



Nipopyy: A framework for the **organization and decentralized processing** of neuroimaging-clinical studies

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ORIGAMI
Lab

How can we make neuroimaging datasets more FAIR?

- **FAIR**: findable, accessible, interoperable, reusable (Wilkinson *et al.*, 2016)

Existing open standards/tools developed by the community



(Gorgolewski *et al.*, 2016)



(Kurtzer *et al.*, 2017)



(Glatard *et al.*, 2018)

We leveraged existing open science tools to build a flexible framework for data organization and processing of neuroimaging-clinical data

The **Nipoppy** protocol

Capture

data at the **source**



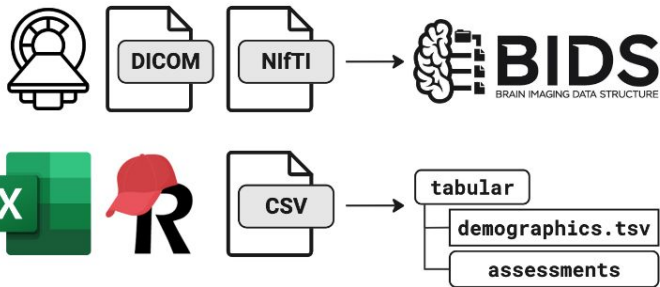
The **Nipoppy** protocol

Capture

Organize

data at the **source**

imaging and non-imaging data



The **Nipoppy** protocol

Capture

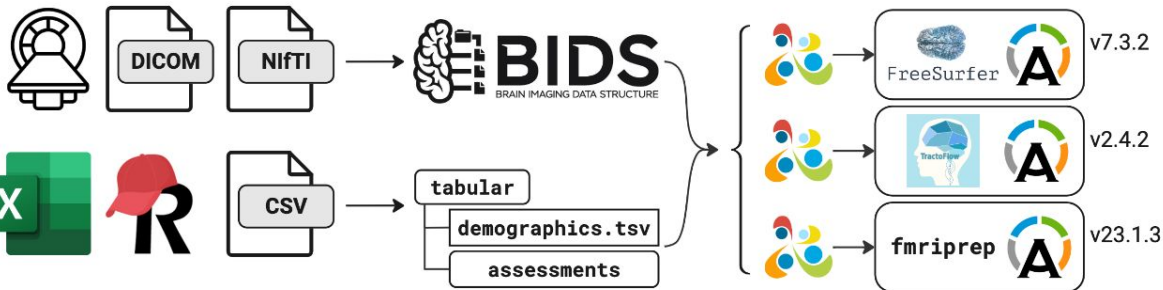
Organize

Process

data at the **source**

imaging and non-imaging data

with **reproducible environments**



The **Nipopy** protocol

Capture

Organize

Process

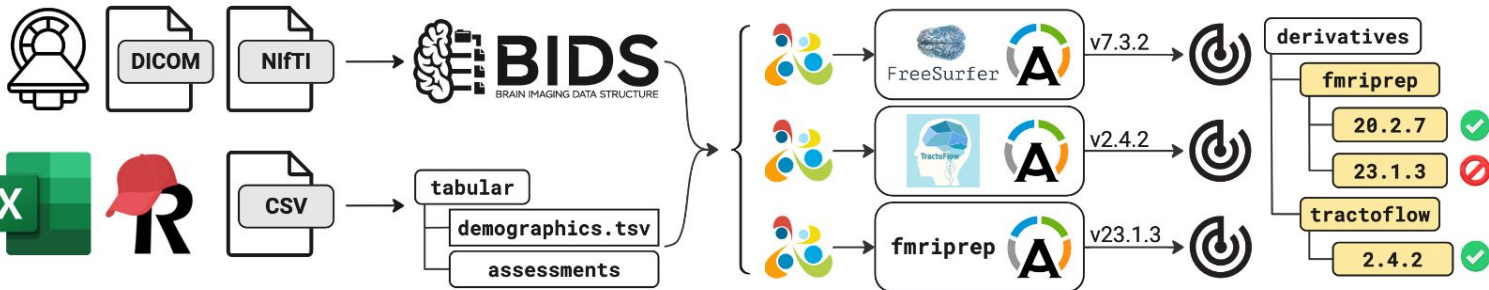
Track

data at the **source**

imaging and non-imaging data

with **reproducible environments**

data availability at the **participant level**



<https://digest.neurobagel.org/>



Neuroimaging and phenotypic dataset exploration beta

[Input schema](#) [Example input files](#) [GitHub](#)

Upload your own digest file:

Select imaging CSV file...

Select phenotypic CSV file...

Load an available digest file:

