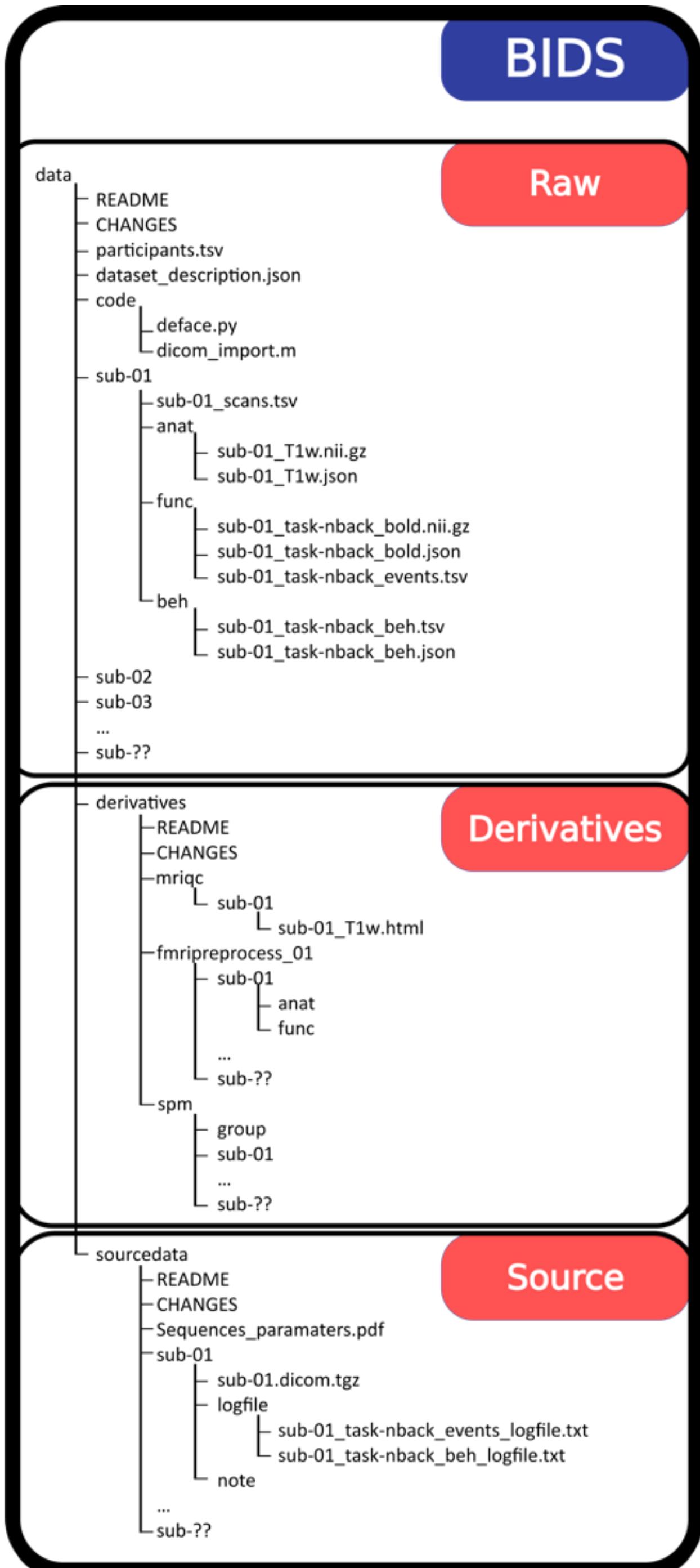
- /code ←scripts used to process/analyse



Data: BIDS

Common principles:

- Raw vs. derived data (separate folders)
- Inheritance principle
- NIfTI: use JSON for meta-data
- Tsv file (also for data), missing data ‘n/a’, can be combined with data dictionary
- Required, recommended and optional metadata



BIDS

Data: BIDS

- Only few required metadata and files:

/anat: specify type (e.g. T1 or T2 weighted)

/func: task name, TR, event onset and duration

Recommended: e.g., slice timing, phase encoding etc.

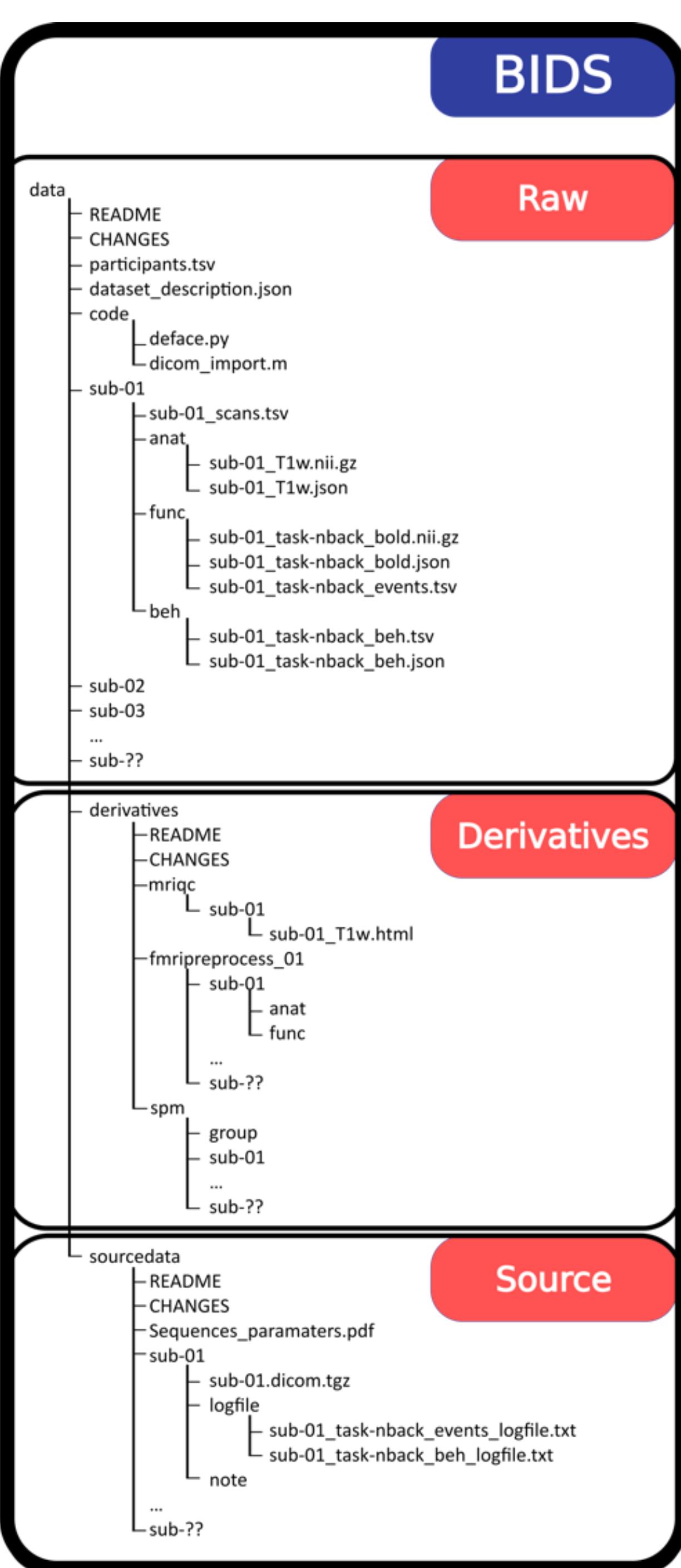
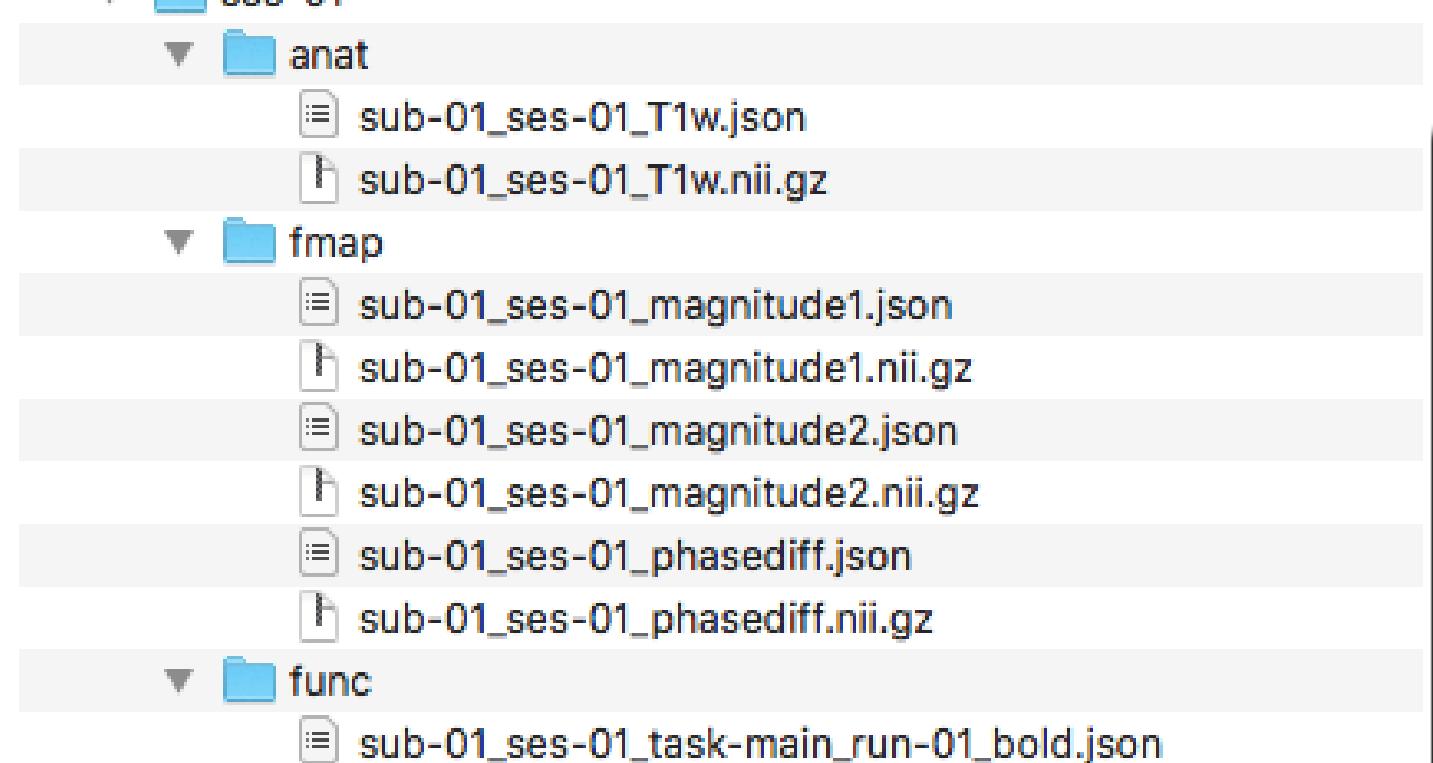
Optional: e.g., scanner software version, head coil name etc.

BIDS validator will report missing metadata

Logic is: sub-<label>_ses-<label>_modality (e.g. bold, t1w)

Func: _task-<label>_run-<index>

Echo's: _echo-<label>



Data: BIDS

Common principles:

- Subject (zero padding is recommended)
- Session: also when going out of the scanner; different modalities across two days can be one session
- Data type:

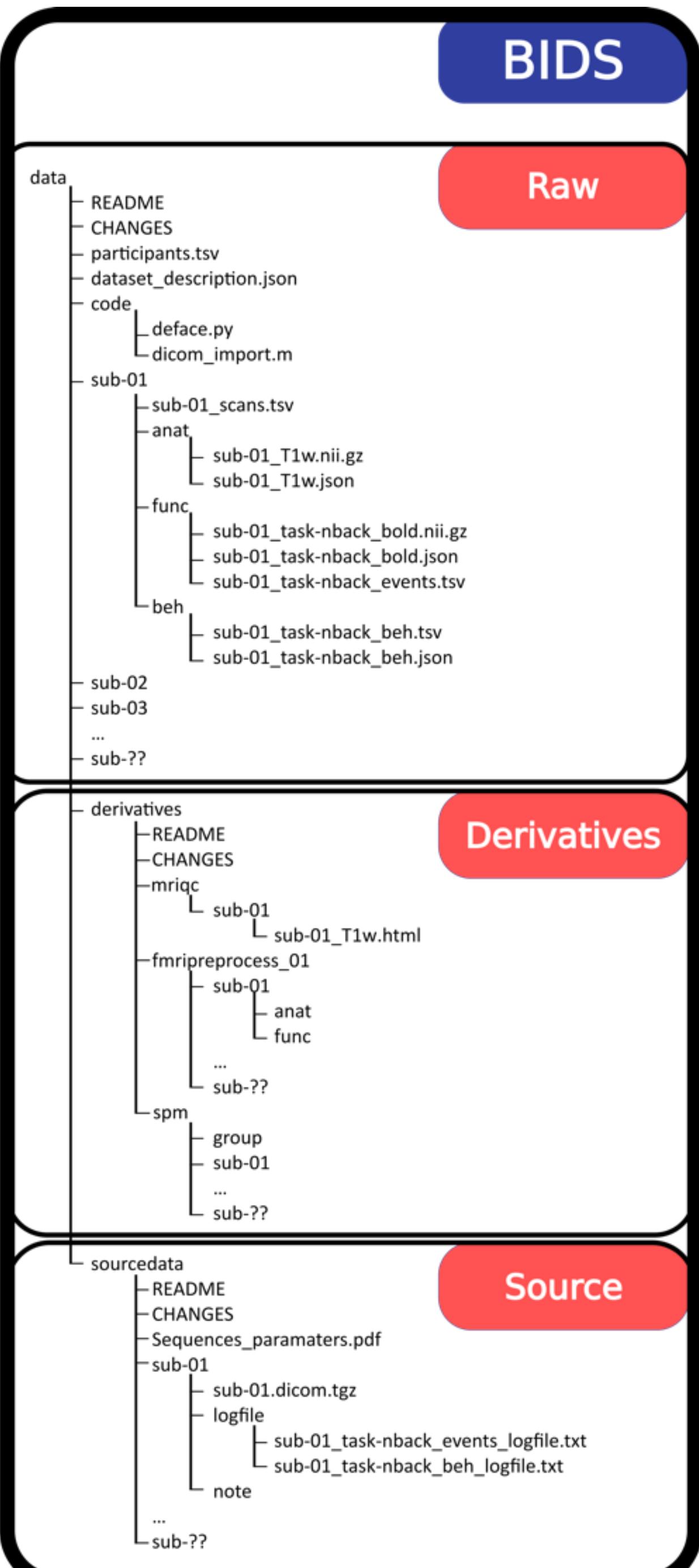
/func /anat /dwi /fmap /meg /eeg /ieeg /beh

