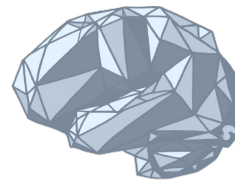


Nipoppy and Neurobagel: Practical tools to navigate barriers for FAIR research

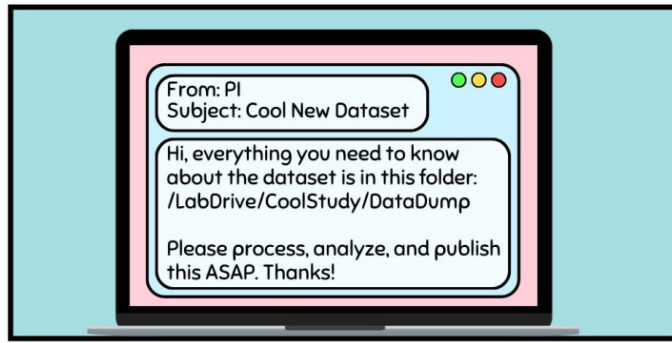
Michelle Wang
PhD candidate, NeuroDataScience-ORIGAMI Lab (JB Poline)

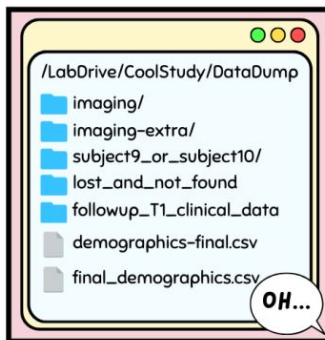
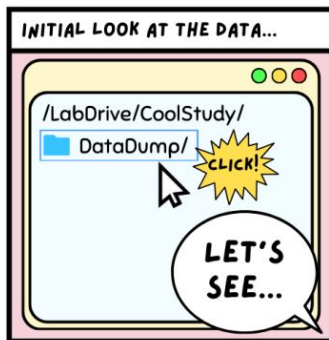
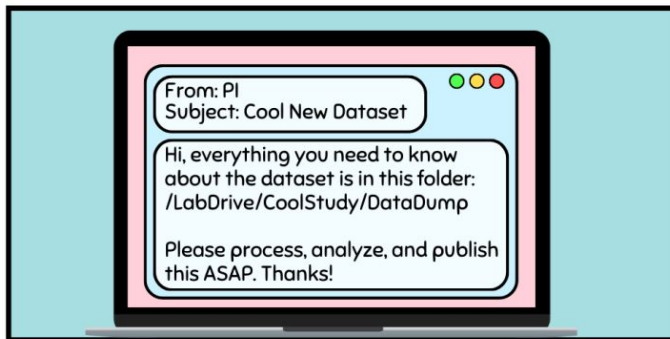
2025 June 18



ORIGAMI
Lab





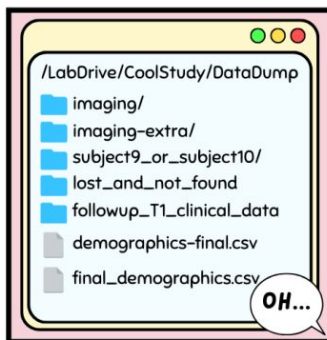
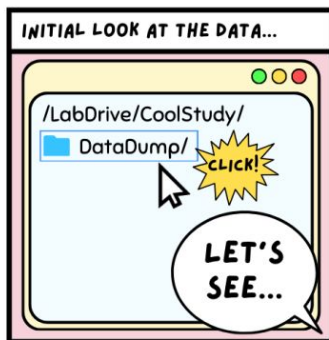
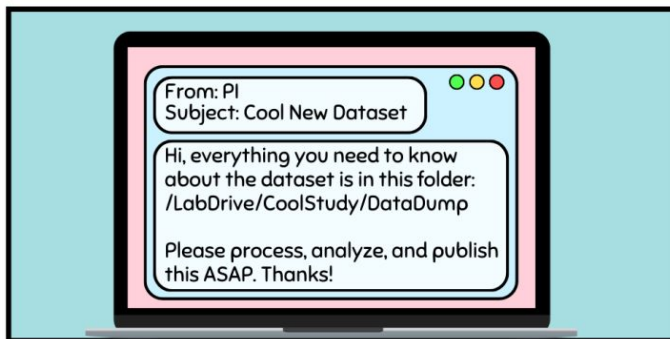


demographics-final.csv

SUBJECT_ID	age	age (good)	Sex
001	21?	22	F
002_fixed	25	25	M
003		30	Male
004_T!	-1	26	0
004_T2	27	27	1
005	29	29	1
6	>18		997
007	26	999	F
008_bad	27	27	M
009	NA	26	F
010	25	25	

??





demographics-final.csv

SUBJECT_ID	age	age (good)	Sex
001	21?	22	F
002_fixed	25	25	M
003		30	Male
004_T!	-1	26	0
004_T2	27	27	1
005	29	29	1
6	>18		997
007	26	999	F
008_bad	27	27	M
009	NA	26	F
010	25	25	

??



The ORIGAMI Lab

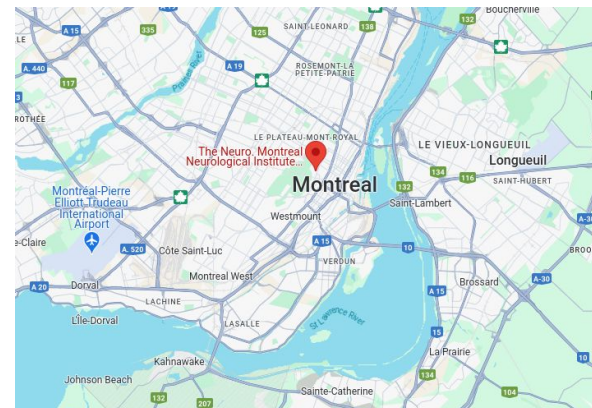
- **Promote** FAIR neuro-data-science
- **Build** neuroinformatic workflows
- **Improve** clinical research practices



JB Poline



McGill
UNIVERSITY





Data challenges in **multicentric** studies

- **Curation:** inevitability of heuristics
- **Processing:** reproducibility and versioning
- **Harmonization:** clinical knowledge
- **Sharing:** privacy, access control



A lot of time-consuming manual work that is difficult to coordinate!



ORIGAMI solutions

Nipoppy (curate + process)



A protocol for organizing and processing neuroimaging data

Neurobagel (annotate + search)



Tools for decentralized data harmonization and search



ORIGAMI solutions

Nipoppy (curate + process)



A protocol for organizing and processing neuroimaging data

Neurobagel (annotate + search)



Tools for decentralized data harmonization and search



Bagel



ORIGAMI solutions

Nipoppy (curate + process)

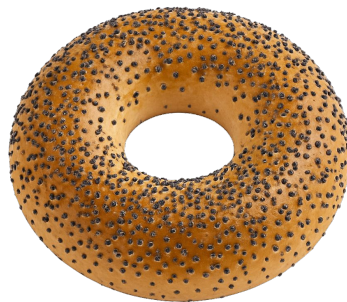


A protocol for organizing and processing neuroimaging data

Neurobagel (annotate + search)



Tools for decentralized data harmonization and search



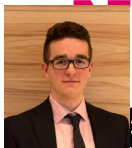
Poppy seed bagel



Michelle Wang



Nikhil Bhagwat



Mathieu Dugré



Julia O'Leary



Brent McPherson



Jean-Baptiste Poline



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



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

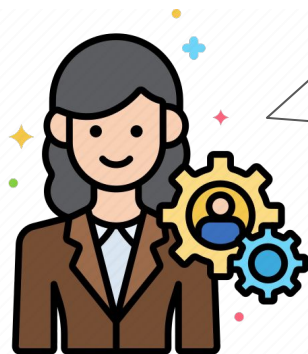


<https://github.com/nipoppy/nipoppy>

Neuroimaging-clinical datasets are **messy**



- **Curating/processing** the data is time-consuming and error-prone
 - Reproducibility concerns
- **Linking** data is difficult



How many participants with

- Parkinson's disease diagnosis
 - age under 65
 - two imaging sessions
 - processed with FreeSurfer
- are in my dataset?