Available imaging digests ▾

Available phenotypic digests ▾



The **Nipopy** protocol

Capture

Organize

Process

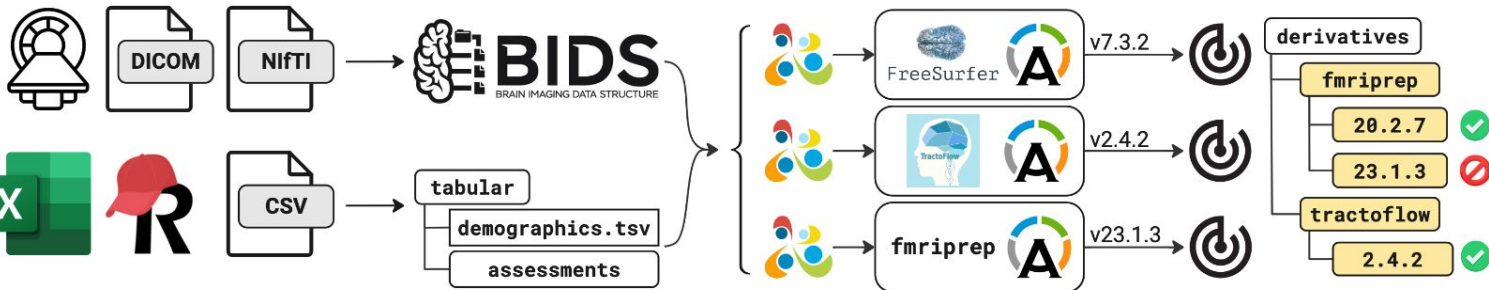
Track

data at the **source**

imaging and non-imaging data

with **reproducible environments**

data availability at the **participant level**



The **Nipopy** protocol

Capture

Organize

Process

Track

Extract

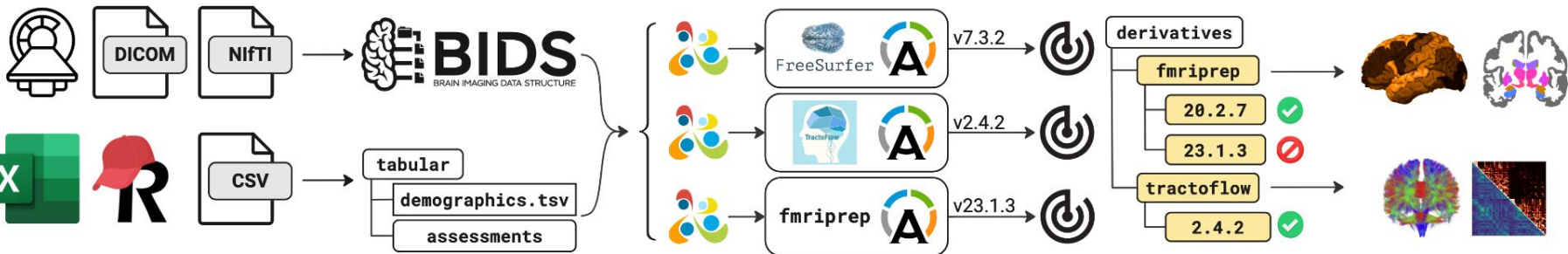
data at the **source**

imaging and non-imaging data

with **reproducible** environments

data availability at the **participant level**

analysis-ready features



The **Nipoppy** protocol and software tools



<https://nipoppy.readthedocs.io/>



<https://github.com/nipoppy/nipoppy>

Capture

Organize

Process

Track

Extract

```
Usage: nipoppy [-h] [--version] {init,doughnut,reorg,bidsify,run,track,extract} ...

Organize and process neuroimaging-clinical datasets.

Options:
  -h, --help            Show this help message and exit.
  --version              Show version number and exit.

Subcommands:
  {init,doughnut,reorg,bidsify,run,track,extract}
  init                  Initialize a new dataset.
  doughnut              Create/update a dataset's doughnut file.