- Use README's for /raw /derivatives /sourcedata

Summary:
493 Files, 15.16GB
10 – Subjects
2 – Sessions

Available Tasks:
main
movie
person

Available Modalities:
T1w
bold
events
fieldmap



Data: BIDS

How to:

1. DICOM → NIfTI ←/raw to /sourcedata (remove CCNI codes)
2. Create structure ←manually or converter using heuristic
3. Add remaining data ←Events (.tsv)
4. Add missing metadata: ←E.g. Intended_for /fmap
5. Validate the dataset ←Docker or validator

I use Heudiconv: <https://github.com/nipy/heudiconv> (heuristic-centric DICOM converter)

Tutorials:

<https://github.com/INCF/bids-starter-kit>

<http://reproducibility.stanford.edu/bids-tutorial-series-part-1a/>

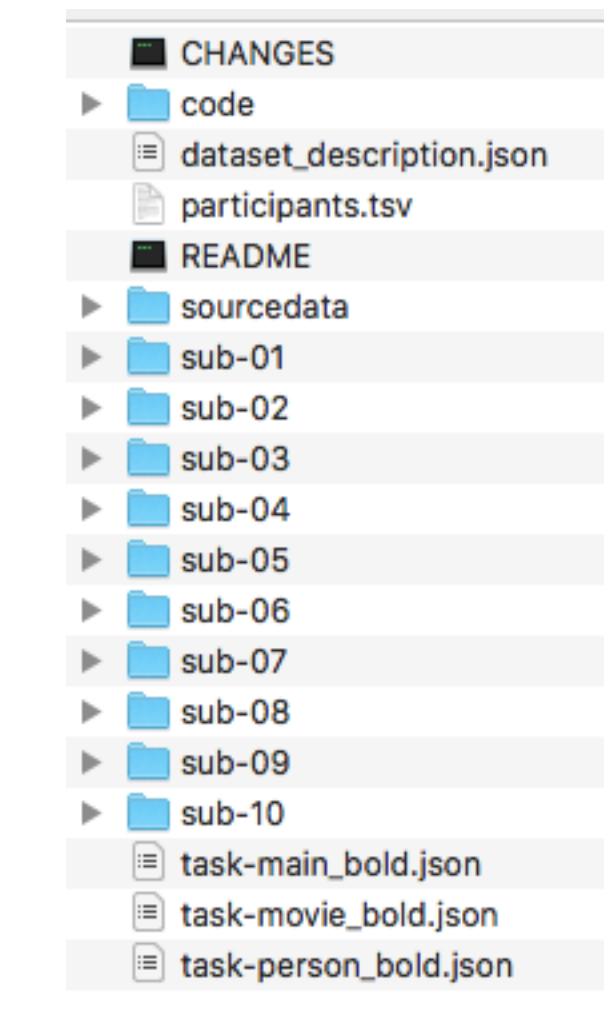
Data: BIDS

How to

AnThroM

1. Details
- 2. BIDS dataset**
3. Preprocessing
4. Analyses
5. IDAQ
6. fROI results
7. IDAQ and ROI Analysis

center the variables



Data: BIDS and beyond

- iEEG/EEG/MEG

- psych-ds

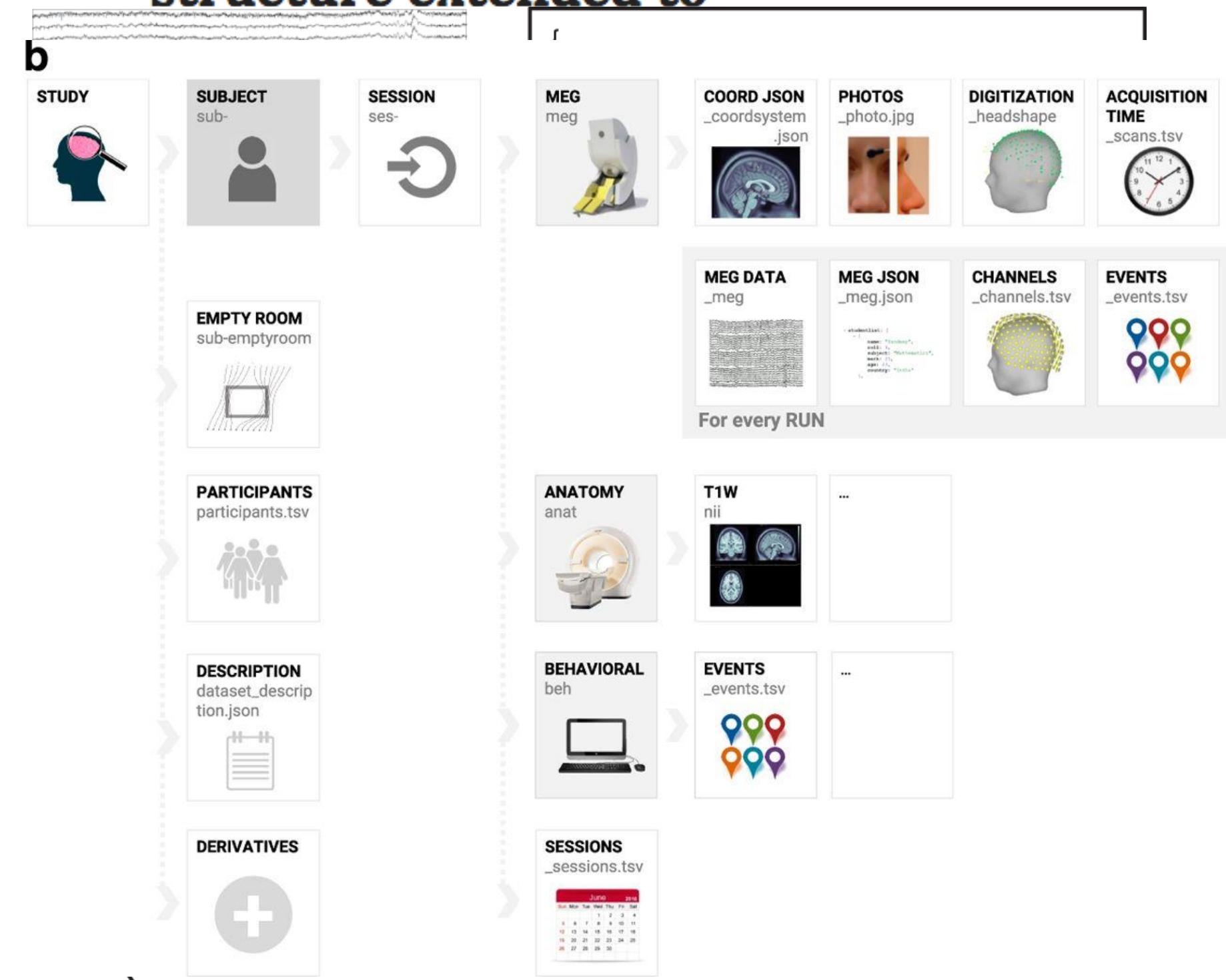
- Lisa's and Daniel Laken's Scienceverse

Links:

- <https://bids-specification.readthedocs.io/en/latest/04-modality-specific-files/>
- <https://github.com/psych-ds/psych-DS>
- <https://scienceverse.github.io/scienceverse/index.html>



MEG-BIDS, the brain imaging data structure extended to



iEEG-BIDS, extending the Brain Imaging Data Structure specification to human intracranial electrophysiology

Data: BIDS

- Other

Physiological and other continuous recordings

Template:

```
sub-<label>/[ses-<label>/]  
  func/  
    <matches>[_recording-<label>]_physio.tsv.gz  
    <matches>[_recording-<label>]_physio.json  
    <matches>[_recording-<label>]_stim.tsv.gz  
    <matches>[_recording-<label>]_stim.json
```

Optional: Yes

Where `<matches>` corresponds to task file name without the `_bold.nii[.gz]` suffix. For example: `sub-control01_task-nback_run-1`. If the same continuous recording has been used for all subjects (for example in the case where they all watched the same movie) one file can be used and placed in the root directory. For example: `task-movie_stim.tsv.gz`

Physiological recordings such as cardiac and respiratory signals and other continuous measures (such as parameters of a film or audio stimuli) can be specified using two files: a gzip compressed TSV file with data (without header line) and a JSON for storing the following metadata fields:

Behavioral experiments (with no MRI)

Template:

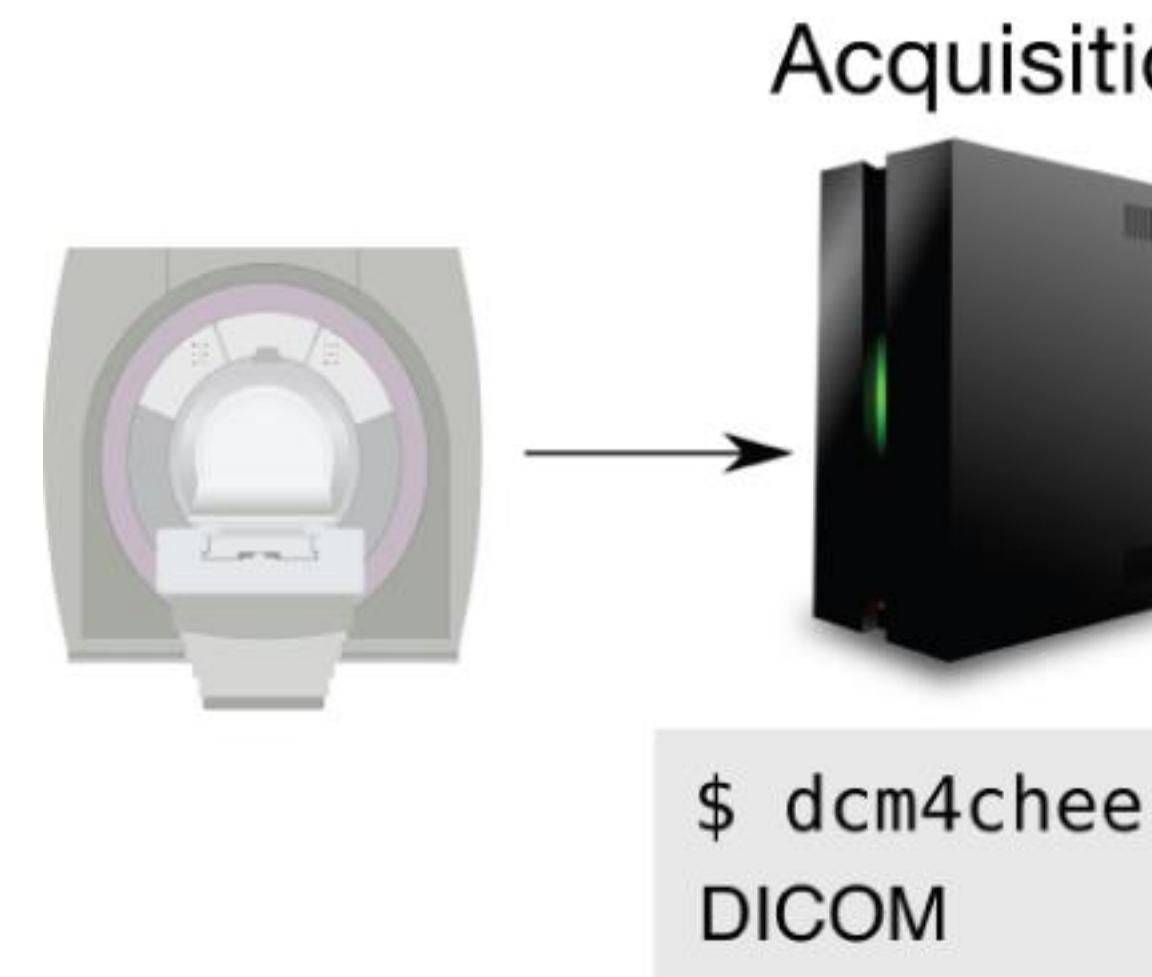
```
sub-<label>/[ses-<label>/]  
  beh/  
    sub-<label>[_ses-<label>]_task-<task_name>_events.tsv  
    sub-<label>[_ses-<label>]_task-<task_name>_events.json  
    sub-<label>[_ses-<label>]_task-<task_name>_beh.tsv  
    sub-<label>[_ses-<label>]_task-<task_name>_beh.json  
    sub-<label>[_ses-<label>]_task-<task_name>_physio.tsv.gz  
    sub-<label>[_ses-<label>]_task-<task_name>_physio.json  
    sub-<label>[_ses-<label>]_task-<task_name>_stim.tsv.gz  
    sub-<label>[_ses-<label>]_task-<task_name>_stim.json
```

In addition to logs from behavioral experiments performed along imaging data acquisitions one can also include data from experiments performed outside of the scanner. The results of those experiments can be stored in the beh folder using the same formats for event timing (`_events.tsv`), metadata (`_events.json`), physiological (`_physio.tsv.gz`, `_physio.json`) and other continuous recordings (`_stim.tsv.gz`, `_stim.json`) as for tasks performed during MRI acquisitions. Additionally, events files that do not include the mandatory `onset` and `duration` columns can still be included, but should be labelled `_beh.tsv` rather than `_events.tsv`.