How can we make neuroimaging data 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

Introducing the **Nipoppy** framework



1. **Protocol** for best practices (FAIR principles) in organization/processing of neuroimaging-clinical datasets

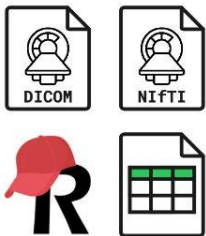
Introducing the **Nipoppy** framework



1. **Protocol** for best practices (FAIR principles) in organization/processing of neuroimaging-clinical datasets

Capture

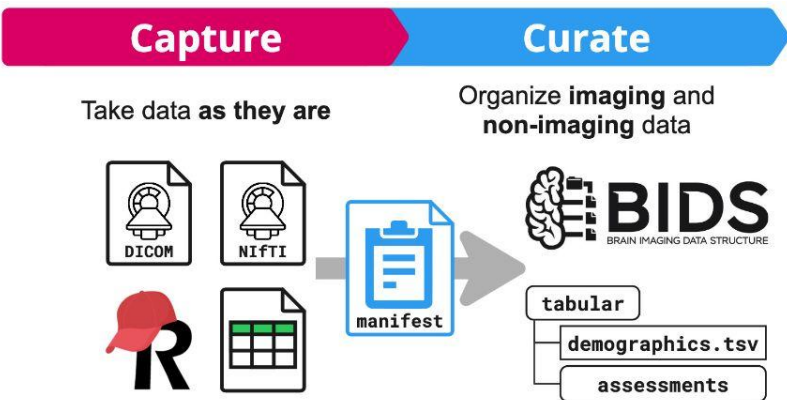
Take data **as they are**



Introducing the **Nipoppy** framework



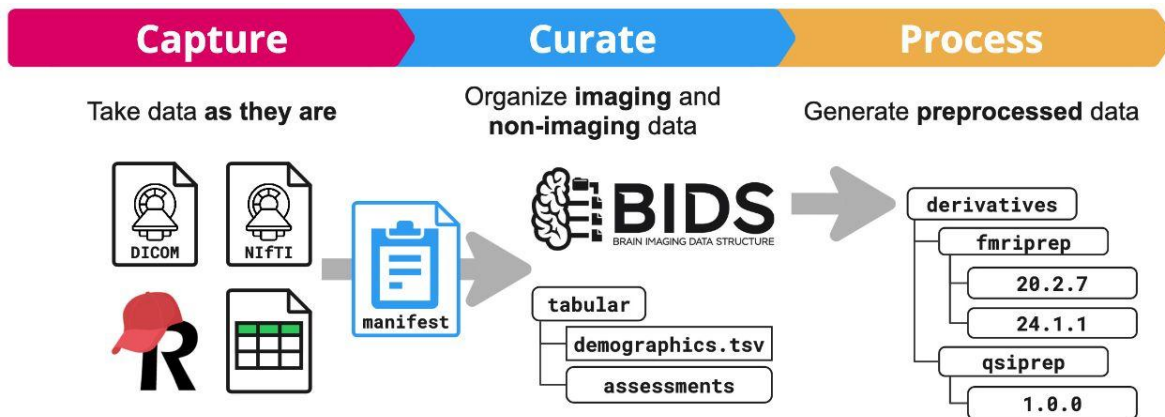
1. **Protocol** for best practices (FAIR principles) in organization/processing of neuroimaging-clinical datasets



Introducing the **Nipoppy** framework



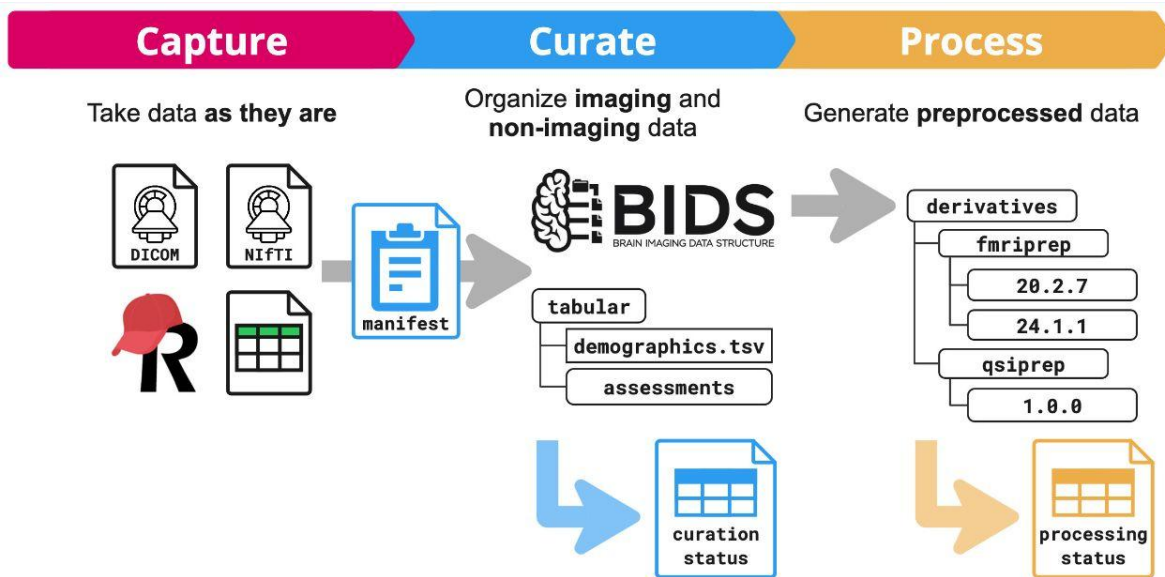
1. **Protocol** for best practices (FAIR principles) in organization/processing of neuroimaging-clinical datasets



Introducing the **Nipoppy** framework



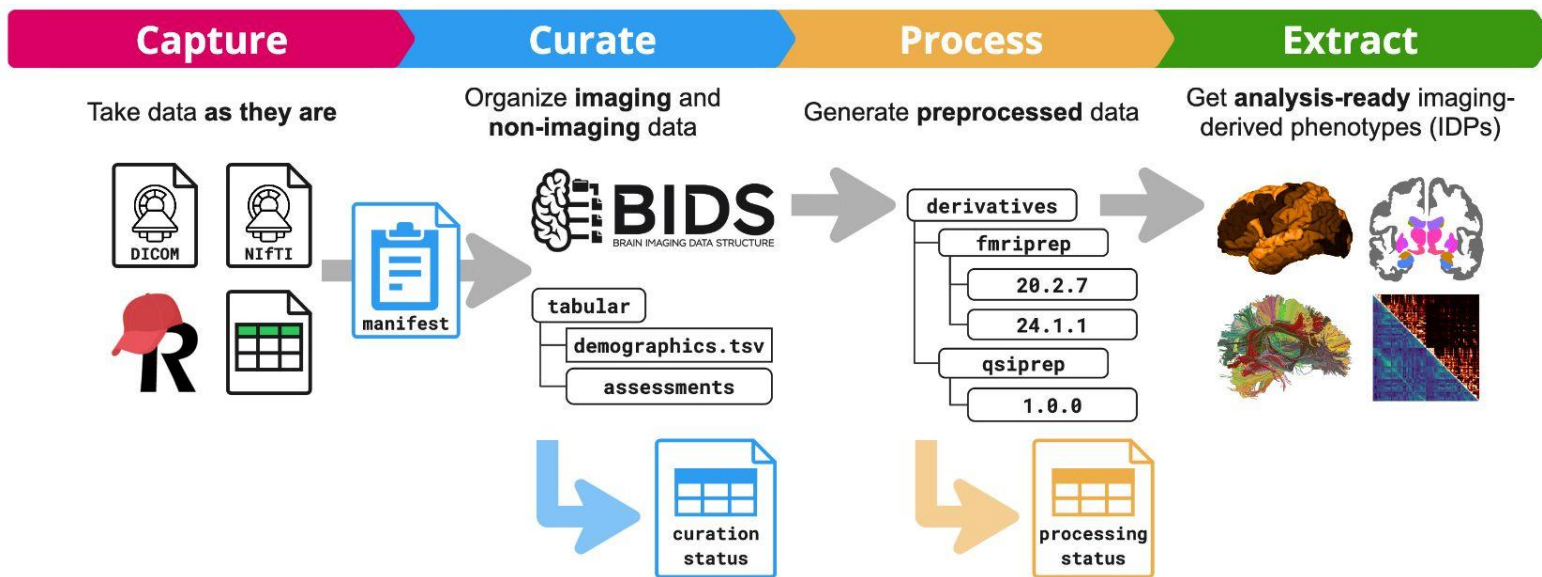
1. **Protocol** for best practices (FAIR principles) in organization/processing of neuroimaging-clinical datasets



