



# Assessing analytical variability with **Nipoppy**

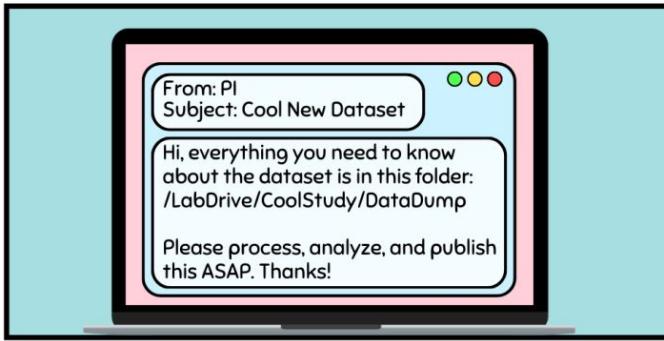
**Michelle Wang**

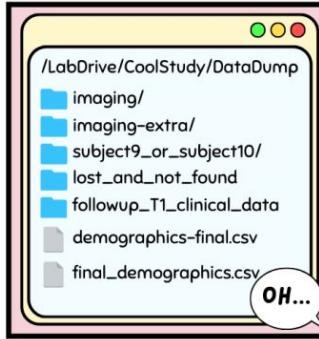
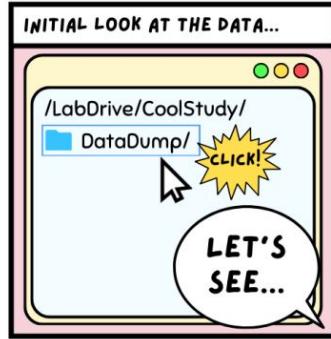
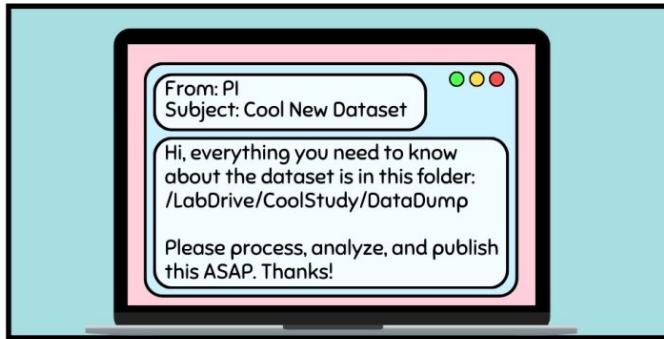
NeuroDataScience-ORIGAMI Lab (JB Poline)  
McGill University

2025 June 24



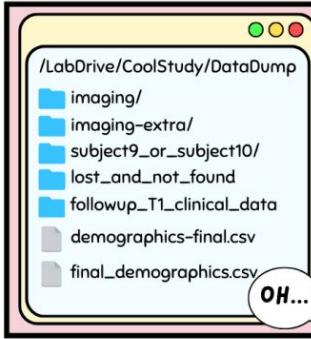
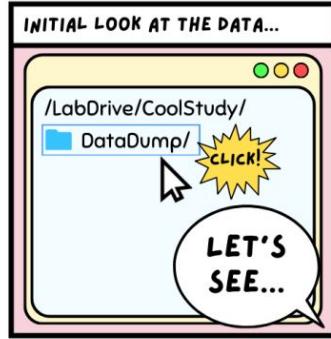
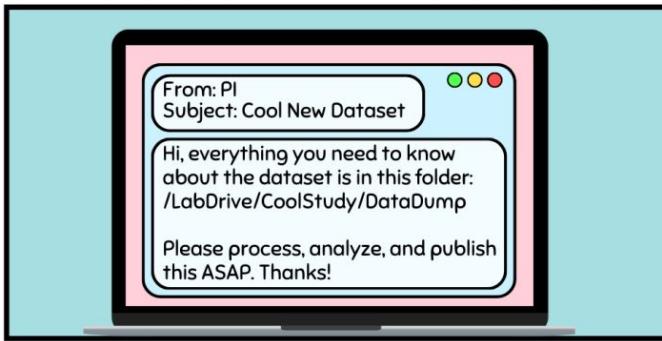






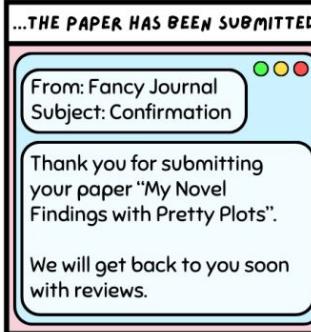
SUBJECT_ID	age	age (good)	Sex
001	21?	22	F
002_fixed	25	25	M
003		30	Male
004_T!	-1	26	O
004_T2	27	27	1
005	29	29	1
6	>18		997
007	26	999	F
008_bad	27	27	M
009	NA	26	F
010	25	25	





demographics-final.csv			
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???