Data: BIDS

ReproNim:

- HeuDiConv-based turnkey solution
- Automated version-controlled BIDS datasets
- Supported by DataLad (optional)



Images from: <https://github.com/ReproNim/repronim>

Figure 1. ReproNim workflow in use at t

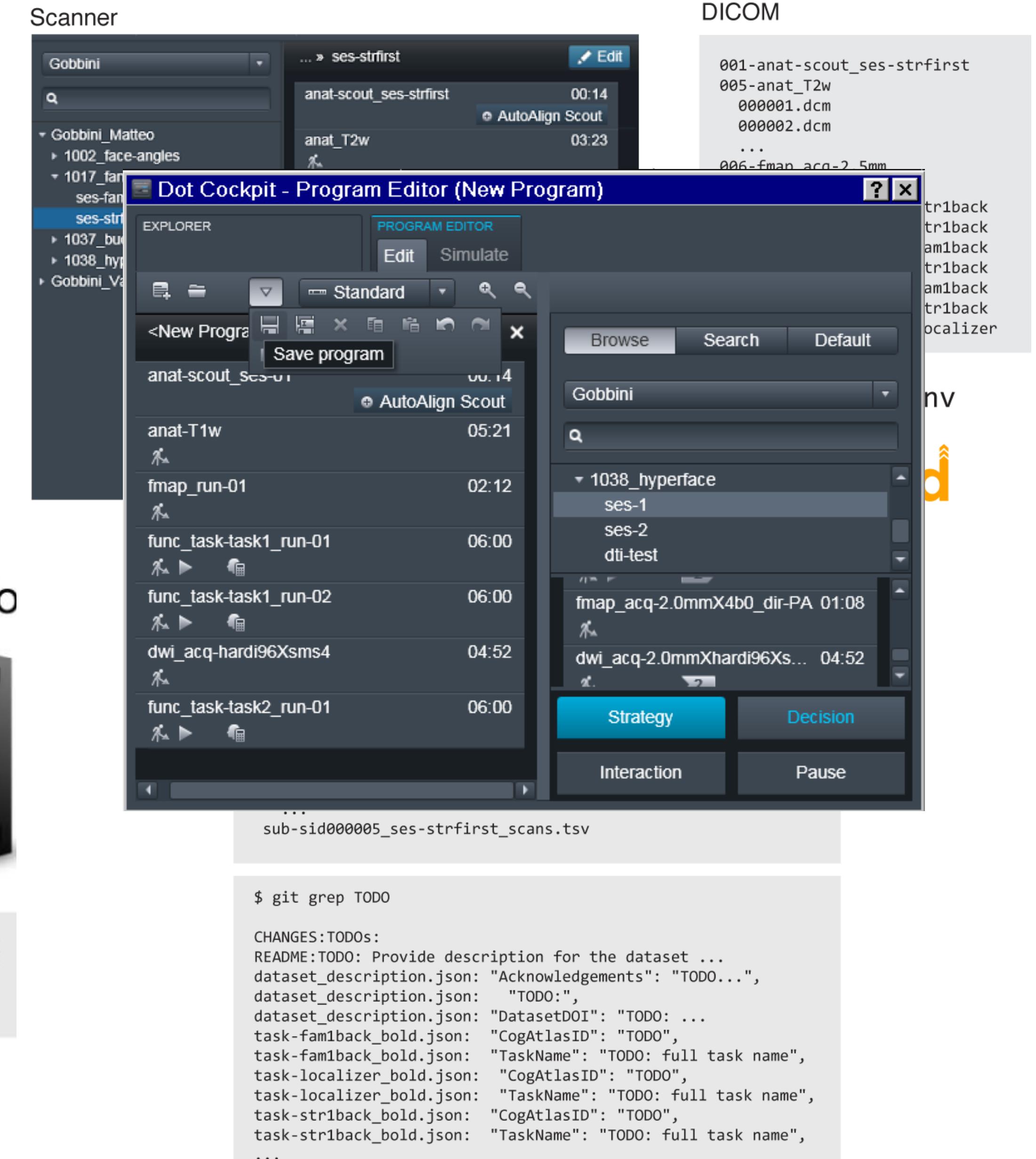
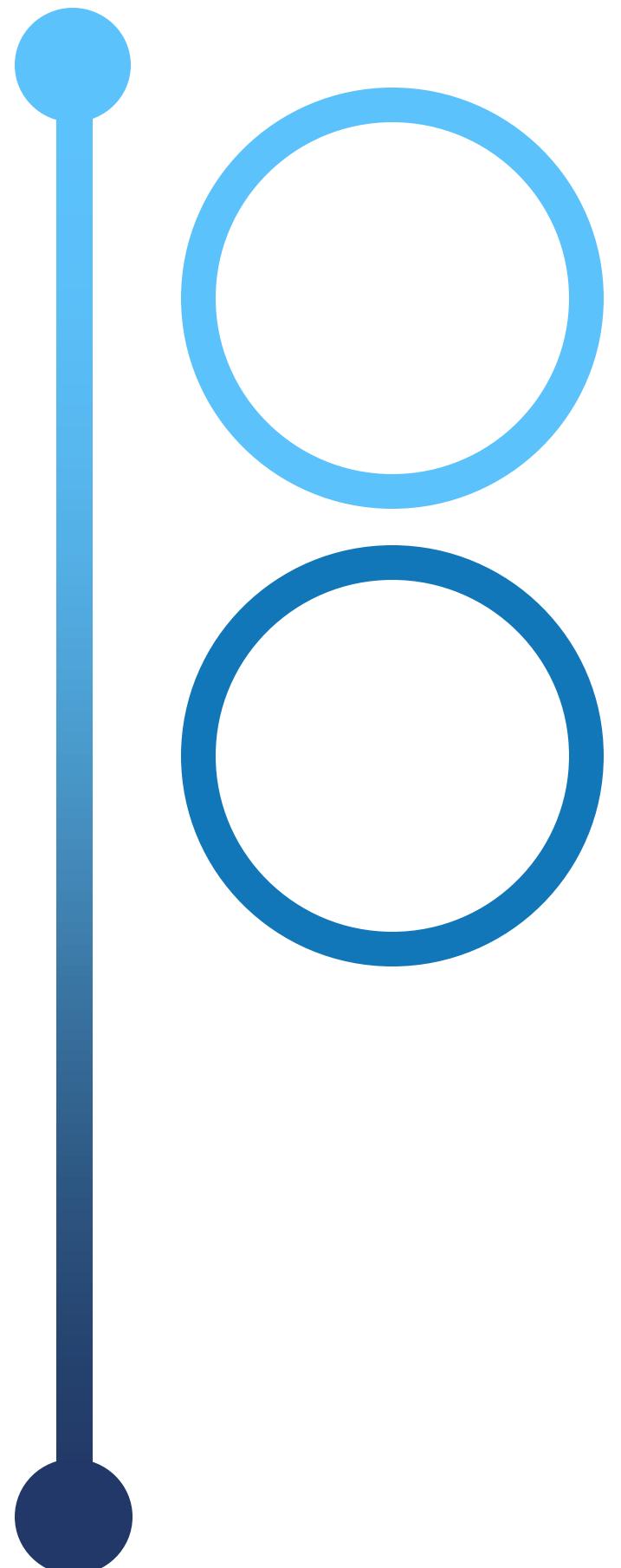


Figure 2. Example of the naming scheme at the scanner console, the resulting DICOM folder structure, and the automatically converted BIDS dataset. The user can quickly find what needs to be added by executing a simple git grep TODO, since the entire dataset is under git and DataLad control.

How to foster transparency and reproducibility

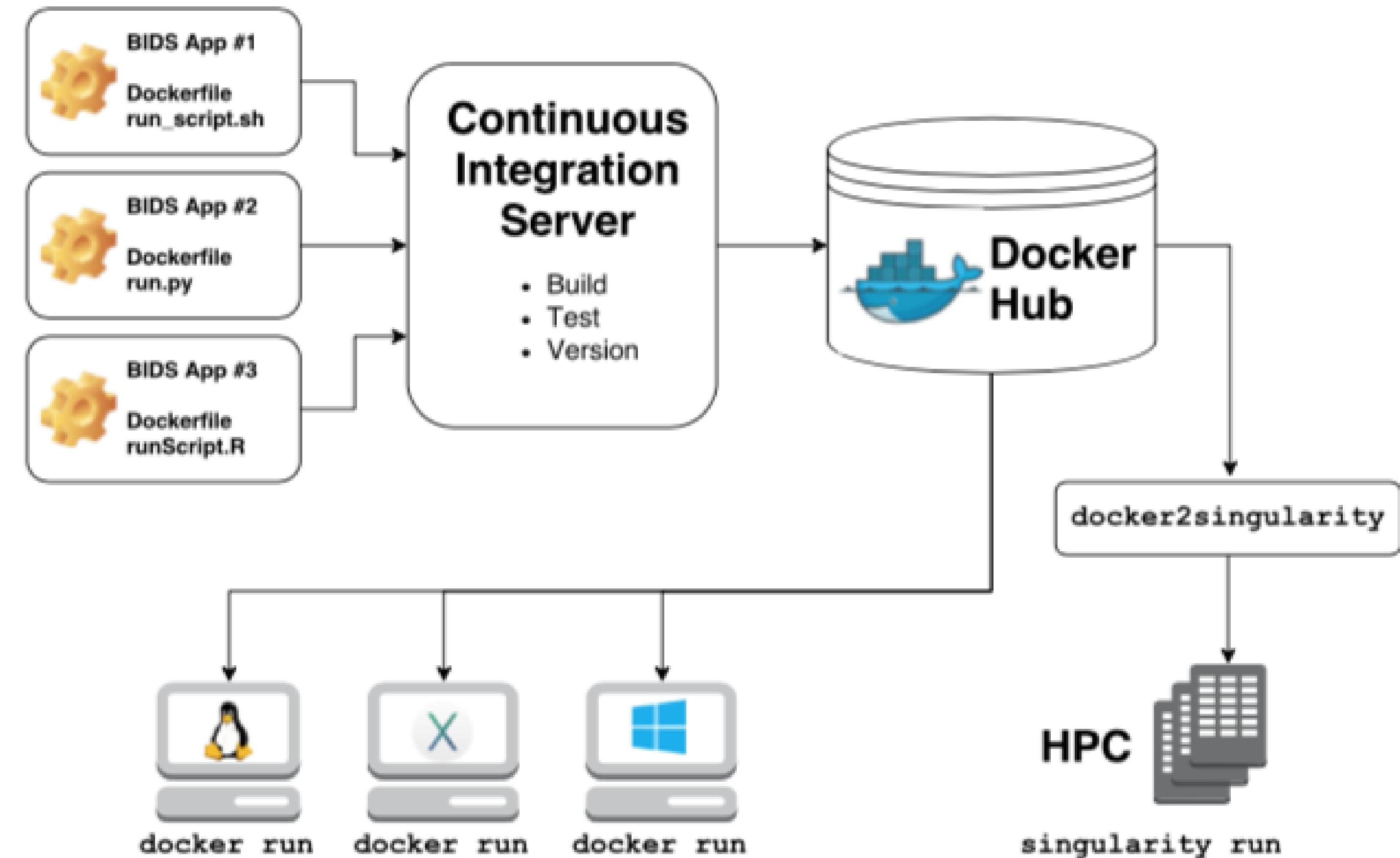


Data: BIDS

Code: BIDS apps [[MRIQC](#), [MRIQCception](#), [fMRIprep](#)]