Introducing the **Nipoppy** framework



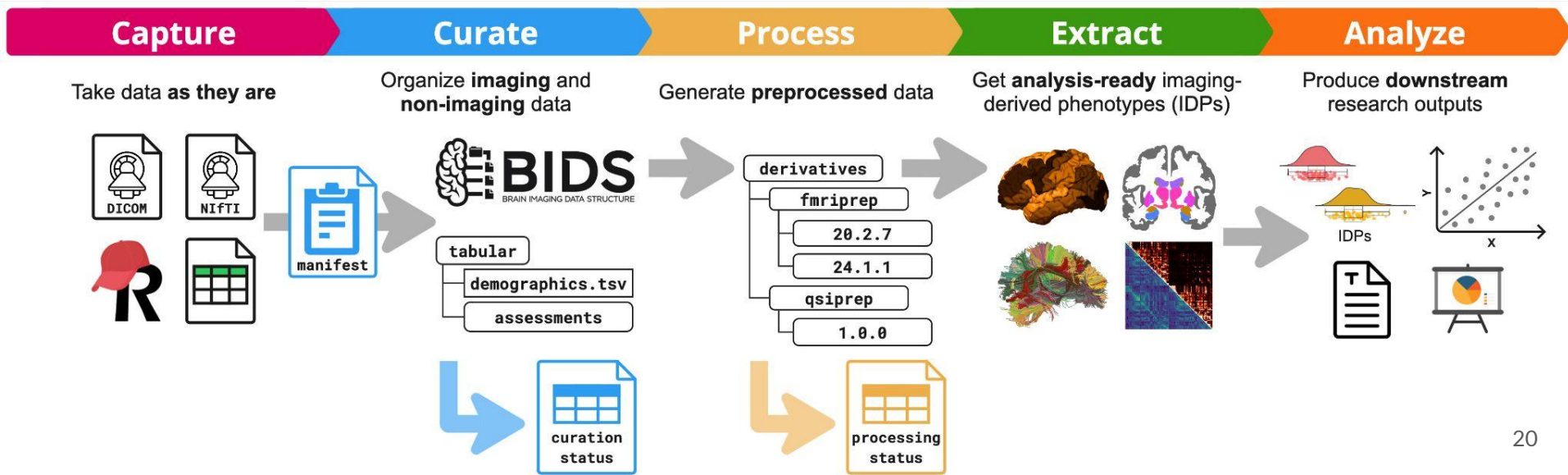
1. **Protocol** for best practices (FAIR principles) in organization/processing of neuroimaging-clinical datasets



Introducing the **Nipoppy** framework



1. **Protocol** for best practices (FAIR principles) in organization/processing of neuroimaging-clinical datasets

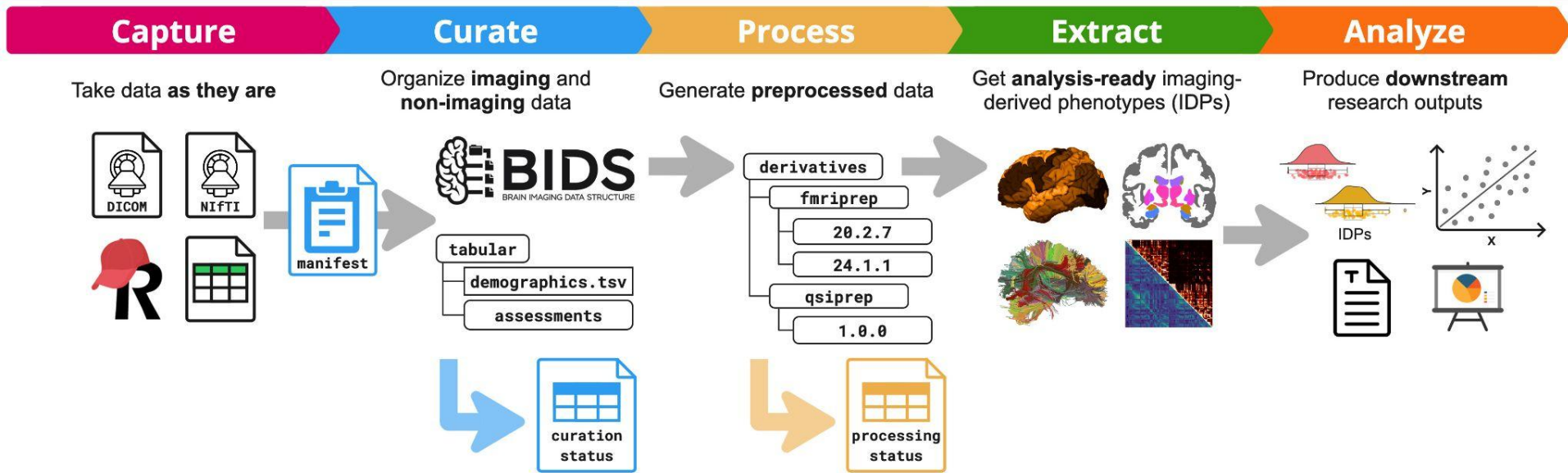


Introducing the **Nipoppy** framework



1. **Protocol** for best practices (FAIR principles) in organization/processing of neuroimaging-clinical datasets
 - a. From raw scanner data to extracted imaging-derived phenotypes (IDPs)
 - b. Visualizing tabular data/metadata on a dashboard

(<https://dicost.neurobase.org/>)



<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 ▾



Introducing the **Nipoppy** framework



1. **Protocol** for best practices (FAIR principles) in organization/processing of neuroimaging-clinical datasets
 - a. From raw scanner data to extracted imaging-derived phenotypes (IDPs)
 - b. Visualizing tabular data/metadata on a dashboard

[\(https://dicost.neurobase.org/\)](https://dicost.neurobase.org/)

Capture

Curate

Process

Extract

Analyze

Introducing the **Nipoppy** framework



1. **Protocol** for best practices (FAIR principles) in organization/processing of neuroimaging-clinical datasets
 - a. From raw scanner data to extracted imaging-derived phenotypes (IDPs)
 - b. Visualizing tabular data/metadata on a dashboard

[\(https://dicom-nipoppy.org/\)](https://dicom-nipoppy.org/)

Capture

Curate

Process

Extract

Analyze

2. Data organization **specification**
 - a. For imaging and non-imaging data
 - b. At the whole study level

Introducing the **Nipoppy** framework



1. **Protocol** for best practices (FAIR principles) in organization/processing of neuroimaging-clinical datasets
 - a. From raw scanner data to extracted imaging-derived phenotypes (IDPs)
 - b. Visualizing tabular data/metadata on a dashboard

[\(https://dicom-nipoppy.org/\)](https://dicom-nipoppy.org/)

Capture

Curate

Process

Extract

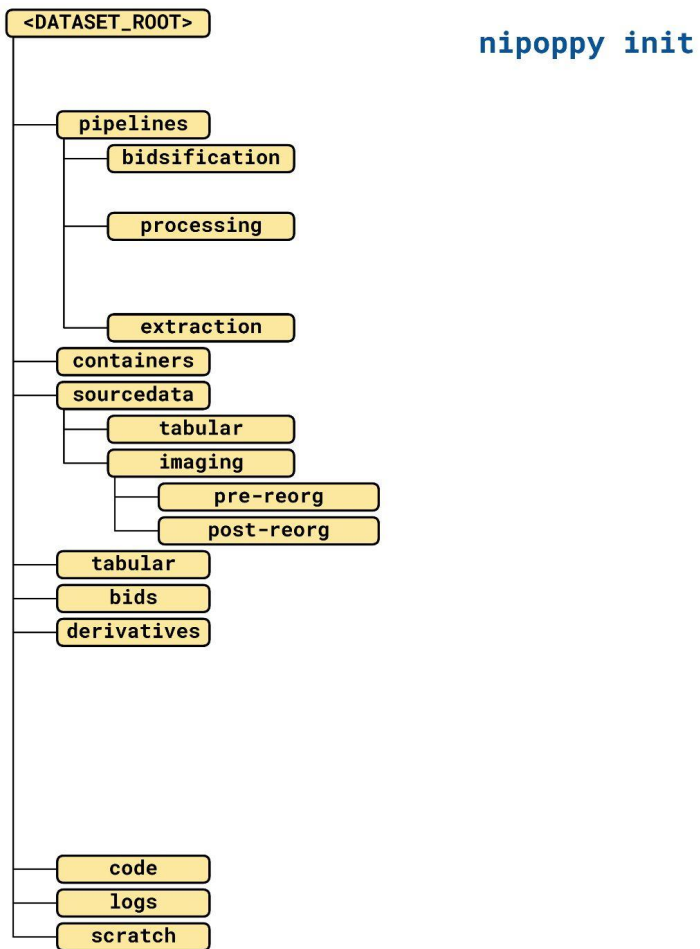
Analyze

2. Data organization **specification**
 - a. For imaging and non-imaging data
 - b. At the whole study level
3. Software package with **tools** to help work with this framework **locally**