# 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

# Introducing the **Nipopy** framework

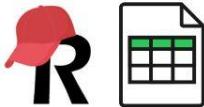
1. **Protocol** for best practices (FAIR principles) in organization/processing of neuroimaging-clinical datasets

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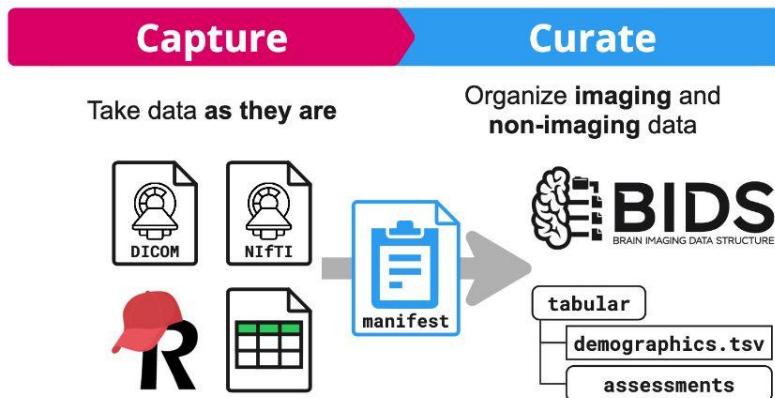
## Capture