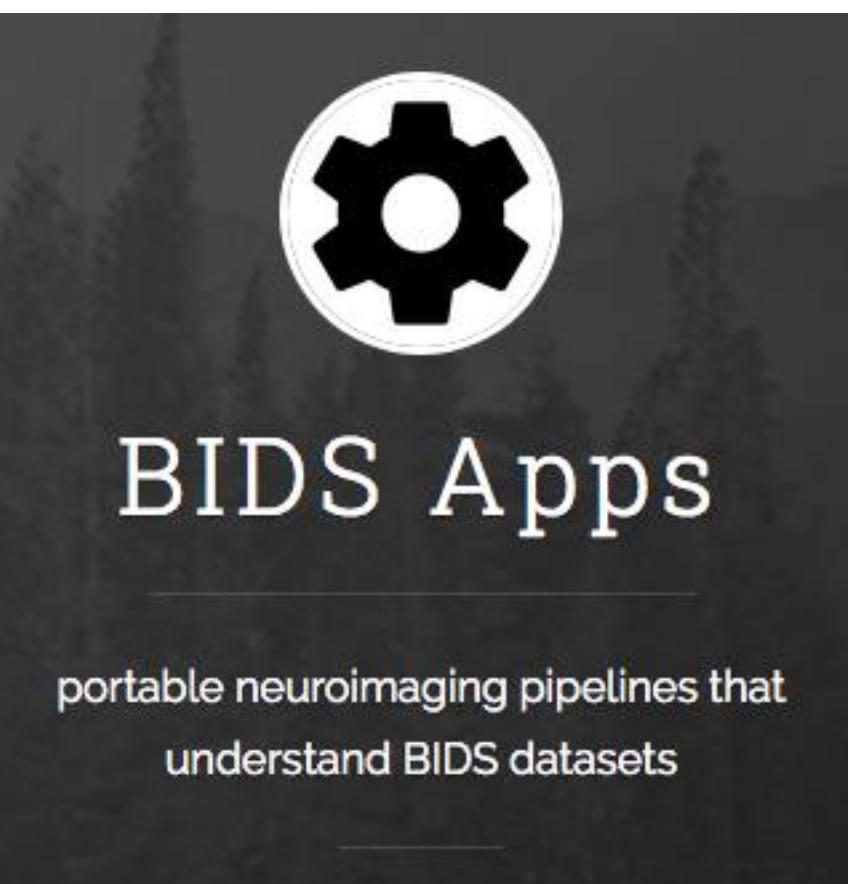
Code: BIDS apps

- “a container image capturing a neuroimaging pipeline that takes a BIDS-formatted dataset as input”
- Docker or Singularity
- Docker requires root permissions
- Use singularity on the grid
- Run for ‘participants’ or ‘group’



Code: BIDS apps

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



Available BIDS Apps

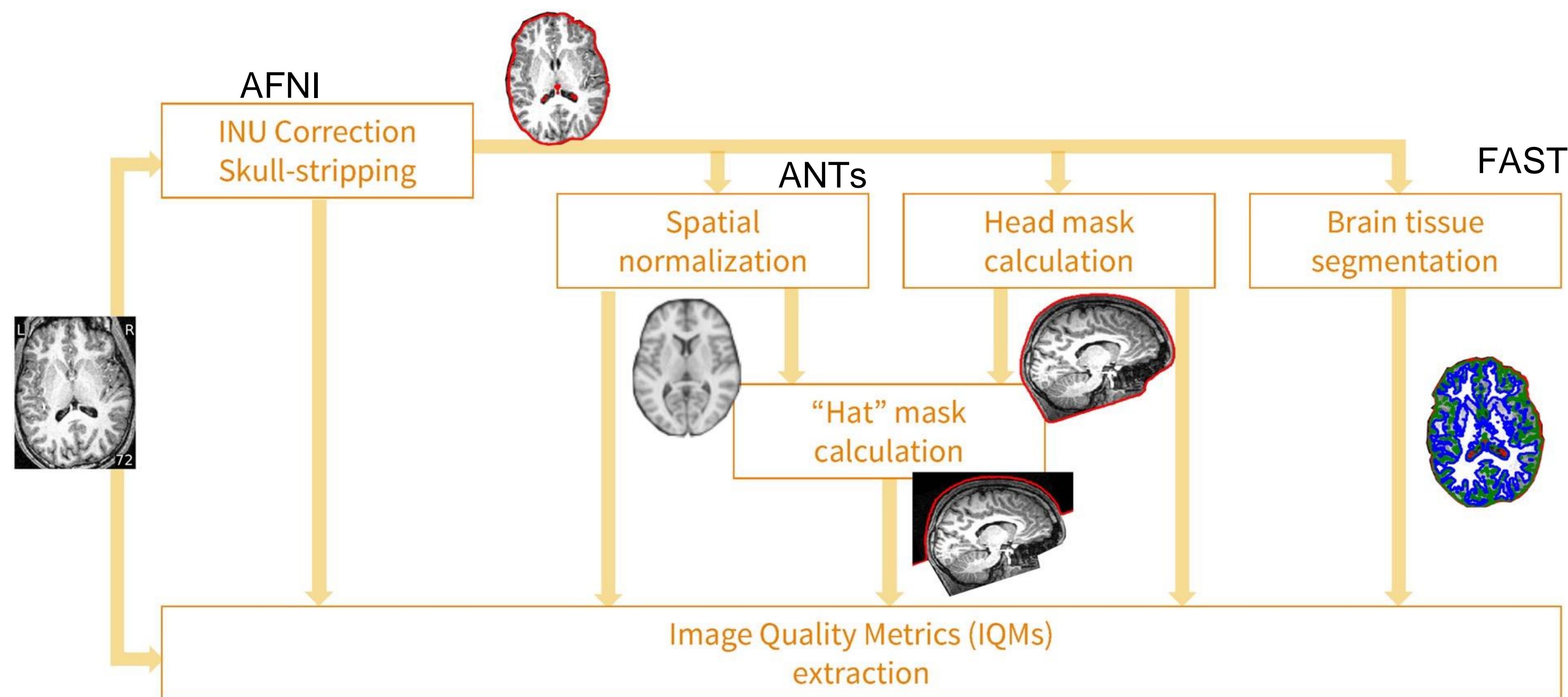
BIDS-Apps/example	version 0.0.7	open bug issues 0	build passing	open bug pull requests 0	docker pulls 13k	439.5MB 23 layers
BIDS-Apps/freesurfer	version	open bug issues 0	build failing	open bug pull requests 0	docker pulls 10k	2.6GB 52 layers
BIDS-Apps/ndmg	version v0.1.0	open bug issues 0	build passing	open bug pull requests 0	docker pulls 7.9k	920.9MB 31 layers
BIDS-Apps/BROCCOLI	version v1.0.1	open bug issues 1	build passing	open bug pull requests 0	docker pulls 505	3GB 21 layers
BIDS-Apps/FibreDensityAndCrosssection	version v0.0.1	open bug issues 0	build passing	open bug pull requests 0	docker pulls 237	576.8MB 31 layers
BIDS-Apps/SPM	version v0.0.15	open bug issues 0	build passing	open bug pull requests 0	docker pulls 1.4k	2GB 24 layers
poldracklab/mriqc	version 0.15.0	open bug issues 1	build passing	open bug pull requests 0	docker pulls 28k	3GB 41 layers
BIDS-Apps/QAP	Image not found	open bug issues 0	build passing	open bug pull requests 0	docker pulls 7	Image not found
BIDS-Apps/CPAC	version v1.0.1a_22	open bug issues 0	build passing	open bug pull requests 0	docker pulls 3.2k	1.6GB 45 layers
BIDS-Apps/hyperalignment	Image not found	open bug issues 0	build passing	open bug pull requests 0	docker pulls 165	Image not found
BIDS-Apps/mindboggle	version 0.0.4-1	open bug issues 2	build passing	open bug pull requests 0	docker pulls 647	1.9GB 81 layers
BIDS-Apps/MRtrix3_connectome	version latest	open bug issues 0	build passing	open bug pull requests 0	docker pulls 1.2k	7.3GB 56 layers
BIDS-Apps/rs_signal_extract	version 0.1	open bug issues 0	build passing	open bug pull requests 0	docker pulls 226	240MB 17 layers
BIDS-Apps/aa	version v0.2.0	open bug issues 0	build passing	open bug pull requests 0	docker pulls 259	6.3GB 30 layers
BIDS-Apps/niak	version latest	open bug issues 1	build passing	open bug pull requests 0	docker pulls 263	2.7GB 103 layers
BIDS-Apps/oppni	version v0.7.0-1	open bug issues 0	build passing	open bug pull requests 0	docker pulls 303	2.9GB 41 layers
poldracklab/fmriprep	version 1.5.0	open bug issues 19	build passing	open bug pull requests 0	docker pulls 331k	5GB 49 layers
BIDS-Apps/brainiak-srm	version latest	open bug issues 0	build failing	open bug pull requests 0	docker pulls 198	559.3MB 13 layers
BIDS-Apps/nipypipelines	version 0.3.0	open bug issues 0	build passing	open bug pull requests 0	docker pulls 291	478.1MB 20 layers
BIDS-Apps/HCPPipelines	version v3.17.0-18	open bug issues 0	build passing	open bug pull requests 0	docker pulls 1.7k	4GB 31 layers
BIDS-Apps/MAGeTbrain	Image not found	open bug issues 0	build passing	open bug pull requests 0	docker pulls 444	Image not found
BIDS-Apps/tracula	version v6.0.0-4	open bug issues 0	build passing	open bug pull requests 0	docker pulls 649	3.4GB 57 layers
BIDS-Apps/baracus	Image not found	open bug issues 0	build passing	open bug pull requests 0	docker pulls 1.1k	Image not found
BIDS-Apps/antsCorticalThickness	version v2.2.0-1	open bug issues 0	build passing	open bug pull requests 0	docker pulls 196	351.9MB 21 layers
BIDS-Apps/DPARSF	version v4.3.12	open bug issues 0	build passing	open bug pull requests 0	docker pulls 296	1.4GB 28 layers
BIDS-Apps/afni_proc	Image not found	open bug issues 0	build passing	open bug pull requests 0	docker pulls 186	Image not found

Code: MRIQC

- MRI Quality Control
- Can be run on OpenNeuro or locally
- Nipype workflow toolboxes from *FSL*, *ANTs* and *AFNI*.
- Requires minimal preprocessing
- Image Quality Metrics
- <https://mriqc.readthedocs.io/en/stable/>

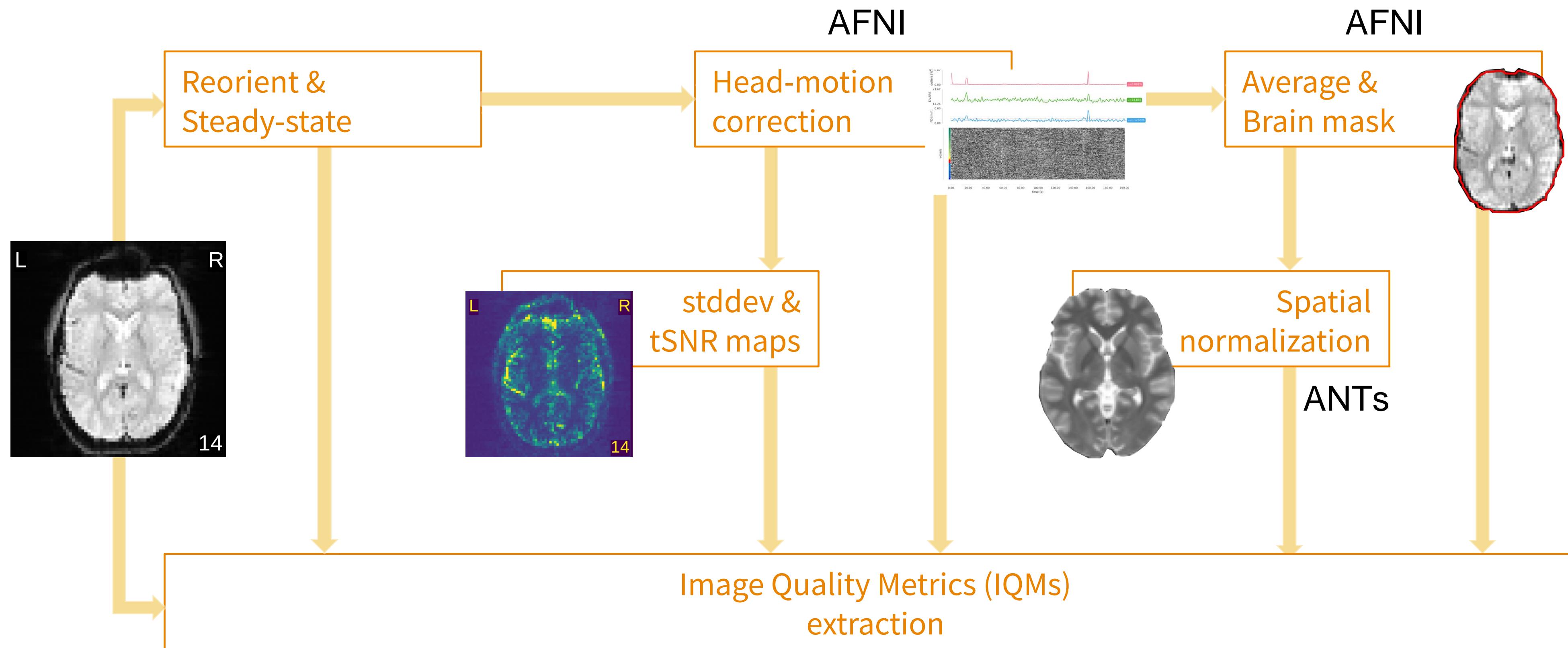
Code: MRIQC

- Anatomical workflow



Code: MRIQC

- Functional workflow



Code: MRIQC

- No-reference Image Quality Metrics (based on [QAP](#)):
No ground-truth, no-reference metrics
Stored in the JSON files and TSV files.