A typical **Nipoppy** workflow



A typical **Nipoppy** workflow



Legend

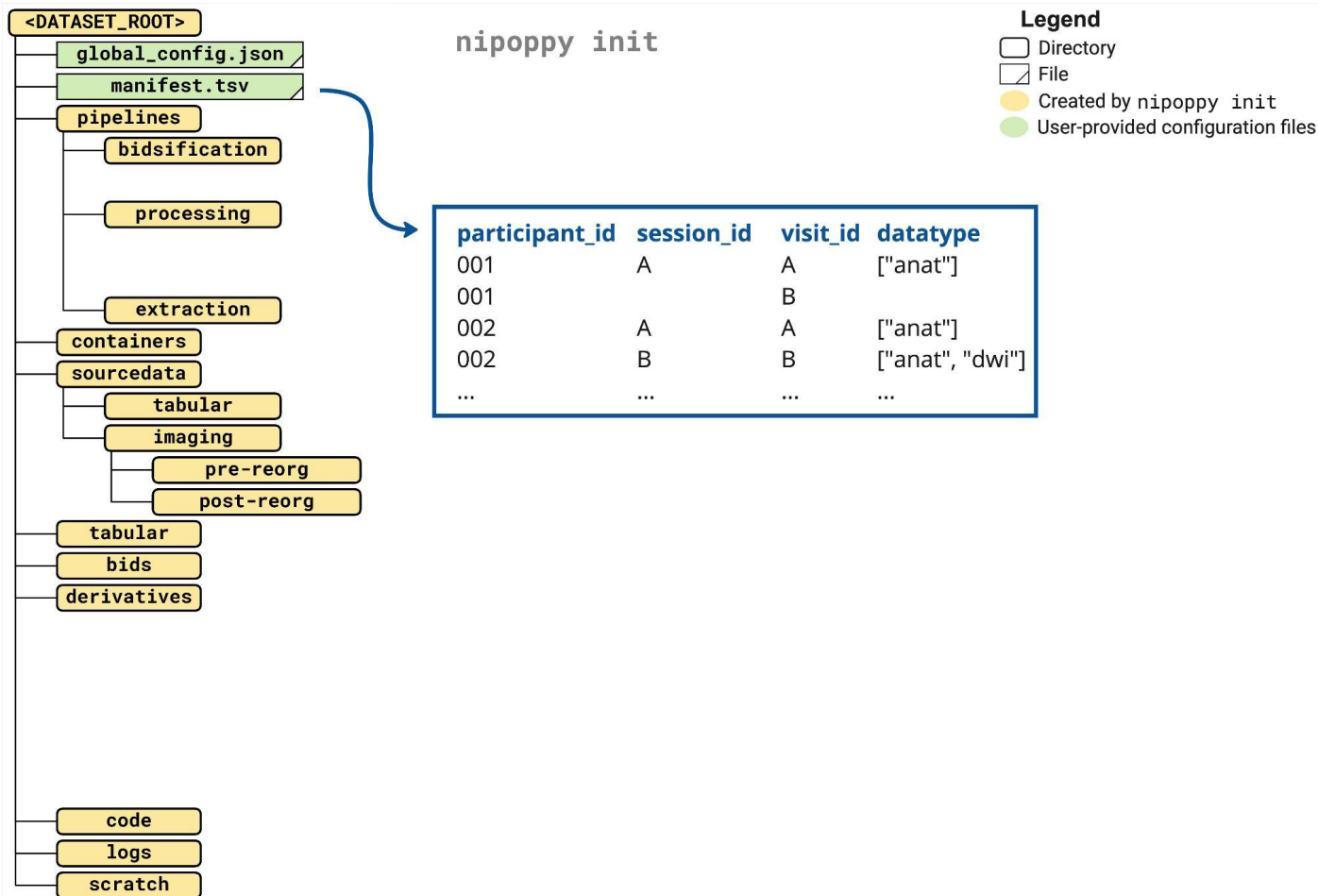
□ Directory

□ File

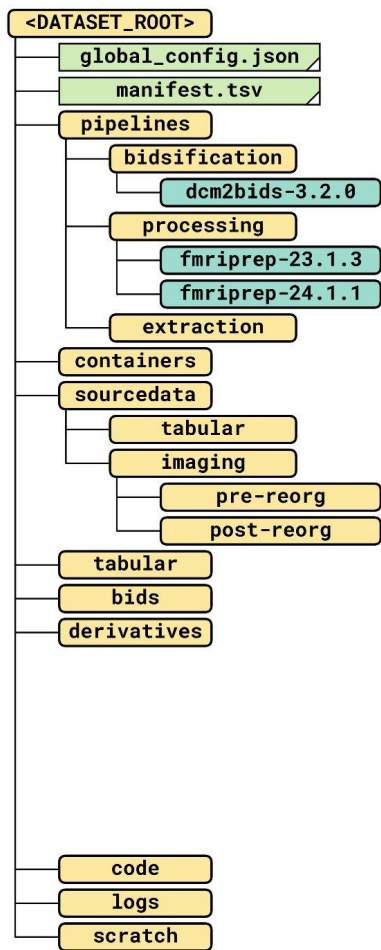
● Created by nipoppy init



A typical Nipoppy workflow



A typical **Nipoppy** workflow



`nipoppy init`

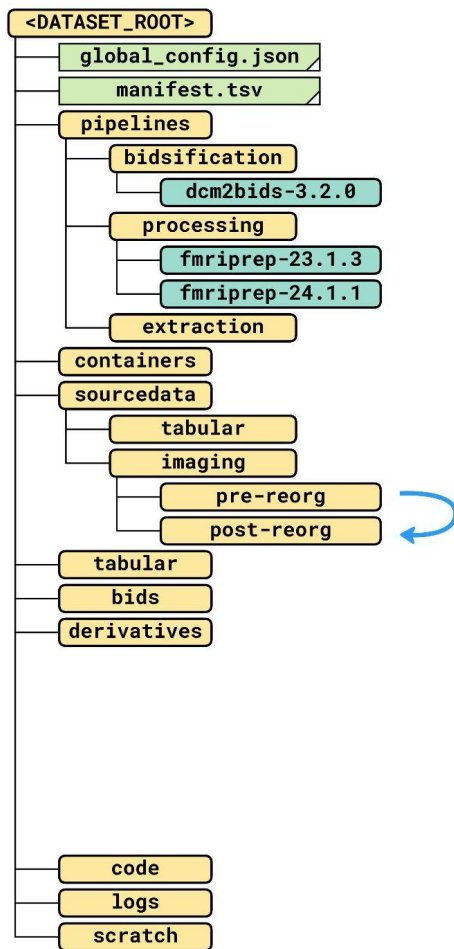
`nipoppy pipeline install`

Legend

- Directory
- File
- Created by `nipoppy init`
- User-provided configuration files
- Pipeline configuration files