Take data **as they are**



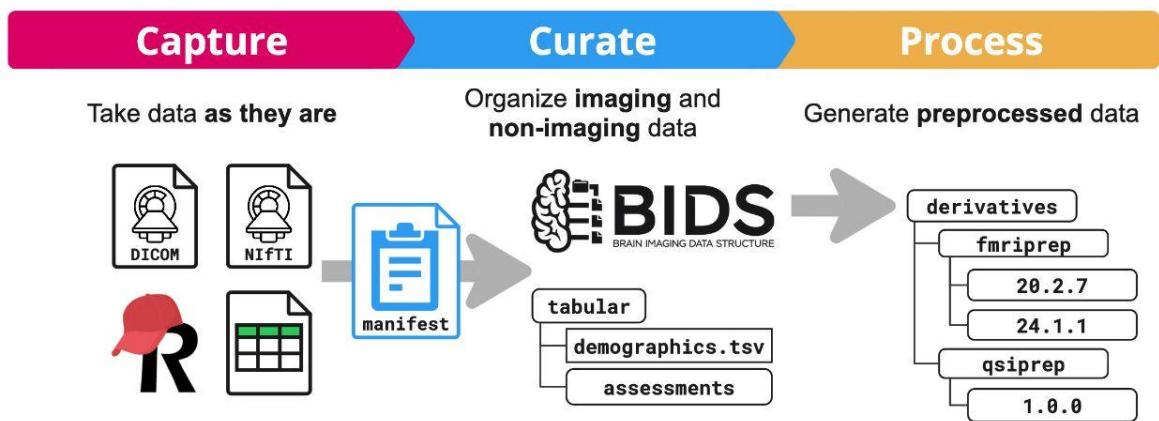
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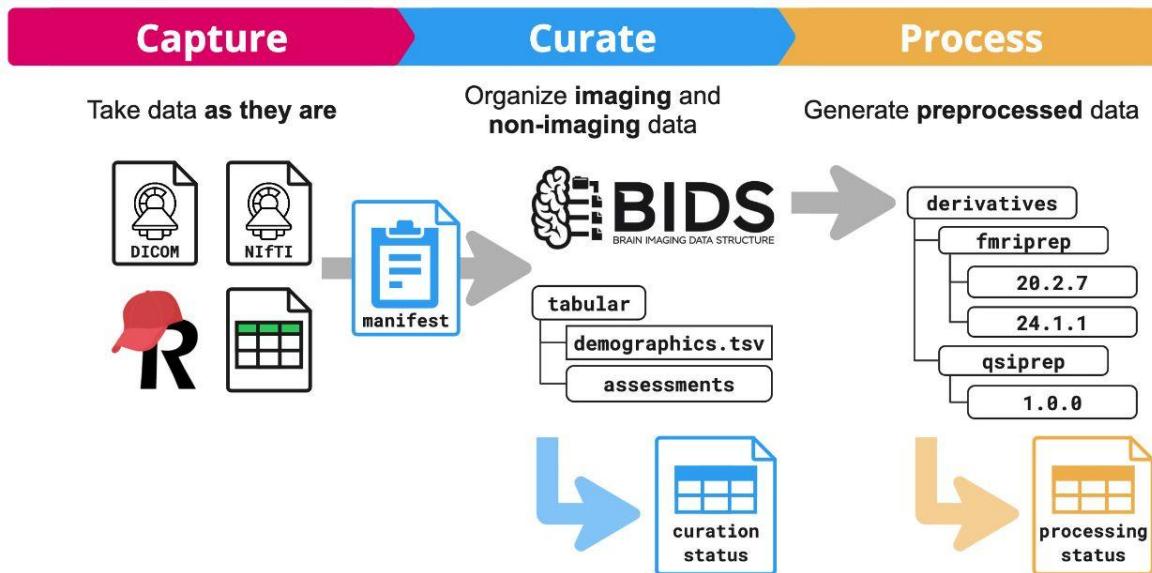
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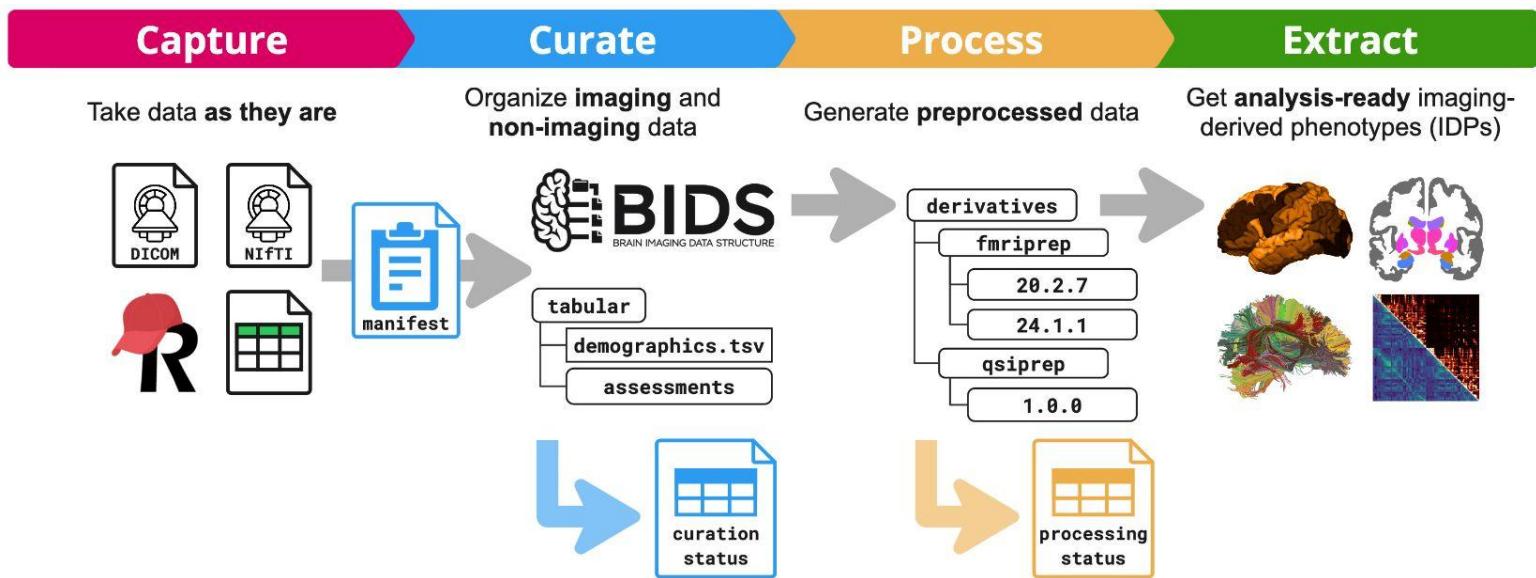