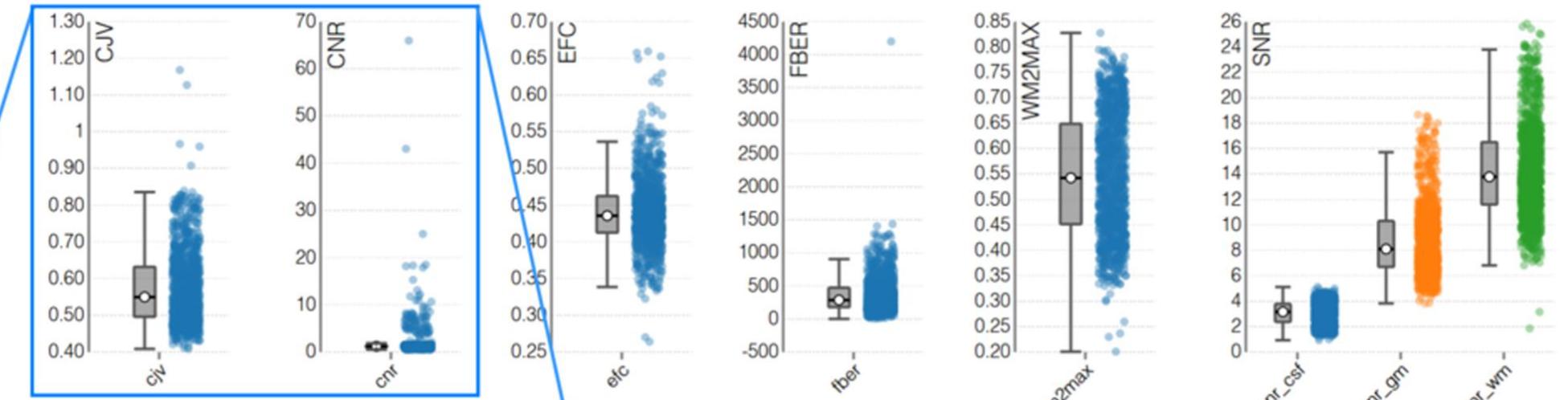
They can be mapped in four categories:

- *The impact of noise*
- *Spatial distribution of information*
- *Artifacts*
- *Other (e.g. tissue distributions, sharpness/blurriness of image)*

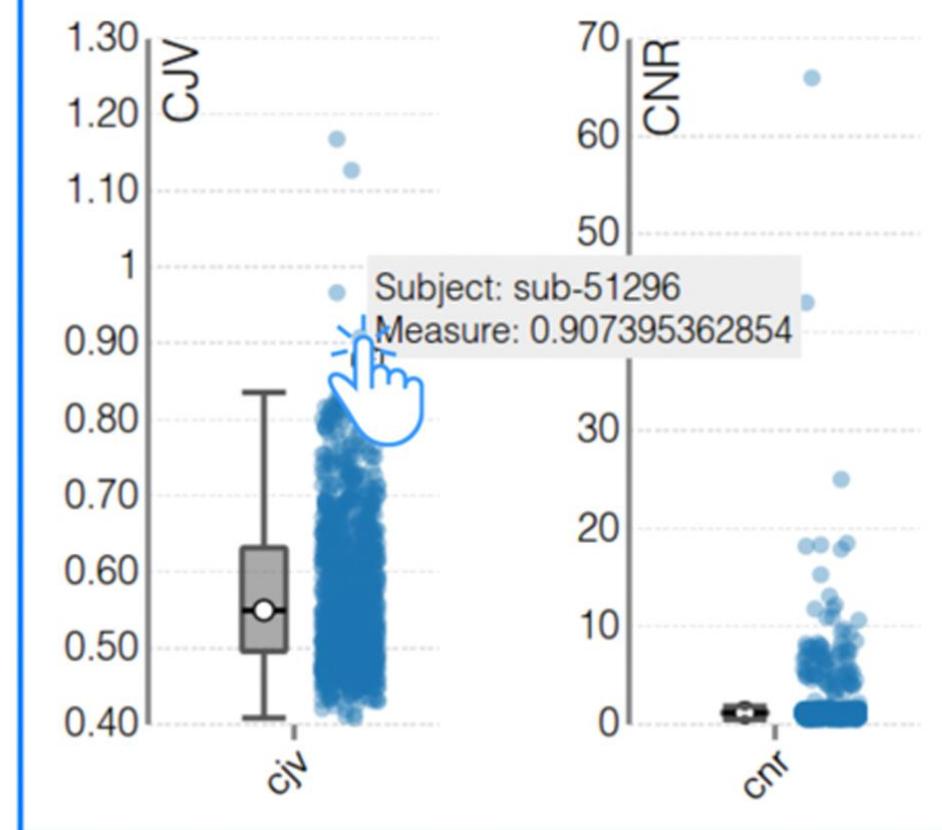
[My notes on the OSF](#)

① MRIQC: group anatomical report Summary

- Date and time: 2017-02-05, 12:27.
- MRIQC version: 0.9.0-rc2.



② MRIQC: individual anatomical report Summary



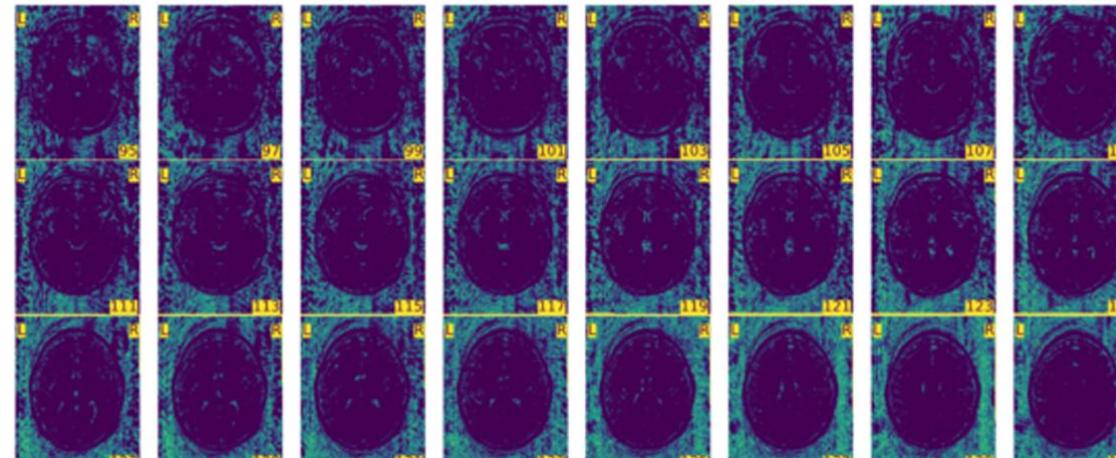
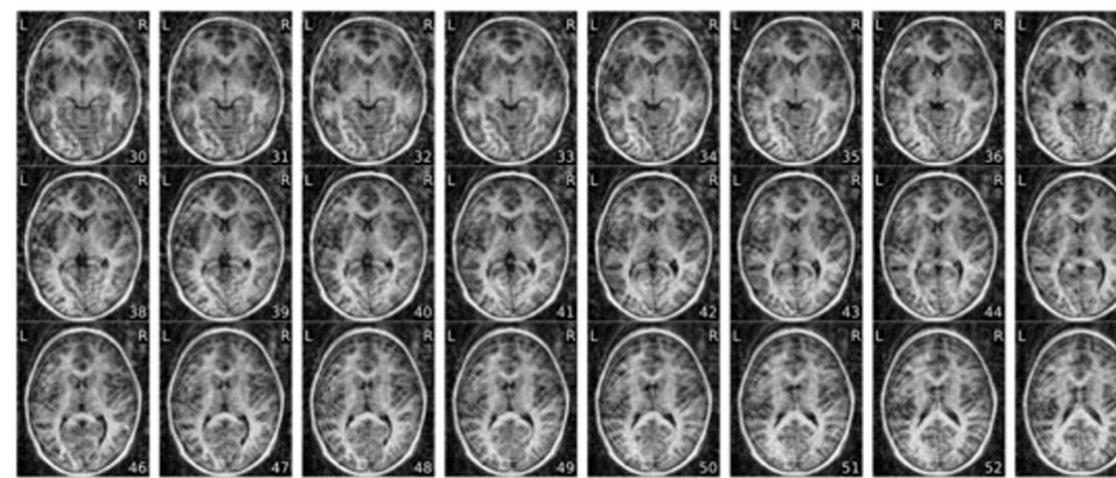
Data points in the scatter plots of the group report can be clicked to open the corresponding individual report. This feature is particularly useful to identify low-quality datasets visually.

③ The individual reports show the calculated IQMs and metadata in the summary, and a series of image mosaics and plots designed for the visual assessment of images.

MRIQC: individual anatomical report

Summary

- Subject ID: 51296.
- Date and time: 2017-02-05, 03:44.
- MRIQC version: 0.9.0-rc2.



Code: MRIQC

- How to

AnThroM

1. Details

2. BIDS dataset

3. Preprocessing

4. Analyses

5. IDAQ

6. fROI results

7. IDAQ and ROI Analysis

center the variables

```
usage: mriqc [-h] [--version]
              [--participant_label [PARTICIPANT_LABEL [PARTICIPANT_LABEL ...]]]
              [--session-id [SESSION_ID [SESSION_ID ...]]]
              [--run-id [RUN_ID [RUN_ID ...]]]
              [--task-id [TASK_ID [TASK_ID ...]]]
              [-m [{T1w,bold,T2w} [{T1w,bold,T2w} ...]])] [--dsname DSNAME]
              [-w WORK_DIR] [--verbose-reports] [--write-graph] [--dry-run]
              [--profile] [--use-plugin USE_PLUGIN] [--no-sub] [--email EMAIL]
              [-v] [--webapi-url WEBAPI_URL] [--webapi-port WEBAPI_PORT]
              [--upload-strict] [--n_procs N_PROCS] [--mem_gb MEM_GB]
              [--testing] [-f] [--ica] [--hmc-afni] [--hmc-fsl]
              [--fft-spikes-detector] [--fd_thres FD_THRES]
              [--ants-nthreads ANTS_NTHREADS] [--ants-float]
              [--ants-settings ANTS_SETTINGS] [--deoblique] [--despike]
              [--start-idx START_IDX] [--stop-idx STOP_IDX]
              [--correct-slice-timing]
              bids_dir output_dir {participant,group} {{participant,group} ...}
```

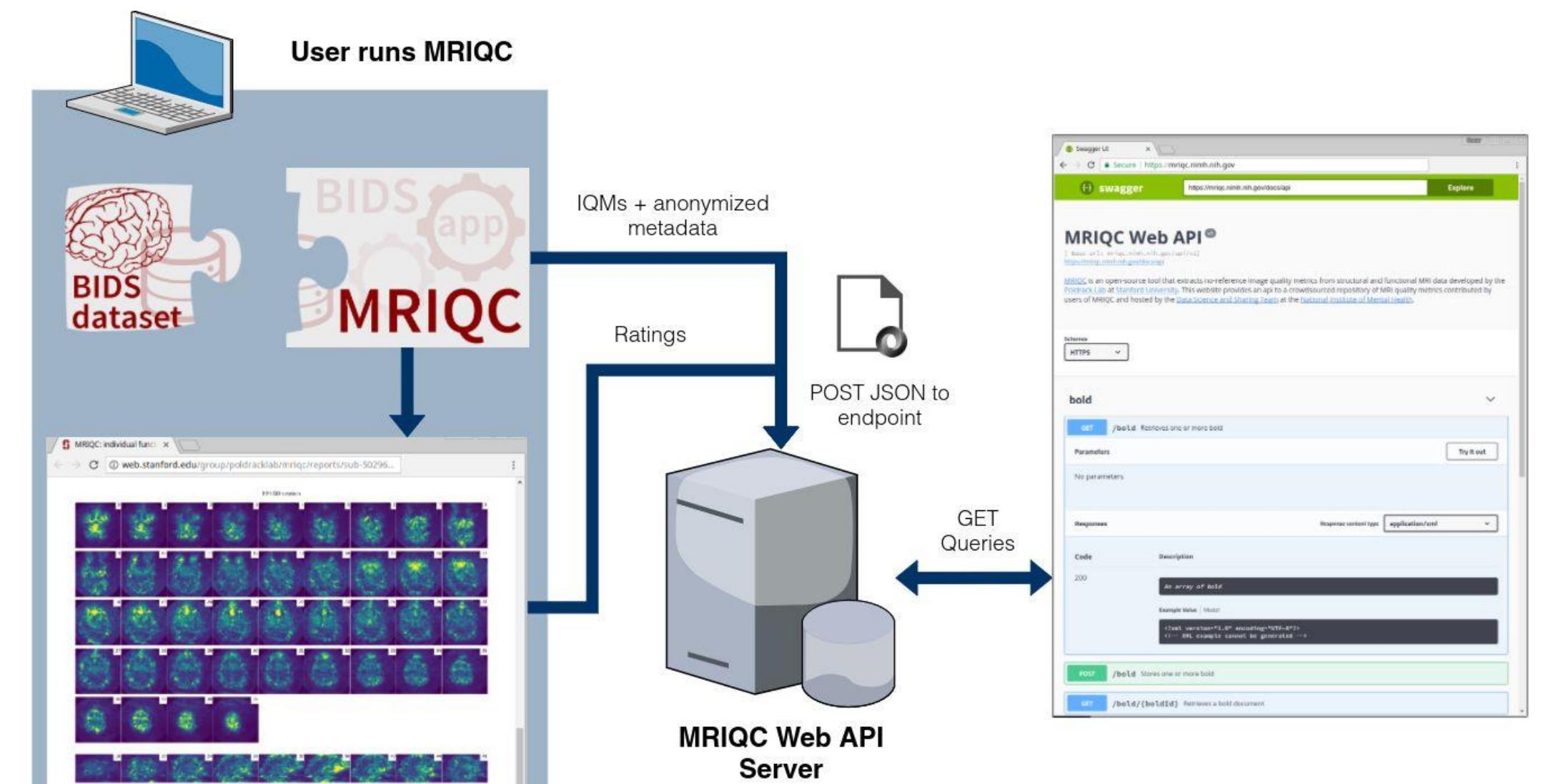
Code: MRIQCception

- No-reference Image Quality Metrics (based on [QAP](#)):
No ground-truth these are considered as no-reference