A typical **Nipoppy** workflow



nipoppy init

nipoppy pipeline install

nipoppy reorg

Legend

□ Directory

▤ File

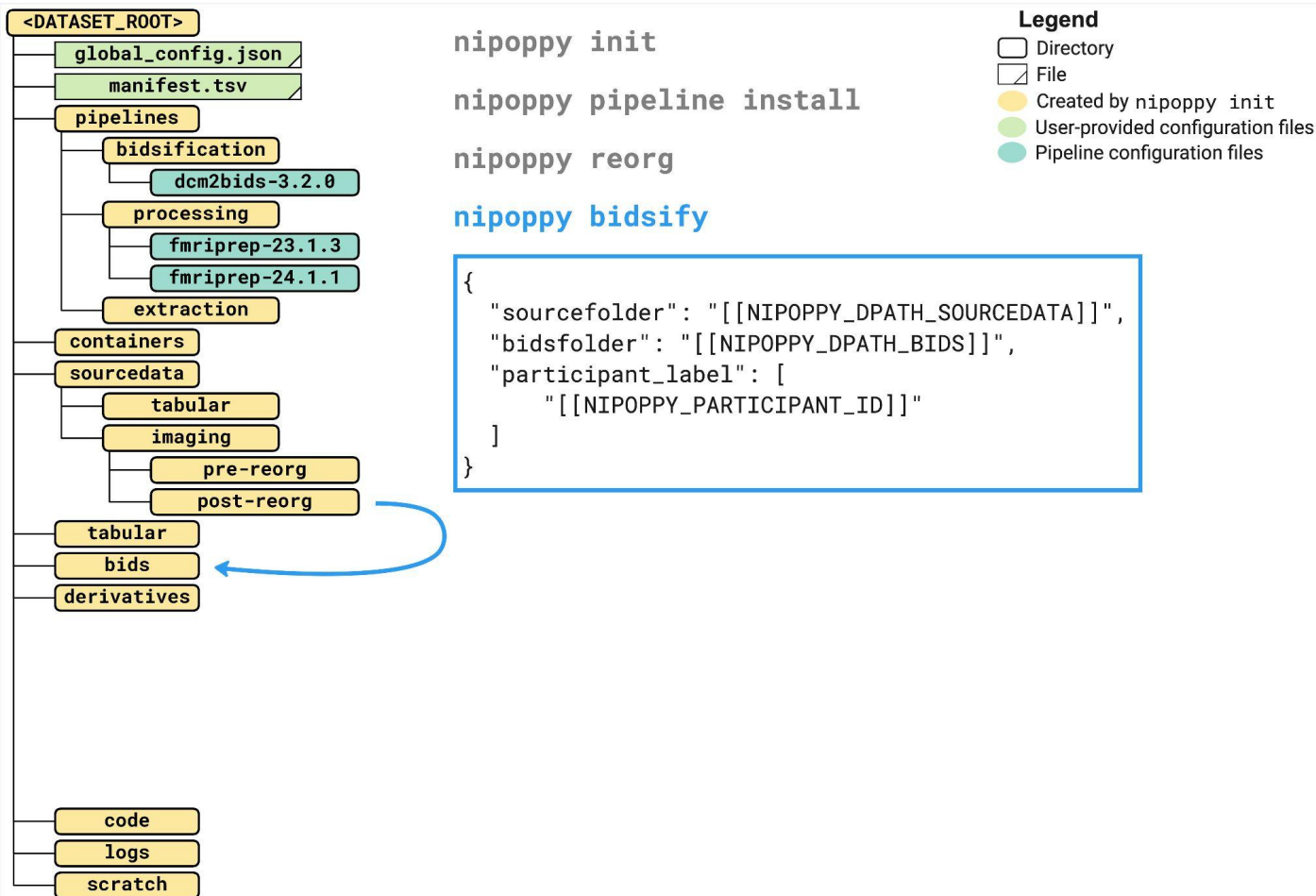
● Created by nipoppy init

● User-provided configuration files

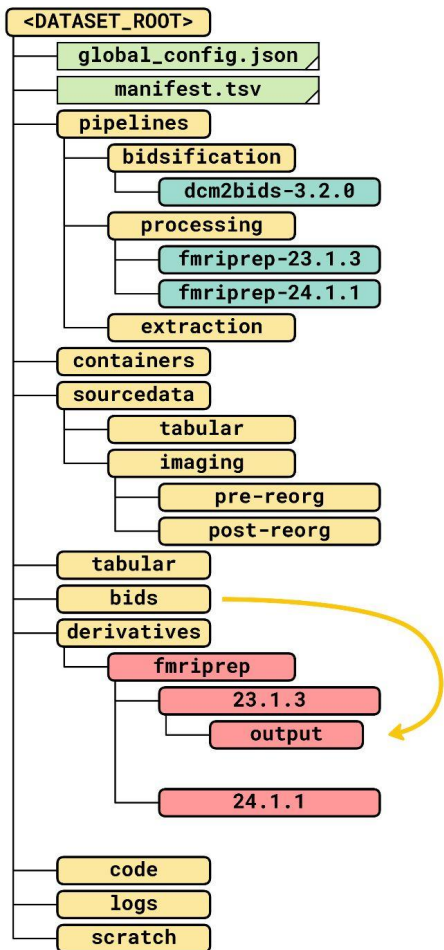
● Pipeline configuration files



A typical Nipoppy workflow



A typical **Nipoppy** workflow



`nipoppy init`

`nipoppy pipeline install`

`nipoppy reorg`

`nipoppy bidsify`

`nipoppy process`

```
{
  "bids_dir": "[[NIPOPPY_DATASET_ROOT]]",
  "output_dir": "[[NIPOPPY_DPATH_PIPELINE_OUTPUT]]",
  "analysis_level": "participant",
  ...
}
```

Legend

□ Directory

▤ File

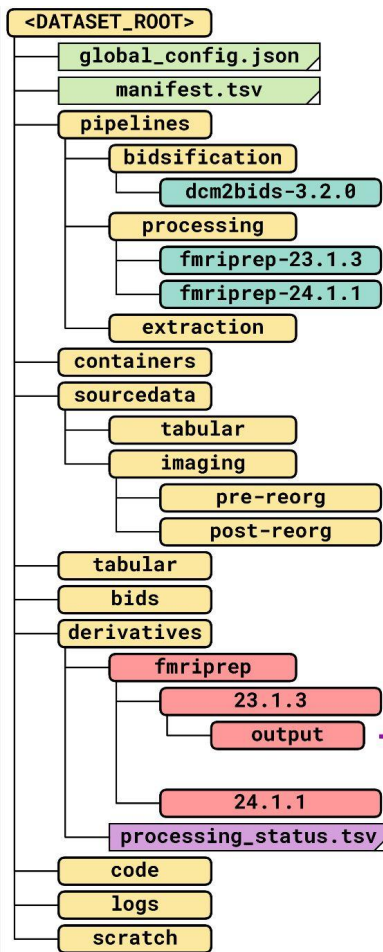
○ Created by `nipoppy init`

○ User-provided configuration files

○ Pipeline configuration files

○ Imaging derivatives data

A typical Nipoppy workflow



nipoppy init

nipoppy pipeline install

nipoppy reorg

nipoppy bidsify

nipoppy process

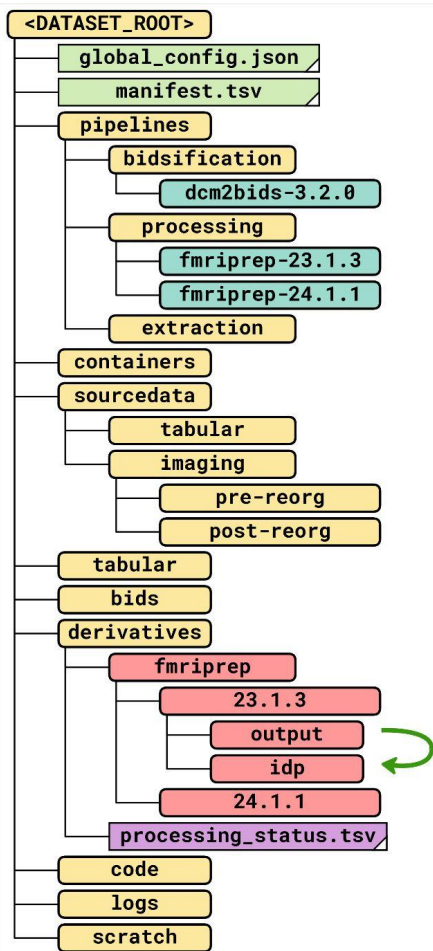
nipoppy track-processing

Legend

- Directory
- File
- Created by nipoppy init
- User-provided configuration files
- Pipeline configuration files
- Imaging derivatives data
- Tracking files

participant_id	session_id	pipeline	version	status
01	A	freesurfer	6.0.0	SUCCESS
01	A	freesurfer	7.4.1	SUCCESS
02	A	freesurfer	6.0.0	FAIL
02	A	freesurfer	7.4.1	FAIL
02	B	freesurfer	6.0.0	INCOMPLETE
02	B	freesurfer	7.4.1	INCOMPLETE
...

A typical Nipoppy workflow



`nipoppy init`

`nipoppy pipeline install`

`nipoppy reorg`

`nipoppy bidsify`

`nipoppy process`

`nipoppy track-processing`

`nipoppy extract`

participant_id	session_id	gm_vol	wm_vol	...
001	A	399445	463167	...
002	A	432054	422803	...
002	B	432913	422634	...
...

Legend

- Directory
- File
- Created by nipoppy init
- User-provided configuration files
- Pipeline configuration files
- Imaging derivatives data
- Tracking files



Demo

The **Nipoppy** pipeline catalog



Available on the [Zenodo](#) data repository

- Community-driven
- Seamless pipeline configuration sharing (container, runtime parameters)

```
(nipoppy) mathdugre@osx ✓ nipoppy_demo % py demo.py
```


Documentation and video tutorials



Written documentation available at <https://nipoppy.readthedocs.io/en/latest/>

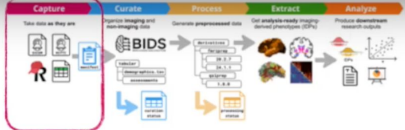
Coming soon: video tutorials on YouTube



nipoppy init

In this video:

- nipoppy init
- Nipoppy specification
- nipoppy status
- manifest.tsv
- track curation



```
$ nipoppy track-curation --dataset my-example-study --regenerate
```