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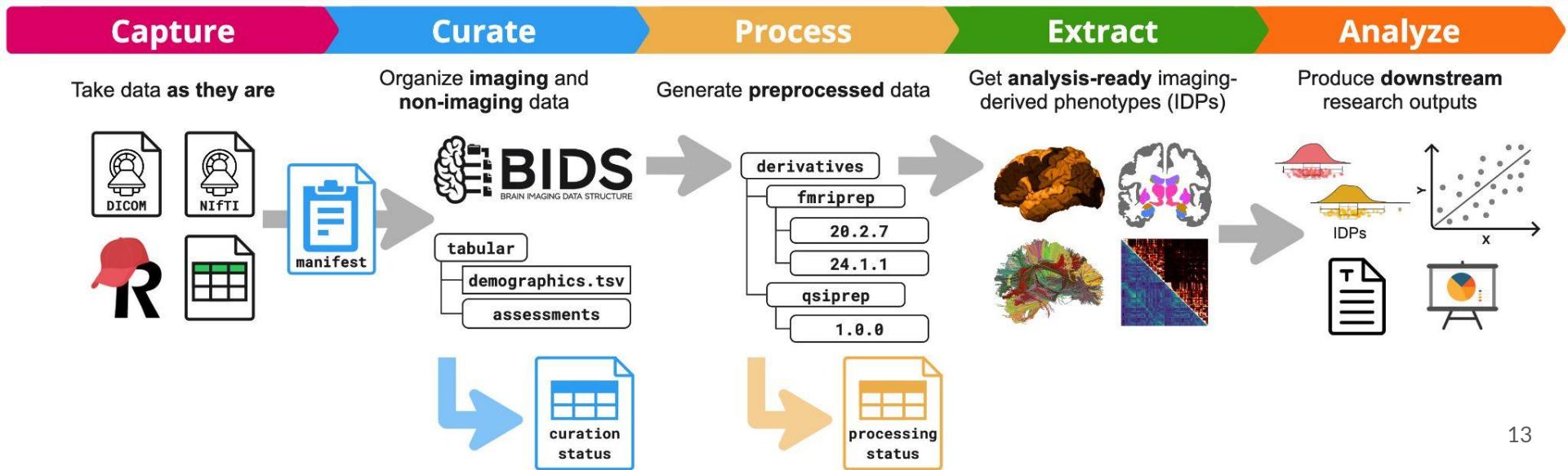
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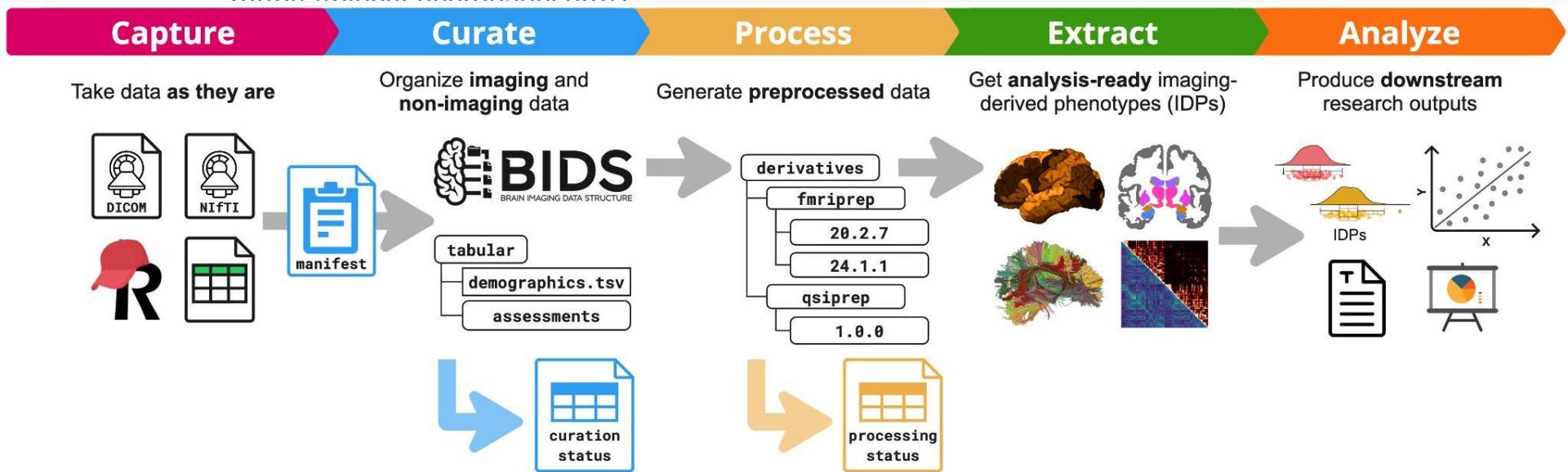
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# Introducing the **Nipopy** framework