Reference point:

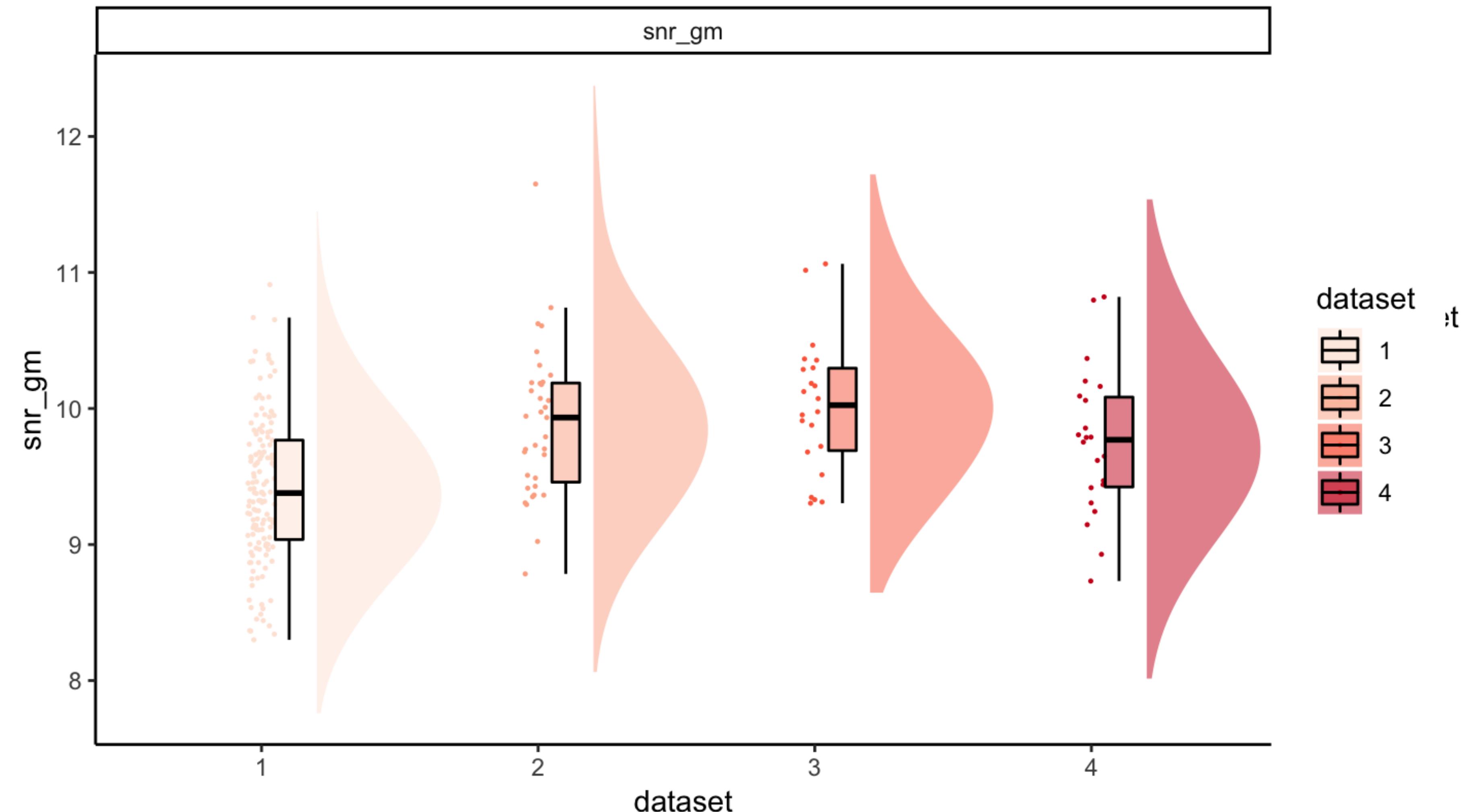
- <https://github.com/elizabethbeard/mriqception>

- Download MRIQC Web-API: >30K (Esteban et al. <https://doi.org/10.1101/216671>):
<https://mriqc.nimh.nih.gov/>



Code: MRIQCception

Comparison of t1w QC measure snr_gm between datasets





Code: fMRIprep

- Preprocessing pipeline:
 - Minimal input
 - Minimal preprocessing (standard, except smoothing)
 - Reproducible, automated pipeline: “analysis-agnostic”
 - Interpretable reports, high-quality processing
 - Nipype combination of: FSL, ANTs, Freesurfer and AFNI
 - Results in a boilerplate for methods!
- Version control, regular updates

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

On the plurality of (methodological) worlds: estimating the analytic flexibility of fMRI experiments

Joshua Carp*

Department of Psychology, University of Michigan, Ann Arbor, MI, USA



ORIGINAL RESEARCH
published: 24 April 2015
doi: 10.3389/fninf.2015.00012

Reproducibility of neuroimaging analyses across operating systems

Tristan Glatard^{1,2}, Lindsay B. Lewis¹, Rafael Ferreira da Silva³, Reza Adalat¹, Natacha Beck¹, Claude Lepage¹, Pierre Rioux¹, Marc-Etienne Rousseau¹, Tarek Sherif¹, Ewa Deelman³, Najmeh Khalili-Mahani¹ and Alan C. Evans^{1*}



OPEN ACCESS Freely available online

The Effects of FreeSurfer Version, Workstation Type, and Macintosh Operating System Version on Anatomical Volume and Cortical Thickness Measurements

Ed H. B. M. Gronenschild^{1,2*}, Petra Habets^{1,2}, Heidi I. L. Jacobs^{1,2,3}, Ron Mengelers^{1,2}, Nico Rozendaal^{1,2}, Jim van Os^{1,2,4}, Machteld Marcelis^{1,2}

¹ Department of Psychiatry and Neuropsychology, School for Mental Health and Neuroscience, Maastricht University Medical Center, Maastricht, Alzheimer Center Limburg, The Netherlands, ² European Graduate School of Neuroscience (EURON), Maastricht University, Maastricht, The Netherlands, ³ Cognitive Neurology Section, Institute of Neuroscience and Medicine-3, Research Centre Jülich, Jülich, Germany, ⁴ King's College London, King's Health Partners, Department of Psychosis Studies Institute of Psychiatry, London, United Kingdom

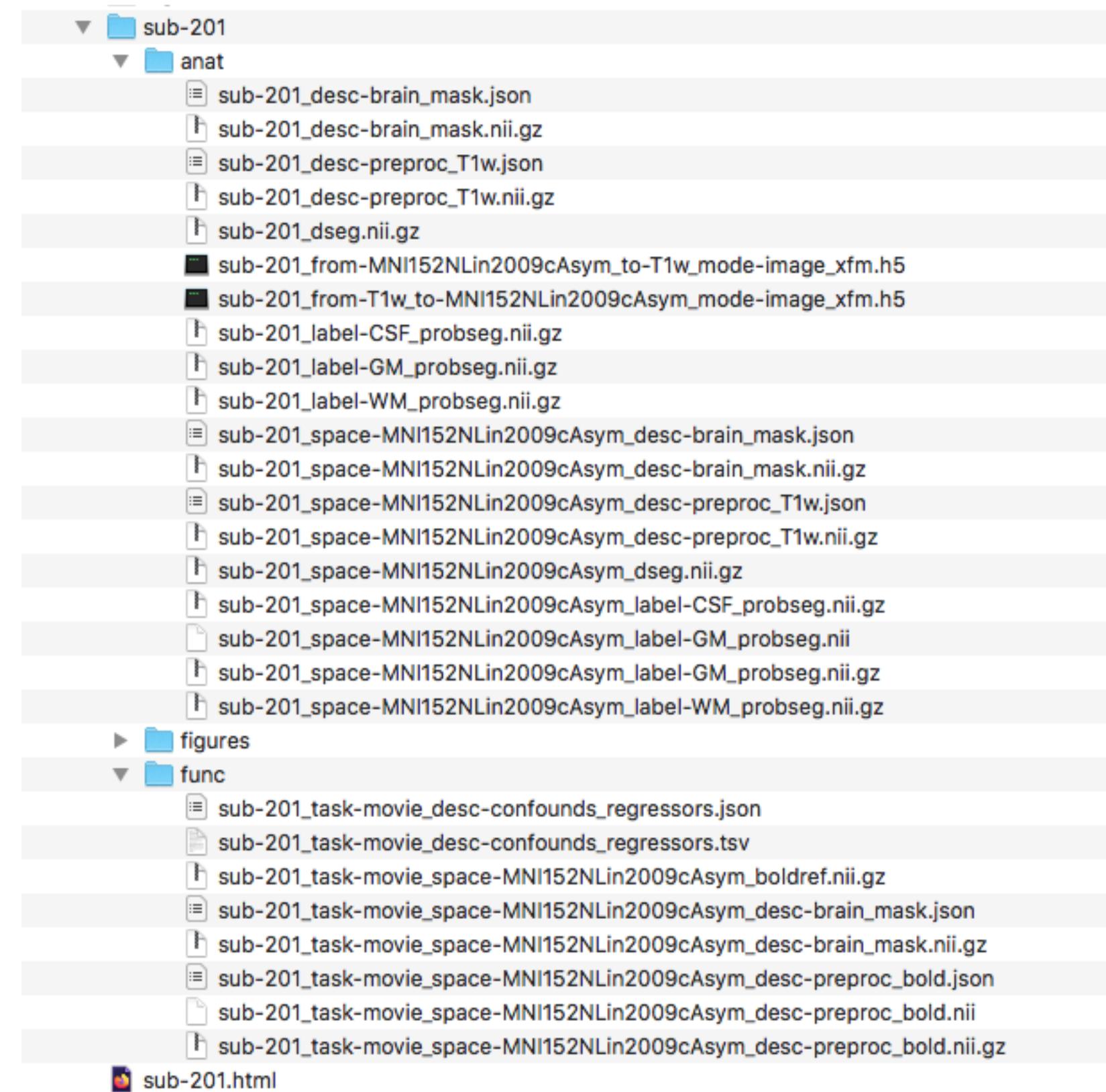
Code: fMRIprep

- 3 principles:
 - Robustness
 - Easy to use
 - “Glass box”

Why not use it:

- narrow FoV (but might in the future)
- Special populations (infants and non-human brains) – but with 1.4.1 new templates
- EPInorm approach is not support (but might be in the future)

Review by Sam Nastase: if you want unlimited flexibility, students to suffer, or if using in-house pipeline



Code: fMRIprep

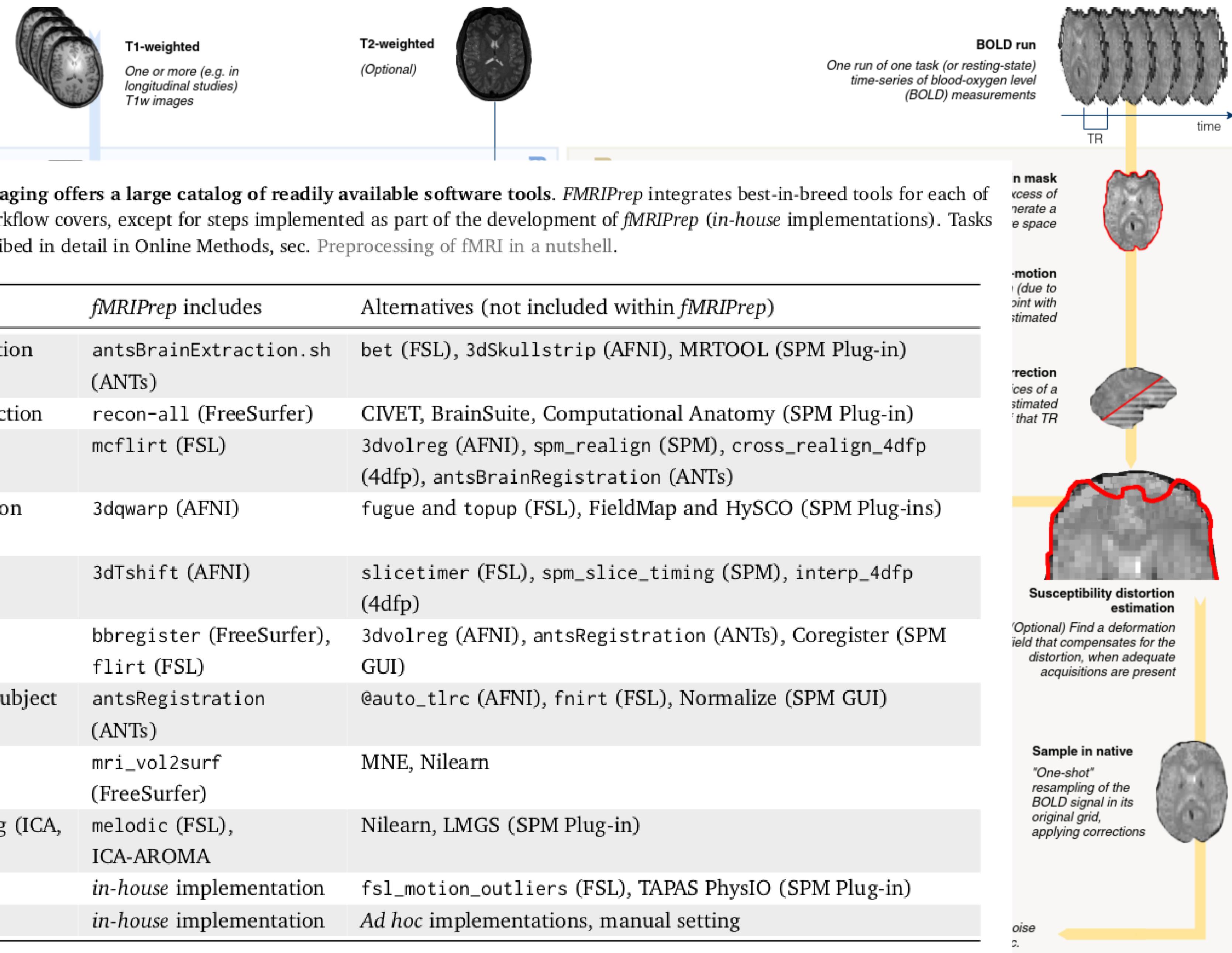


Table 1. State-of-the-art neuroimaging offers a large catalog of readily available software tools. *fMRIprep* integrates best-in-breed tools for each of the preprocessing tasks that its workflow covers, except for steps implemented as part of the development of *fMRIprep* (*in-house* implementations). Tasks listed on the first column are described in detail in Online Methods, sec. Preprocessing of fMRI in a nutshell.