0:53 / 7:42

Scroll for details

Nipoppy takeaways

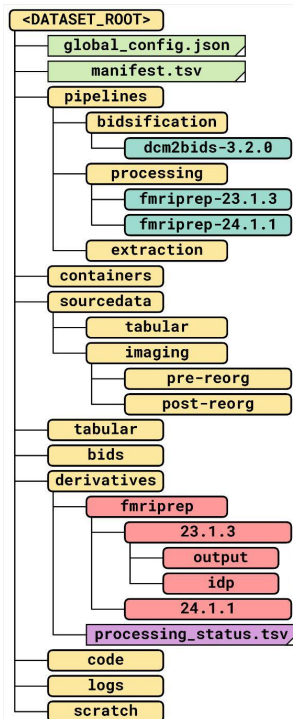
Framework combining **existing tools**



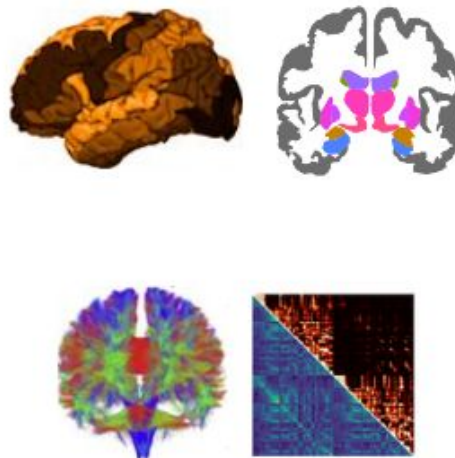
Boutiques



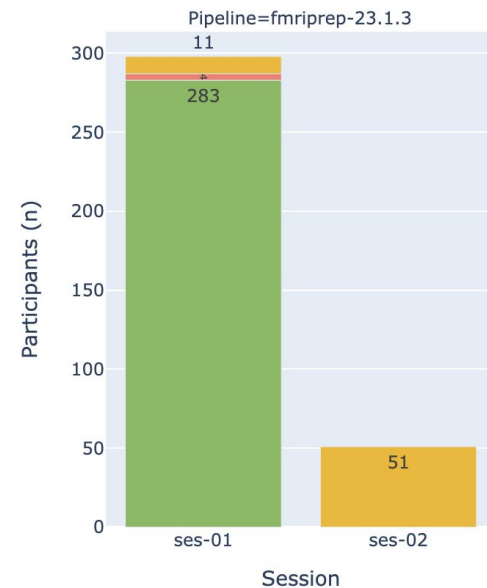
Local data management



Reproducible MRI processing and IDP extraction



Progress tracking



Nipoppy takeaways



For trainees



Best/FAIR practices


For labs



Efficiency and
consistency

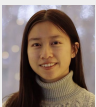
For institutions



Data-sharing
Metadata discovery
with **Neurobagel** 



Alyssa Dai



Rémi Gau



Arman Jahanpour



Brent McPherson



Julia B. Repas
Julia B. Repas Poline



Sebastian Urchs



Michelle Wang



Neurobagel © 2025 by Neurobagel Team, Origami Lab, McGill
slides are licensed under CC BY 4.0



A neuroinformatics framework for
decentralized data harmonization and search



neurobagel



neurobagel.org



HEALTHY BRAINS
HEALTHY LIVES



neuro
Montreal Neurological
Institute-Hospital



CONP
PCNO



National Institutes
of Health



Fondation
Brain Canada
Foundation

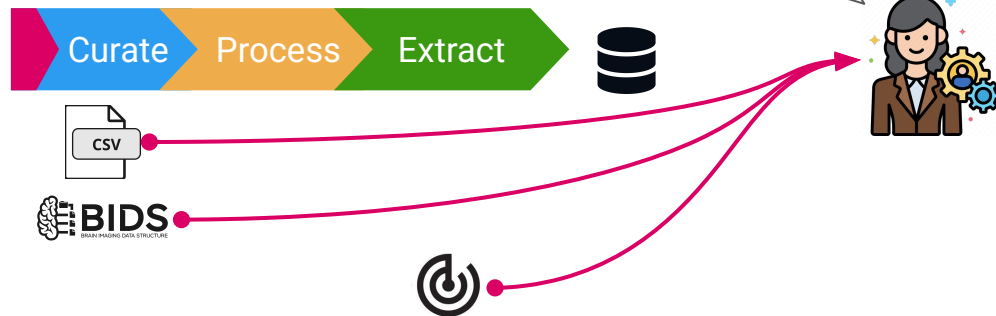




How many participants

- with PD diagnosis
- under 65
- 2 imaging sessions
- run with freesurfer v6

are in **this one dataset?**

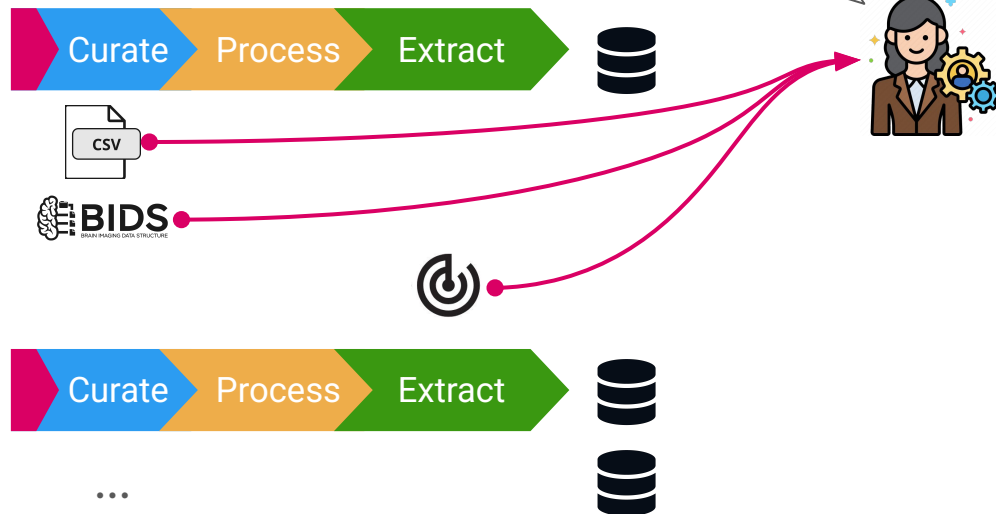




How many participants

- with PD diagnosis
- under 65
- 2 imaging sessions
- run with freesurfer v6

do our PIs have?

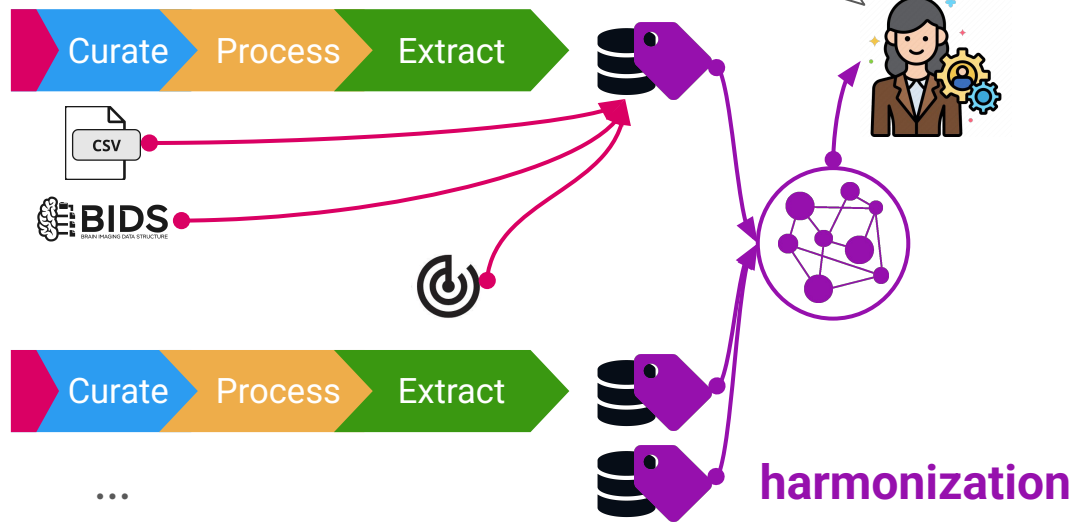




How many participants

- with PD diagnosis
- under 65
- 2 imaging sessions
- run with freesurfer v6

do our PIs have?

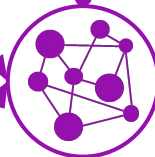




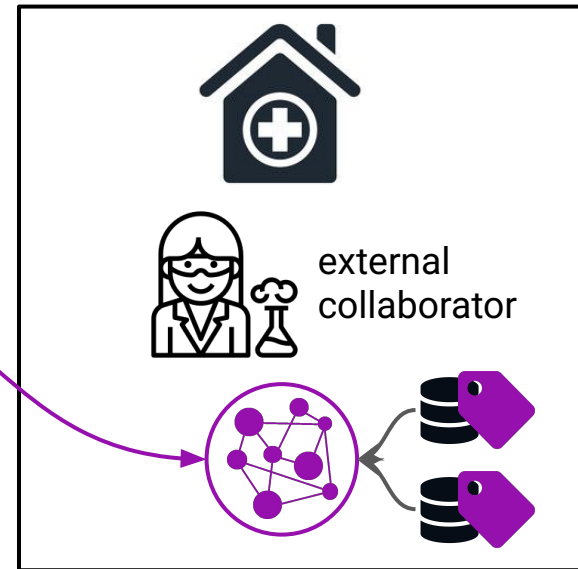
How many participants

- with PD diagnosis
- under 65
- 2 imaging sessions
- run with freesurfer v6

exist within our network?