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://dscntt.neurobboal.org/>)



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

Neuroimaging and phenotypic dataset exploration beta

Upload your own digest file:

Select imaging CSV file... Select phenotypic CSV file...

Load an available digest file:

Available imaging digests ▾ Available phenotypic digests ▾

Input schema Example input files GitHub



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(<https://dicoat.neurobigdata.org/>)

**Capture**

**Curate**

**Process**

**Extract**

**Analyze**

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(<https://discourse.neurobogal.org/>)

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2. Data organization **specification**

- a. For imaging and non-imaging data
  - b. At the whole study level

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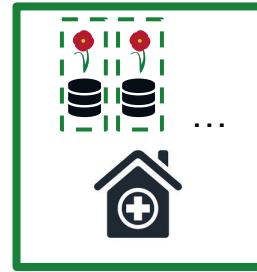
**Extract**

**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**

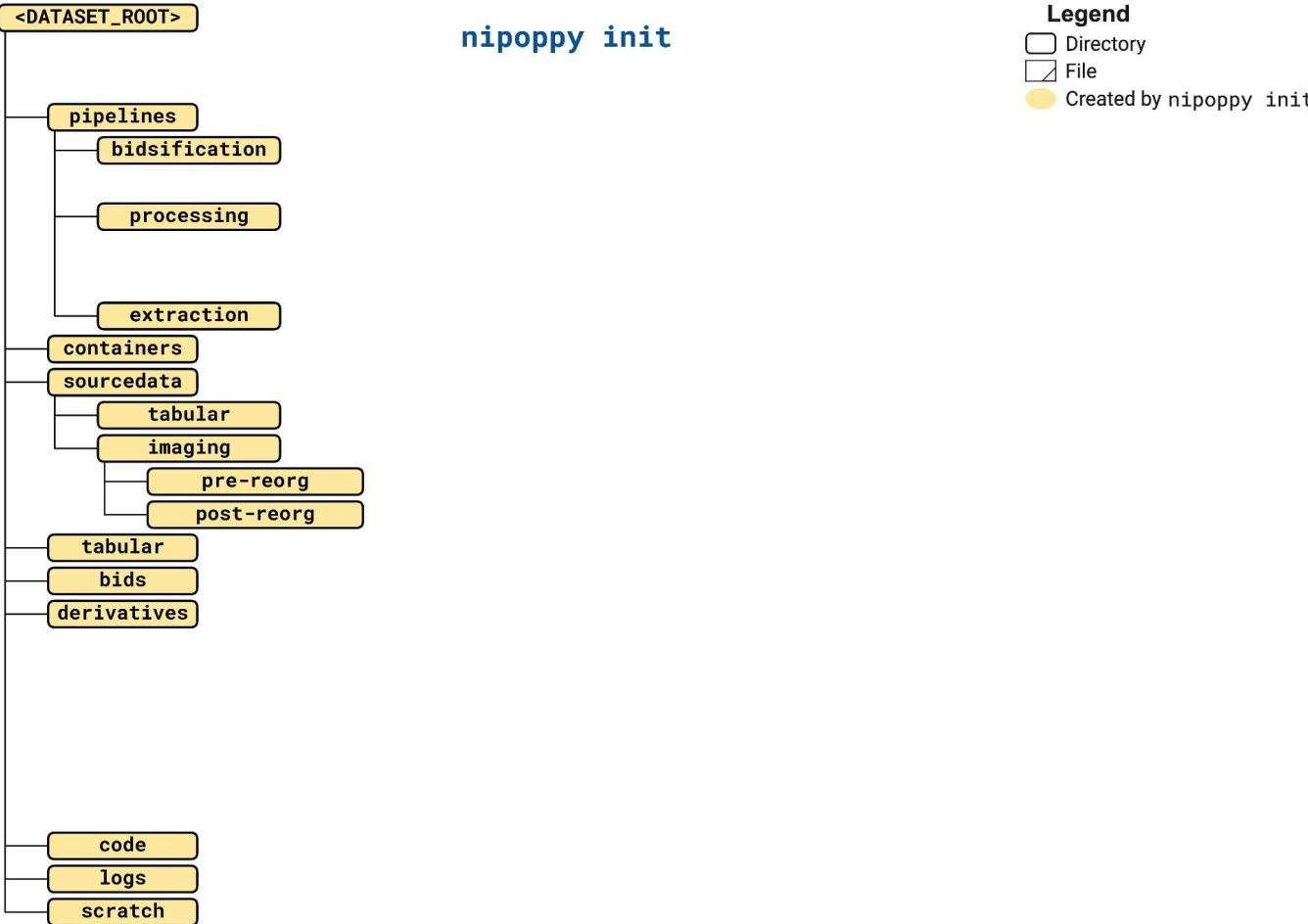
# Nipoppy for decentralized data management/processing