  reorg                 (Re)organize raw (DICOM) files, from the raw DICOM directory
                       (<DATASET_ROOT>/scratch/raw_imaging) to the organized
                       sourcedata directory (<DATASET_ROOT>/sourcedata).
  bidsify               Run a BIDS conversion pipeline.
  run                   Run a processing pipeline.
  track                 Track the processing status of a pipeline.
  extract               Run an extraction pipeline.

Run 'nipoppy COMMAND --help' for more information on a subcommand.
```

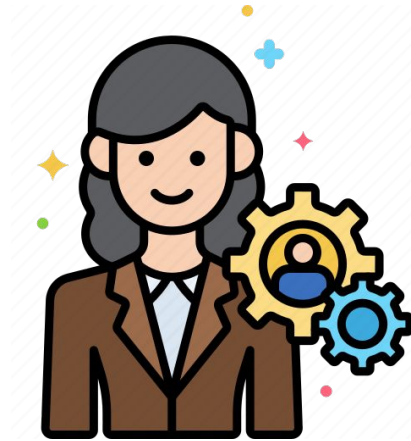
Nipoppy takeaways

For trainees



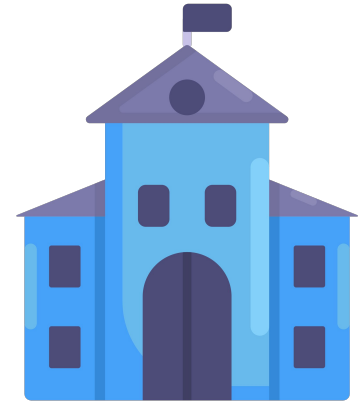
Best/FAIR practices


For labs



Efficiency and consistency

For institutions



Data-sharing
Metadata discovery
with **Neurobagel** 

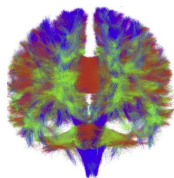
Nipoppy at The Neuro



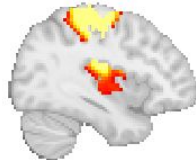
Parkinson's
Progression
Markers
Initiative



Anat. MRI



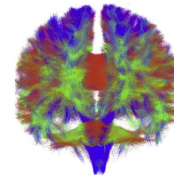
Diff. MRI



Func. MRI



Anat. MRI



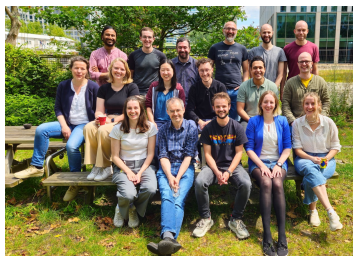
Diff. MRI
(in progress)



Func. MRI
(to come)

Nipoppy beyond The Neuro

ENIGMA-PD working group
(*Ysbrand van der Werf*)



NIMHANS large ongoing PD study in Bangalore, India
(*Shweta Prasad*)