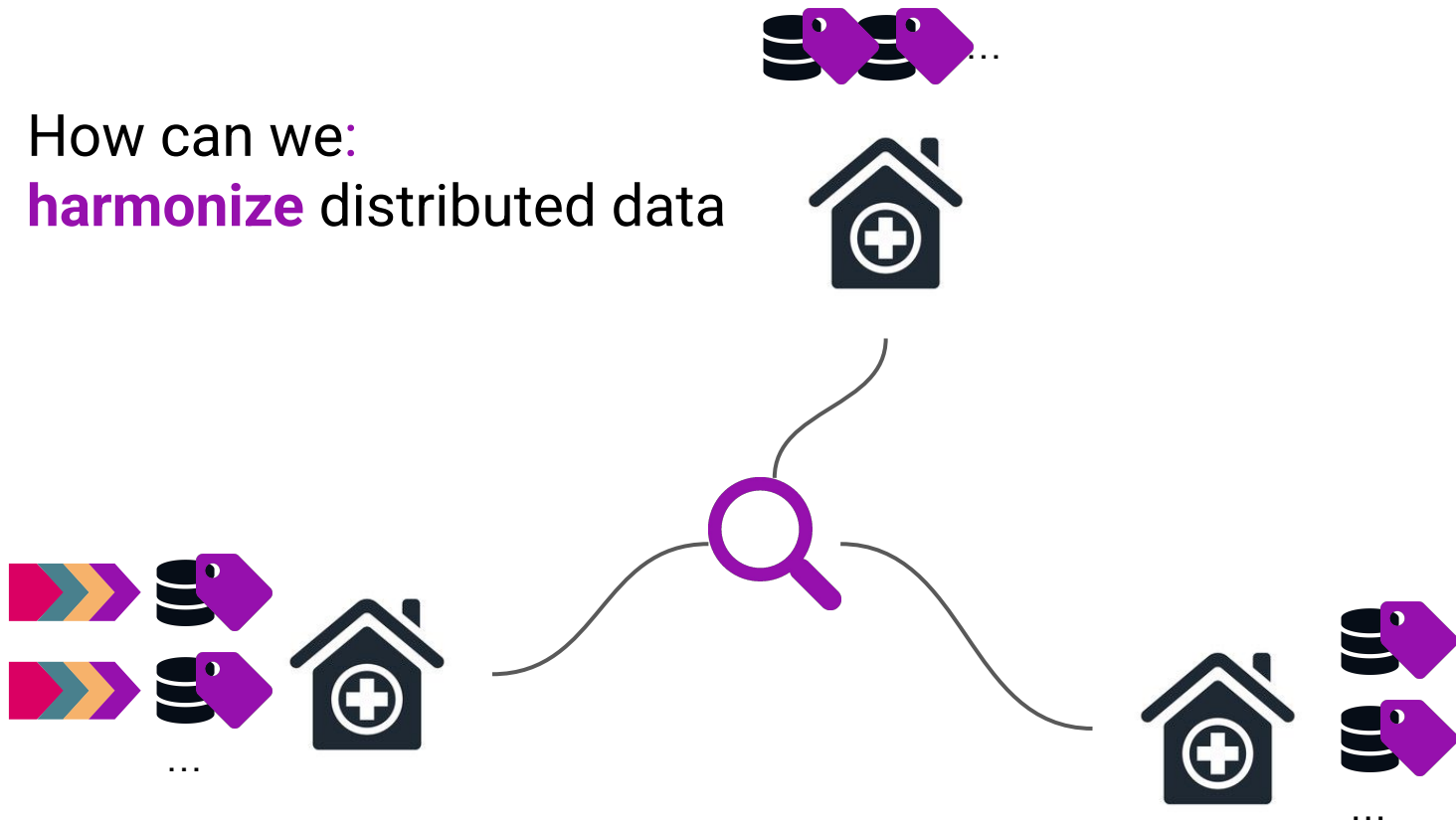


harmonization





How can we:
harmonize distributed data



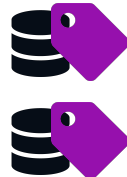
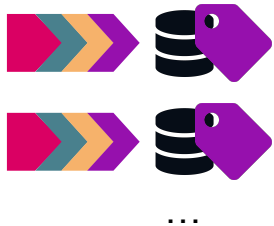


How can we:
harmonize distributed data

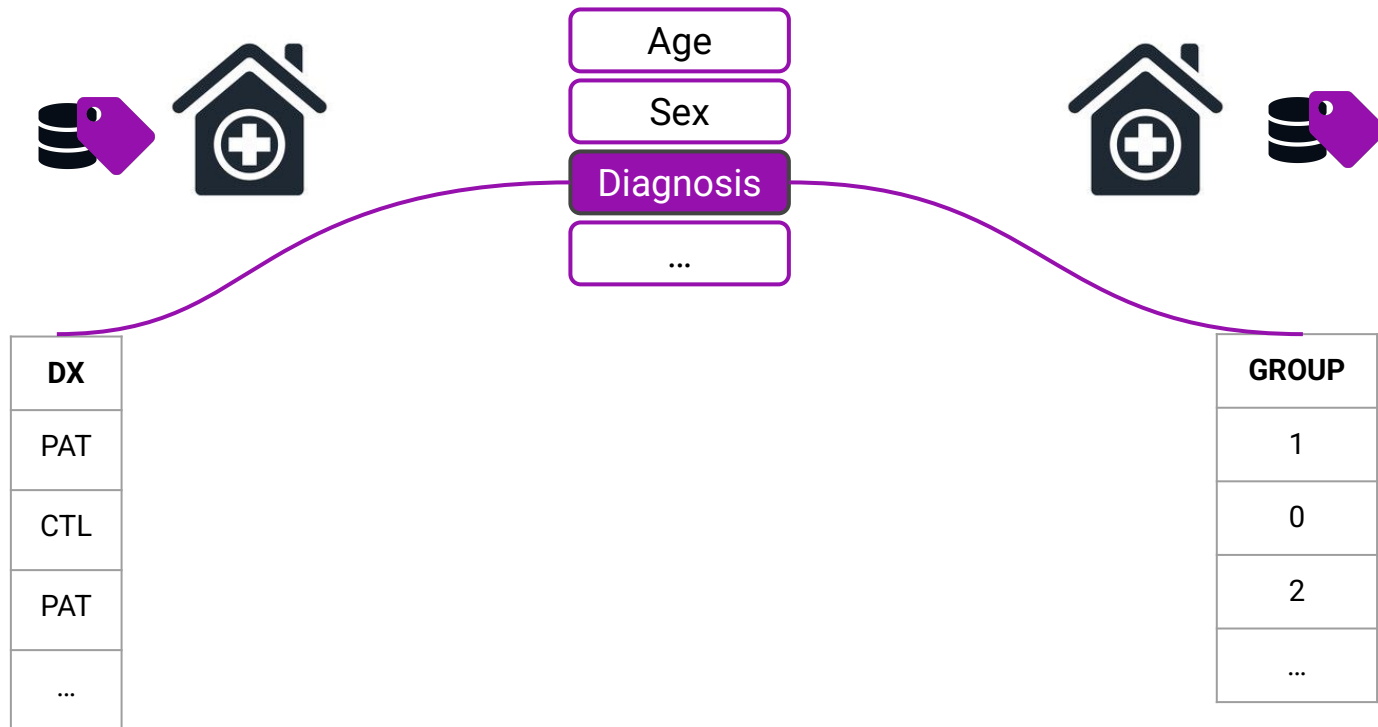


Age
Sex
Diagnosis
...

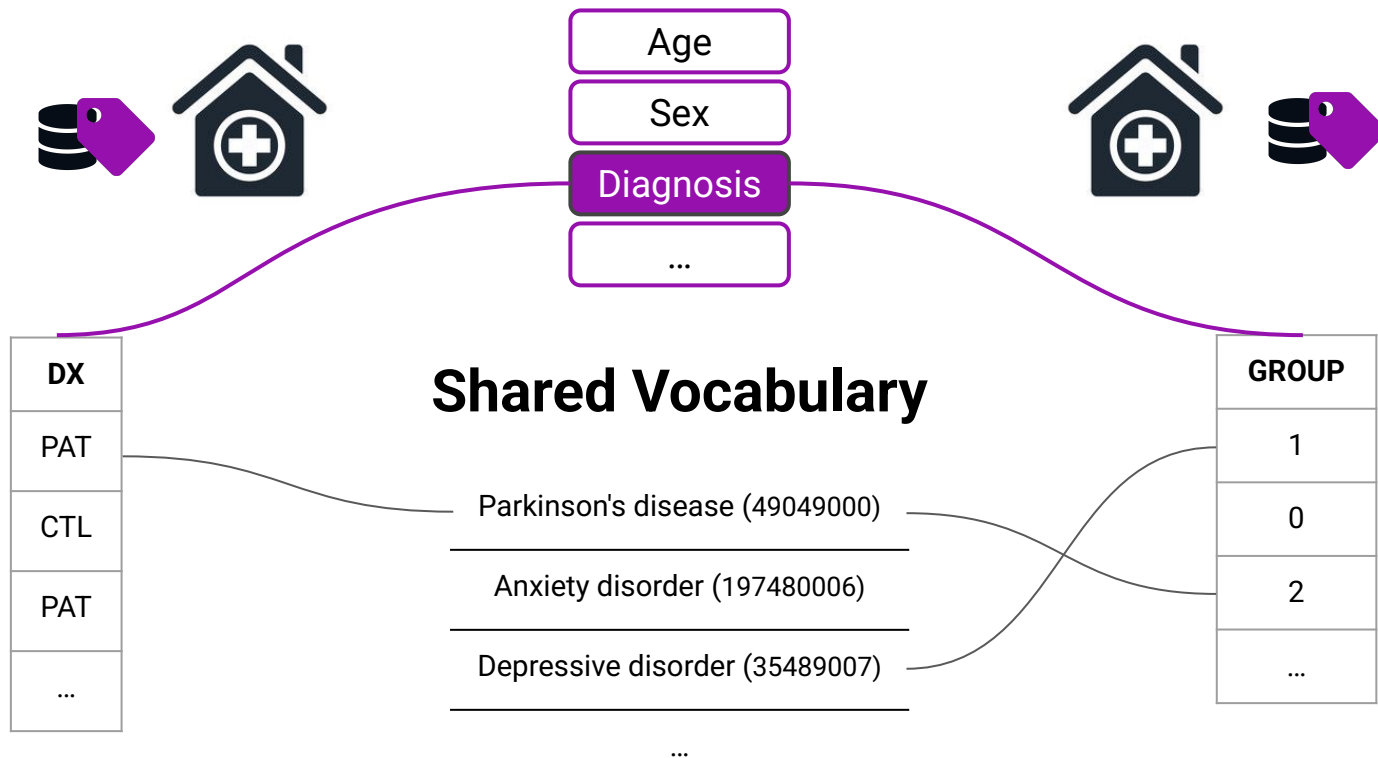
- use common **data model**
- distribute **intuitive GUI**