Code: fMRIprep

- How to

- AnThroM

- 1. Details

- 2. BIDS dataset

- 3. Preprocessing

- 4. Analyses

- 5. IDAQ

- 6. fROI results

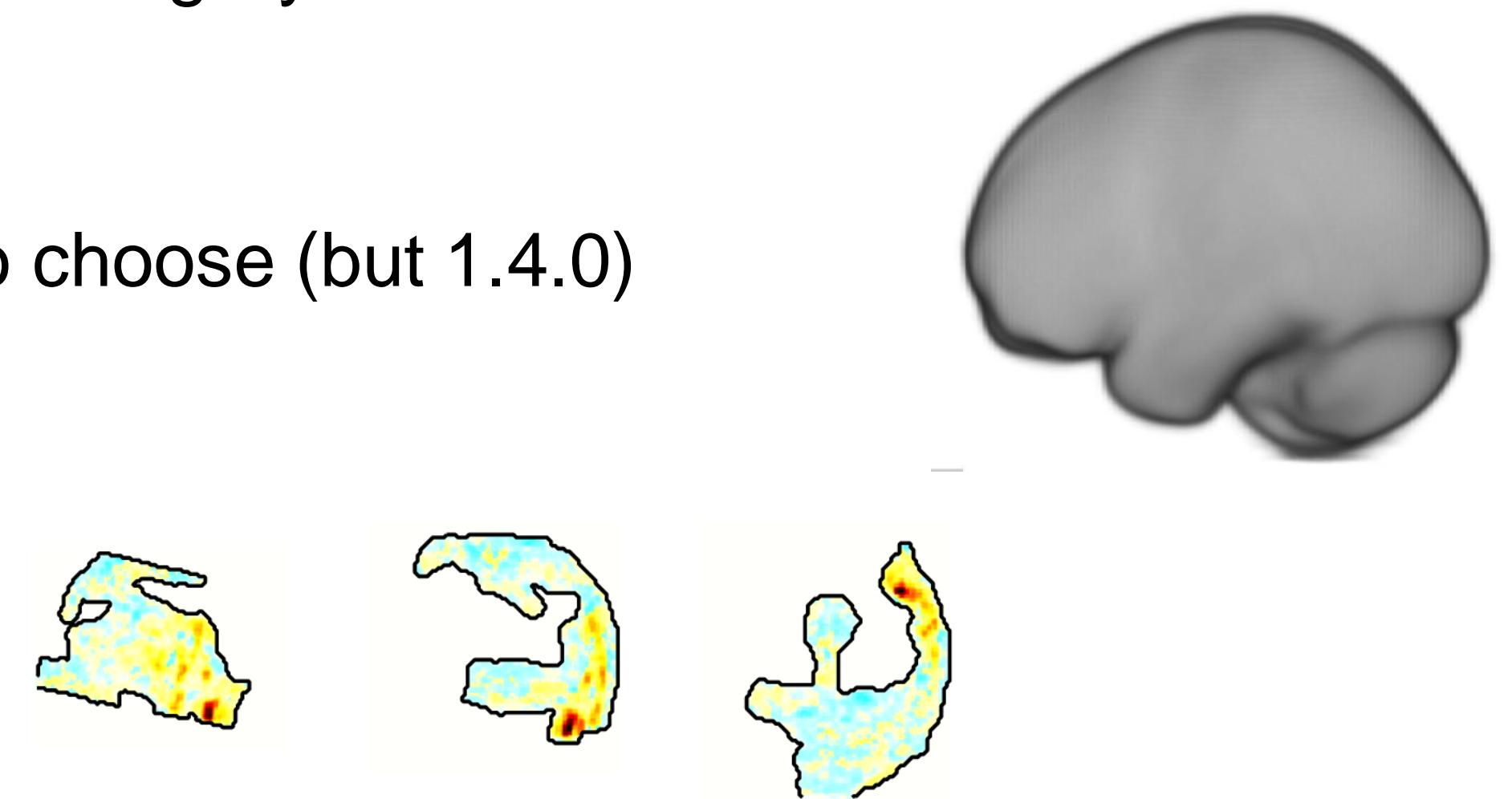
- 7. IDAQ and ROI Analysis

- center the variables

```
usage: fmriprep [-h] [--version] [--skip_bids_validation]
                  [--participant_label PARTICIPANT_LABEL [PARTICIPANT_LABEL ...]]
                  [-t TASK_ID] [--echo-idx ECHO_IDX] [--nthreads NTHREADS]
                  [--omp-nthreads OMP_NTHREADS] [--mem_mb MEM_MB] [--low-mem]
                  [--use-plugin USE_PLUGIN] [--anat-only] [--boilerplate]
                  [--md-only-boilerplate] [--error-on-aroma-warnings] [-v]
                  [--ignore {fieldmaps,slicetiming,sbref} [{fieldmaps,slicetiming,sbref} ...]]
                  [--longitudinal] [--t2s-coreg]
                  [--output-spaces OUTPUT_SPACES [OUTPUT_SPACES ...]]
                  [--bold2t1w-dof {6,9,12}] [--force-bbr] [--force-no-bbr]
                  [--medial-surface-nan] [--dummy-scans DUMMY_SCANS]
                  [--use-aroma]
                  [--aroma-melodic-dimensionality AROMA_MELODIC_DIMENSIONALITY]
                  [--return-all-components]
                  [--fd-spike-threshold FD_SPIKE_THRESHOLD]
                  [--dvars-spike-threshold DVARS_SPIKE_THRESHOLD]
                  [--skull-strip-template SKULL_STRIP_TEMPLATE]
                  [--skull-strip-fixed-seed] [--fmap-bspline] [--fmap-no-demean]
                  [--use-syn-sdc] [--force-syn] [--fs-license-file PATH]
                  [--fs-subjects-dir PATH] [--no-submm-recon]
                  [--cifti-output | --fs-no-reconall] [-w WORK_DIR]
                  [--resource-monitor] [--reports-only] [--run-uuid RUN_UUID]
                  [--write-graph] [--stop-on-first-crash] [--notrack] [--sloppy]
                  bids_dir output_dir {participant}
```

Code: BIDS apps

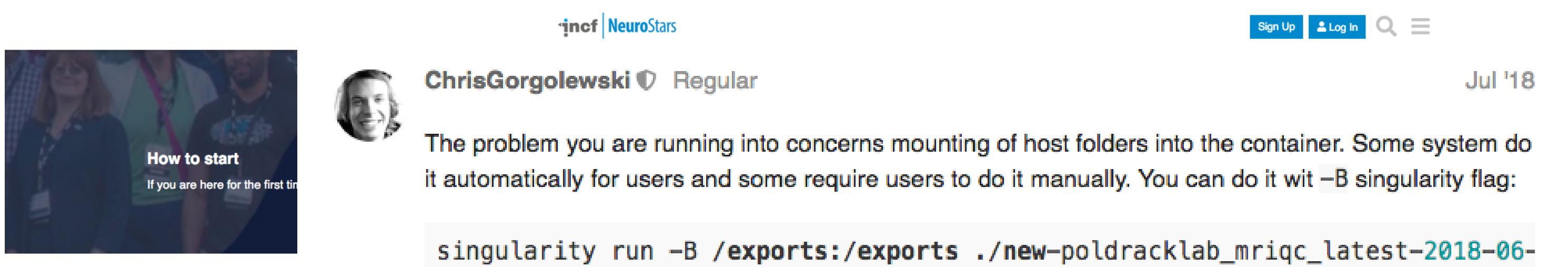
- Some issue:
 - Singularity on the GRID only on CentOS 7.x systems (matlab5-grid.psy.gla.ac.uk and nodes)
 - GRID: Processors: 2 * 8 Core opteron - 128GB Ram memory - Operating System: CentOS 7.x
 - Permission issues (chmod all the way to second-level analysis)
 - Docker: >8GB of RAM
 - hacky way around it) (no --func_only flag, yet)
 - Use runs for So so so many confounds for fMRIprep, which ones to choose (but 1.4.0)
 - /func only (but tasks with only one run ← output of fmriprep)
 - Didn't work for one subject out of >100 (brain mask for bold)
 - BIDS: Check heuristic (changing names between studies)
 - Install dependencies for Pydeface
 - Terminal heavy
- Always always use /work folder (should by outside of /bids_folder)
- Always use one version per study
- Use Rmd or Jupyter notebook



Code: NeuroStars



- <https://neurostars.org/> the stackoverflow for neuroimagers



A screenshot of a NeuroStars post by user ChrisGorgolewski. The post is titled "How to start" and includes the sub-instruction "If you are here for the first time". The post content discusses mounting host folders into a container using the Singularity -B flag. It includes a command-line snippet:

```
singularity run -B /exports:/exports ./new-poldracklab_mriqc_latest-2018-06-
```

If this does not work (Singularity on your system might be configured in a way that does not allow creation of mountpoints inside the container dynamically) you will have to recreate the container with -m flag. See <https://github.com/singularityware/docker2singularity#my-clusterhpc-requires-singularity-images-to-include-specific-mount-points> for more details:

```
docker run \
-v /var/run/docker.sock:/var/run/docker.sock \
-v D:\host\path\where\to\output\singularity\image:/output \
--privileged -t --rm \
singularityware/docker2singularity \
-m "/exports" \
poldracklab/mriqc
```

BTW it seems that the version of singularity you are using might be recent enough to try to build the singularity image on the cluster instead of docker2singularity:

```
singularity build /path/where/you/want/to/store/container/images/mriqc-0.11.
```

How to foster transparency and reproducibility



Data: BIDS

Code: BIDS apps [MRIQC, MRIQCception, fMRIprep]

Paper: NeuroVault, OpenNeuro

Paper: sharing your data

- Derivatives: NeuroVault <https://neurovault.org/>
- Raw: OpenNeuro: <https://openneuro.org/> among others
- Recommended license: CC0
 - unrestricted Public Domain
 - No restrictions
 - Consider the impact of non-commercial clause, no-derivatives clause
- Ask for explicit consent for data sharing! <https://open-brain-consent.readthedocs.io>
- Anonymise (pydeface, no CCNi codes!): https://open-brain-consent.readthedocs.io/en/latest/anon_tools.html

Open Brain Consent
latest

Search docs

Sample consent forms
Recommendations
Discussions
Ultimate consent form
Anonymization tools
Contribute
Contact information

Docs » Make open data sharing a no-brainer for ethics committees. [Edit on GitHub](#)

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

Zenodo badge

Statement of the problem

The ideology of open and reproducible science makes its ways into various fields of science.
Neuroimaging is a driving force today behind many fields of brain sciences. Despite possibly

Sample consent forms

[samples/](#) directory of our [git repository](#) contains samples of the consent forms found online. Because there is no explicit permission allowing their re-distribution we are not including them in this repository/site, but rather link to them as they are available on the web. Our [git repository](#) is



OPEN BRAIN CONSENT FORM

We will give public access to all the data from this project via an open online database. This will allow other researchers to check our analyses or apply their own analyses to our data. The data might be used to address topics other than those of the current project – for instance to develop or validate new analysis methods. Thus, open data sharing can help improve the impact of our research and avoid duplication of research efforts.