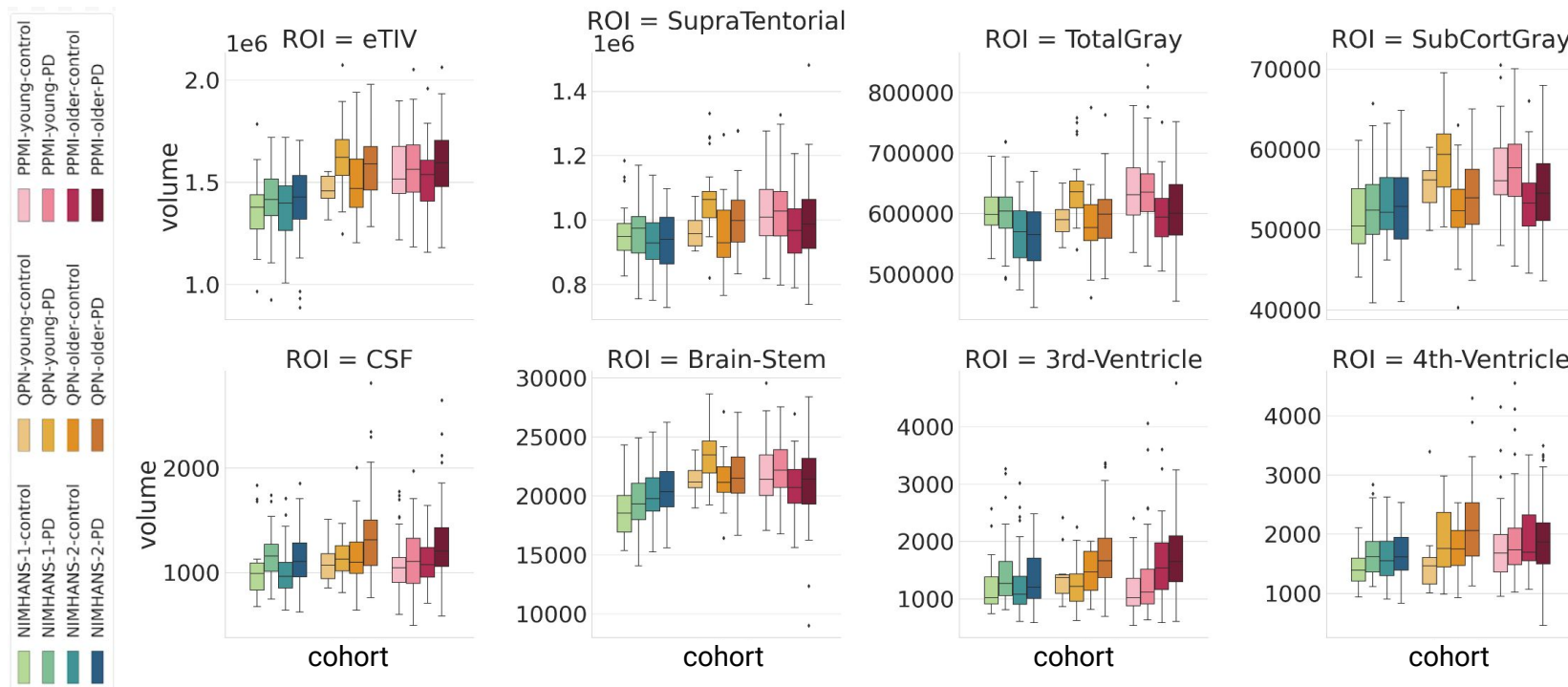
CRIUGM PD-MCI dataset
(*Oury Monchi*)



Douglas research centre
(*Mallar Chakravarty*)

Example **Nipopyy** application

Decentralized data processing → imaging-derived pheno. **sharing** → joint analysis



Thank you!



Nikhil
Bhagwat



Alyssa
Dai



Jacob
Sanz-Robinson



Mathieu
Dugré



Sebastian
Urchs



Mohammad
Torabi



Rémi
Gau



Brent
McPherson



Jean-Baptiste
Poline