Common **participant level** data model




Common participant level data model





Intuitive, web-based annotation tool






Neurobagel Annotate beta
Harmonize phenotypic data

[home](#) [categorization](#) [annotation](#) [download](#) | v0.2.0 [Documentation](#) 




Welcome to the neurobagel annotation tool

This tool allows you to create a machine readable data dictionary in .json format for a tabular phenotypic file in .tsv format ("Data table"). If you already have a [BIDS-like .json data dictionary](#), you can provide it here (under "Data Dictionary") and augment it with more detailed annotations.

 This tool (like all of neurobagel) is under active development and we welcome any feedback or suggestions. Feel free to use our feedback widget on the side of the page.

Summary of annotation steps

Data table



Choose file

 example_synthetic.tsv

Participant Id	Session Id	Pheno Age	Pheno Sex	Pheno Group	Tool1 Item1	Tool1 Item2	Tool2 Item1
sub-01	ses-01	34,1	F	CTRL	good	far	hello
sub-01	ses-02	35,3	F	CTRL	bad	near	world
sub-02	ses-01	NA	M	PAT	ok	missing	hello

We like Feedback

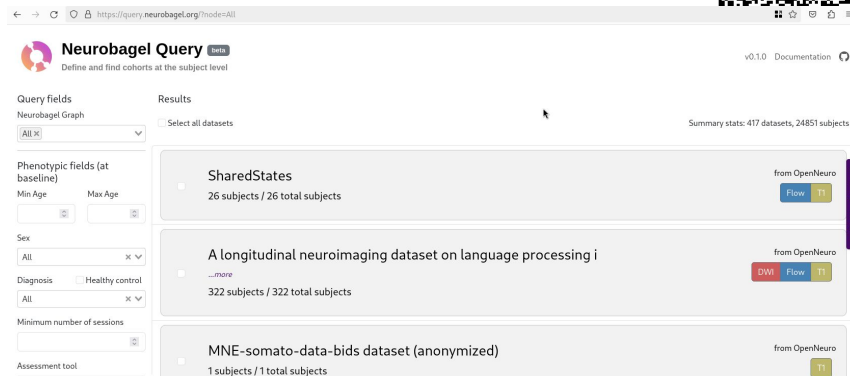
<https://annotate.neurobagel.org/>



How can we:
search distributed data



How can we:
search distributed data




- **create query federation**
- **intuitive search interface**

Web-based federated query tool




← → ↻ 🔒 https://query.neurobagel.org/?node=All



Neurobagel Query beta

Define and find cohorts at the subject level

v0.1.0 [Documentation](#) 

Query fields

Neurobagel Graph

All x

Phenotypic fields (at baseline)

Min Age Max Age

Sex

All x

Diagnosis ☐ Healthy control

All x

Minimum number of sessions

Assessment tool

Results

☐ Select all datasets

Summary stats: 417 datasets, 24851 subjects

☐

SharedStates

26 subjects / 26 total subjects

from OpenNeuro

Flow T1

☐

A longitudinal neuroimaging dataset on language processing i

...more

322 subjects / 322 total subjects

from OpenNeuro

DWI Flow T1

☐

MNE-somato-data-bids dataset (anonymized)

1 subjects / 1 total subjects

from OpenNeuro

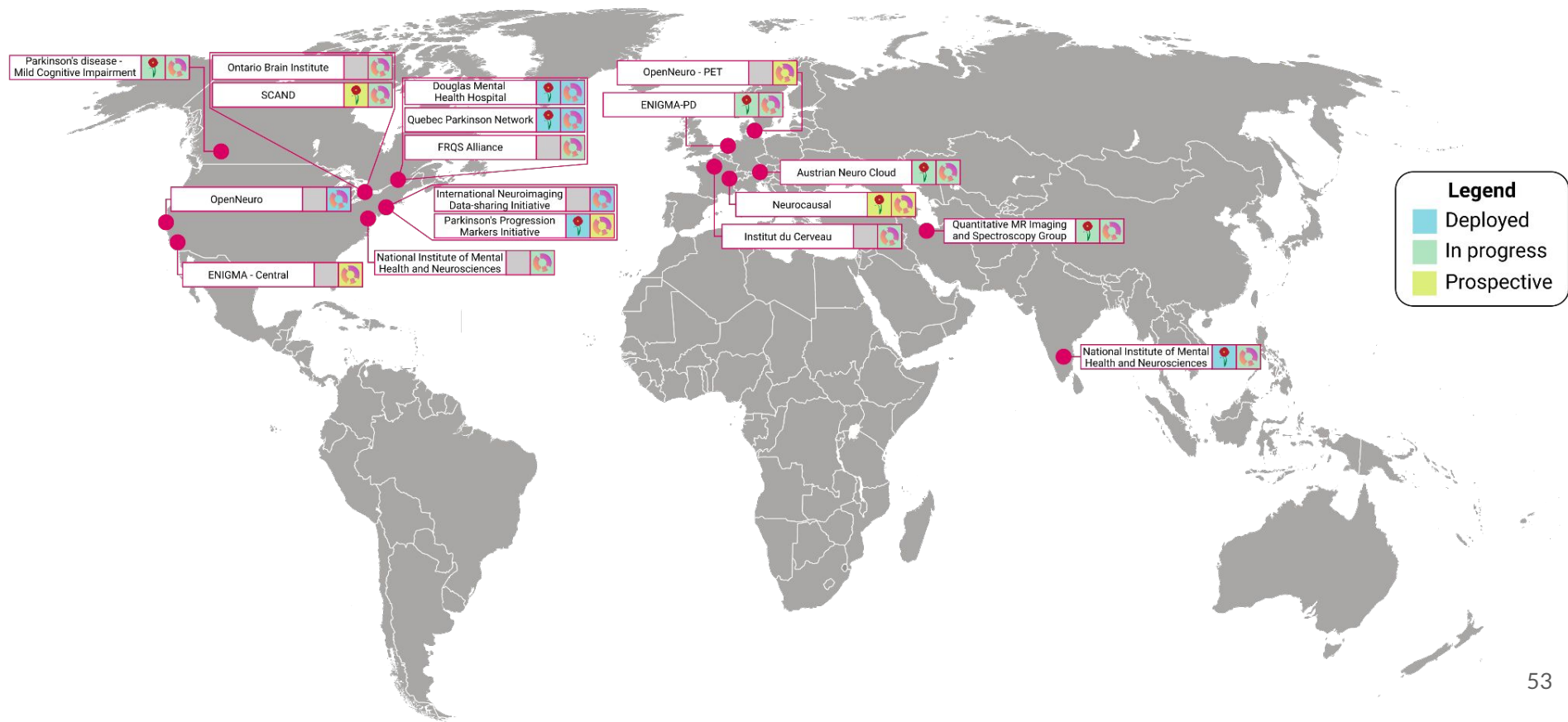
T1

We like Feedback

query.neurobagel.org/

52

Nipoppy and Neurobagel adoption so far



Thank you!



Michelle
Wang



Mathieu
Dugré



Brent
McPherson



Nikhil
Bhagwat



Arman
Jahanpour



Sebastian
Urchs



Alyssa
Dai



Julia
Pfarr



Jean-Baptiste
Poline