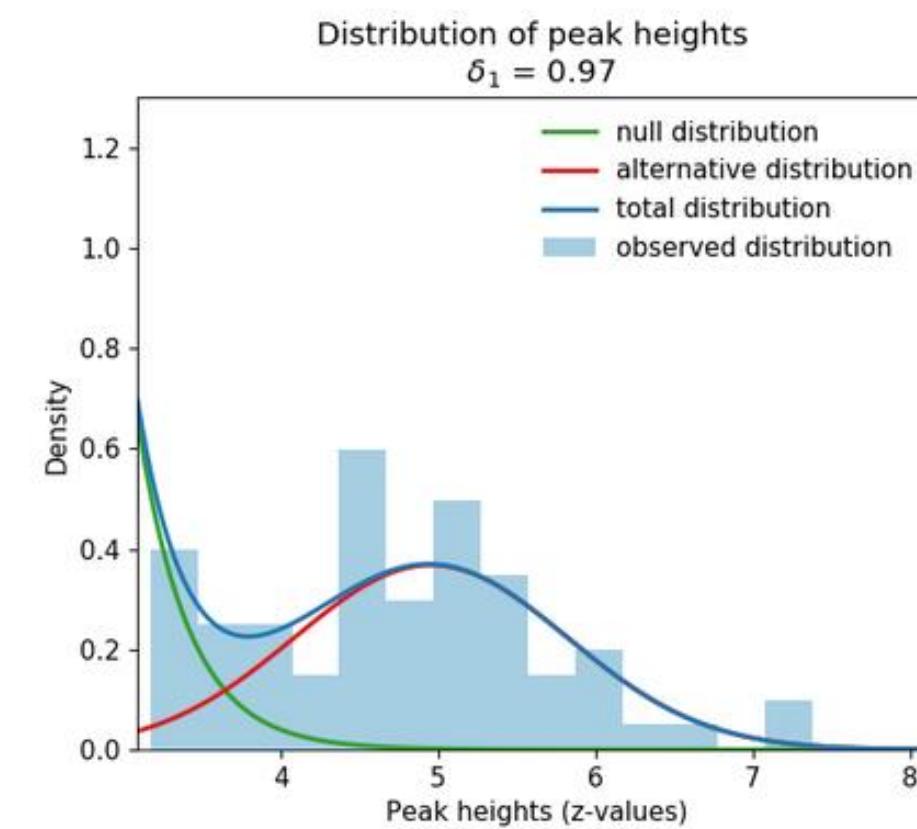
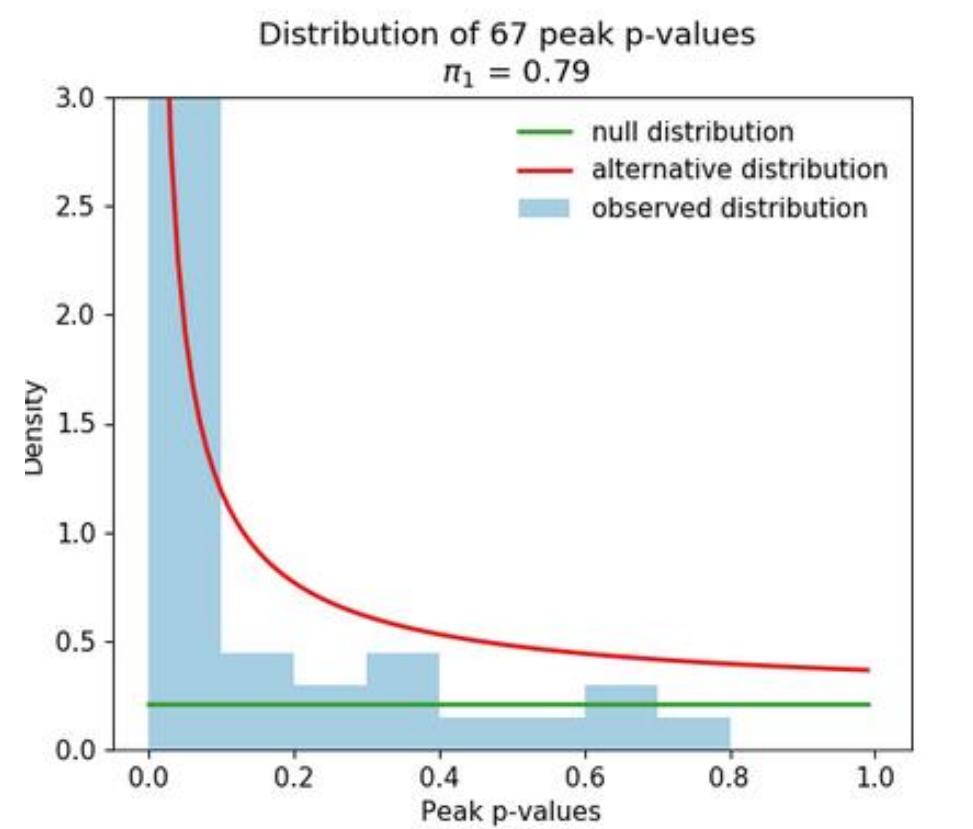
- [UR_Gia_fMRI_Study_Consent_form_UoZ0110.doc](#)
- [USC_Informed-Consent-Template-3-29-13-FMRI.doc](#)
- [psychLMU_ConsentForm_Template_Dyads_German.pdf](#)
- [psychLMU_ConsentForm_Template_NonDyads_German.pdf](#)
- [psychLMU_ConsentForm_Template_easy_German.pdf](#)

Paper: NeuroVault

- www.neurovault.org

Can be used to:

- Publish group maps, parcellations, and atlases
- Perform power analyses
- Run meta-analysis
- Decode activity



NeuroVault Collections ▾ Metaanalyses ▾ About ▾ rhortensius ▾ Search Search

My collections

A collection is a set of images grouped together for some sensible reason. Most commonly, a collection contains all of the images from a single study.

Show 25 entries

Search:

Name	Num. images	Description	Has DOI?
A neurocognitive investigation of the impact of socializing with a robot on empathy for pain	27	Cross, E. S., Riddoch, K. A., Pratts, J., Titone, S., Chaudhury, B., & Hortensius, R. (2019). A neurocognitive investigation of the impact of socialising with a robot on empathy for pain: http://doi.org/10.1101/470534	Yes
AnThrom	5	Testing the relation between Theory-of-Mind network activation and dispositional anthropomorphism	

Showing 1 to 2 of 2 entries

Add new collection

Previous 1 Next

API · Github · Cognitive Atlas · NeuroSynth

What is it?

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

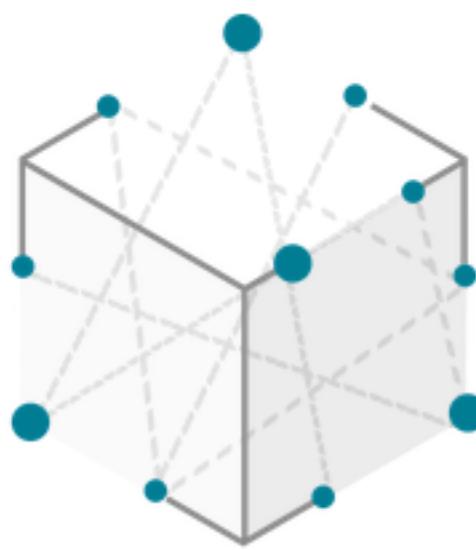
Why use it?

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

Supported by



Paper: OpenNeuro



- Public or restricted for 36 months
- Can be used to run fmriprep
- BIDS data

OpenNEURO

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

CEREBRuM: a 3T MRI segmentation tool

uploaded by Franklin Feingold on 2019-09-26 - 5 months ago
last modified on 2019-09-26 - 5 months ago
authored by Michele Svanera, Lars Muckli
 35 54799

[PUBLIC DATASETS](#) [Download](#) [Analyze on brainlife.io](#)

PUBLIC DATASET R

OpenNeuro Accession Number: ds002207
Files: 10, **Size:** 54.1MB, **Subjects:** 7, **Session:** 1

Cerebellum Retinotopic Mappir **No Available Tasks**
UPLOADED BY Tomas Knapen ON 2020-02-19 - ABC
Available Modalities: T1w
FILES: 324 **SIZE:** 10.07GB **SUBJECT:**

Differential brain mechanisms
UPLOADED BY roman quentin ON 2020-02-12 - 7 D **README**
The dataset is composed by 7 subjects, scanned at the Centre for Cognitive Neuroimaging (CCNi) at the Institute of Neuroscience and Psychology, University of Glasgow.

Protecting the Aging Brain (PAg Psychology, University of Glasgow.
UPLOADED BY Andrew Litten ON 2020-02-12 - 7 D These data serve as testing dataset for the paper:
FILES: 44 **SIZE:** 8.76GB **SUBJECT:** 1

Bontempi, D., Benini, S., Signoroni, A., Svanera, M., & Muckli, L. (2019). CEREBRuM: a Convolutional Encoder-decodeR for Fully Volumetric Fast sEgmentation of BRain MRI. arXiv preprint arXiv:1909.05085.

[PUBLIC DASHBOARD](#) [SUPPORT](#) [FAQ](#) [SIGN IN](#)

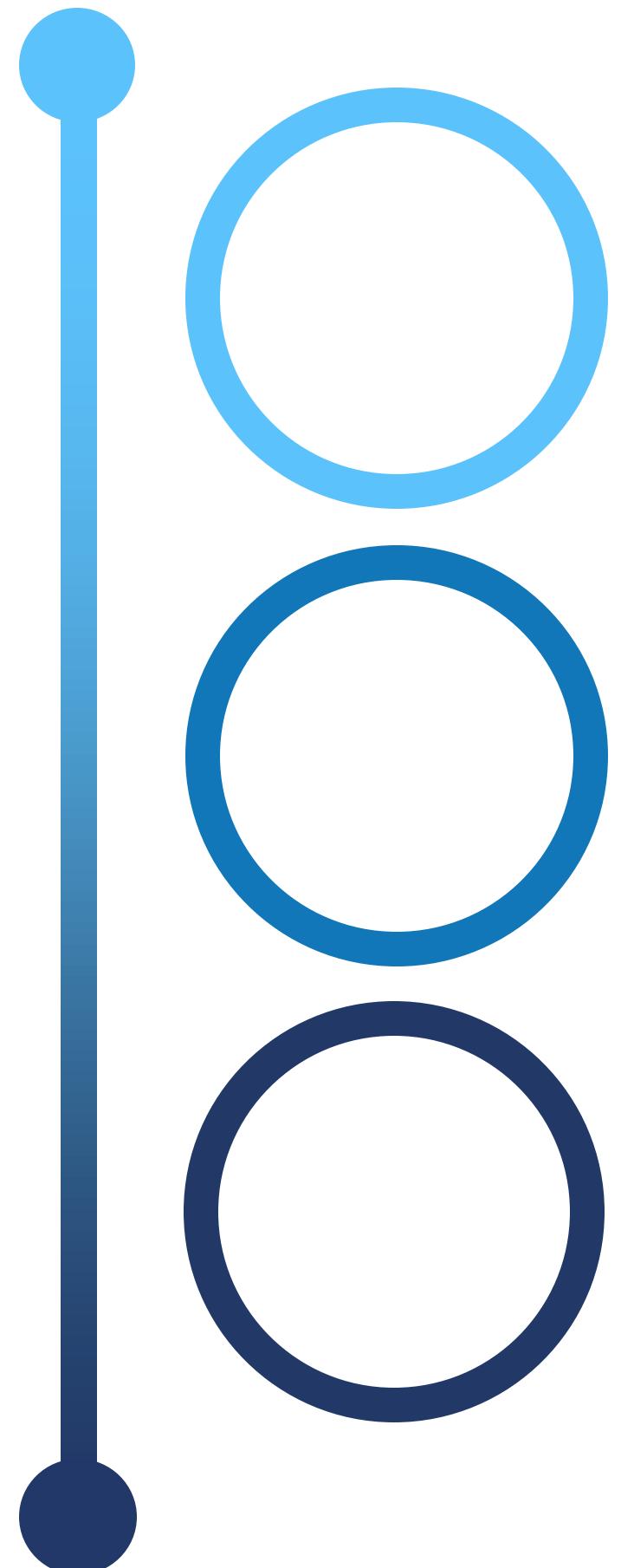
Search Datasets

Eye icon 70 1

Eye icon 197 1

Eye icon 5 **Paw icon** 1152

How to foster transparency and reproducibility



Data: BIDS

Code: BIDS apps [MRIQC, MRIQCception, fMRIprep]

Paper: NeuroVault, OpenNeuro

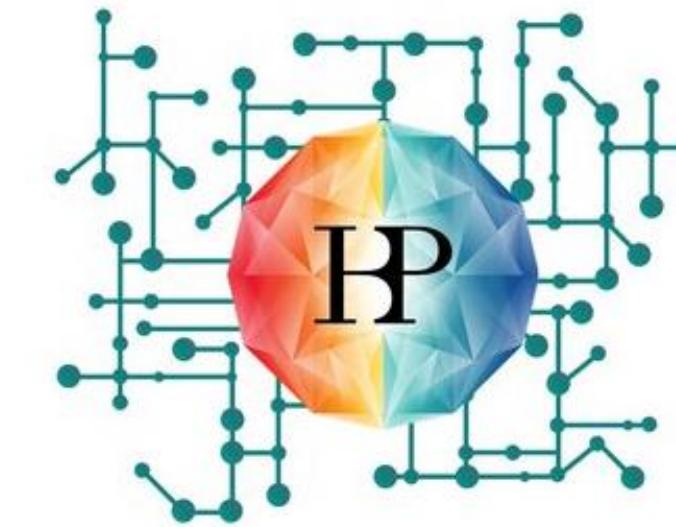
Thank you!

Special shout out to:

<https://www.humanbrainproject.eu/en/explore-the-brain/search/>

FIND data

HBP Knowledge Graph is now part of the EBRAINS platform



Explore HBP's neuroscience datasets shared through EBRAINS' Knowledge Graph [data sharing repository](#)

Resources:

BIDS: <https://bids.neuroimaging.io/>

Docker: <https://www.docker.com/>

MRIQC: <https://mriqc.readthedocs.io/>

MRIQception: <https://github.com/elizabethbeard/mriqception>

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

Neurovault: <https://neurovault.org/>

OpenNeuro: <https://openneuro.org/>

NeuroStars: <https://neurostars.org/>

Slides + material: <https://osf.io/c28jq/>