- pip-installable Python package
- Local processing
- Good for consortium-type settings
  - Independent but consistent processing (same pipelines/parameters)
- “Bring-your-own-pipeline”

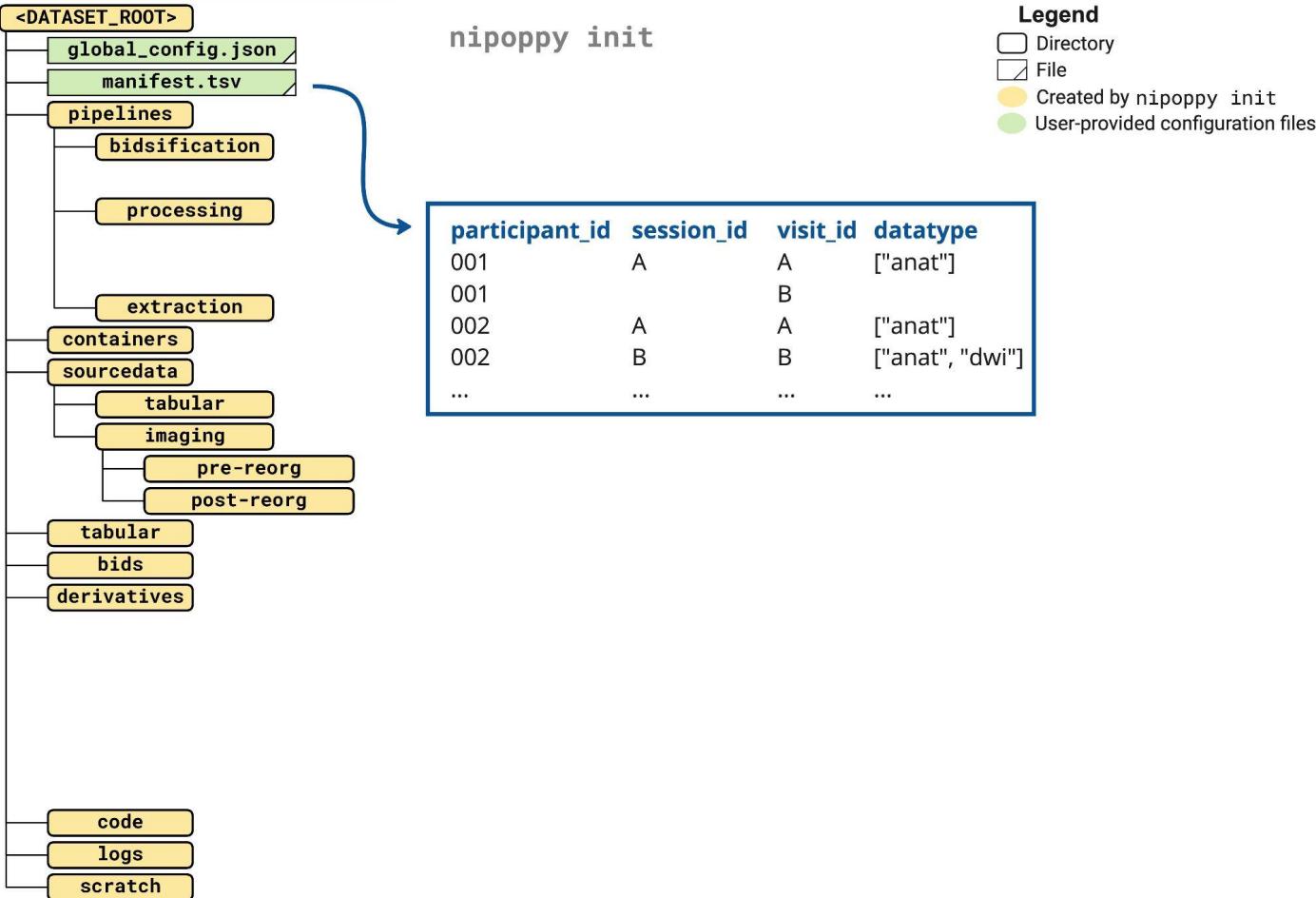


# A typical **Nipopy** workflow

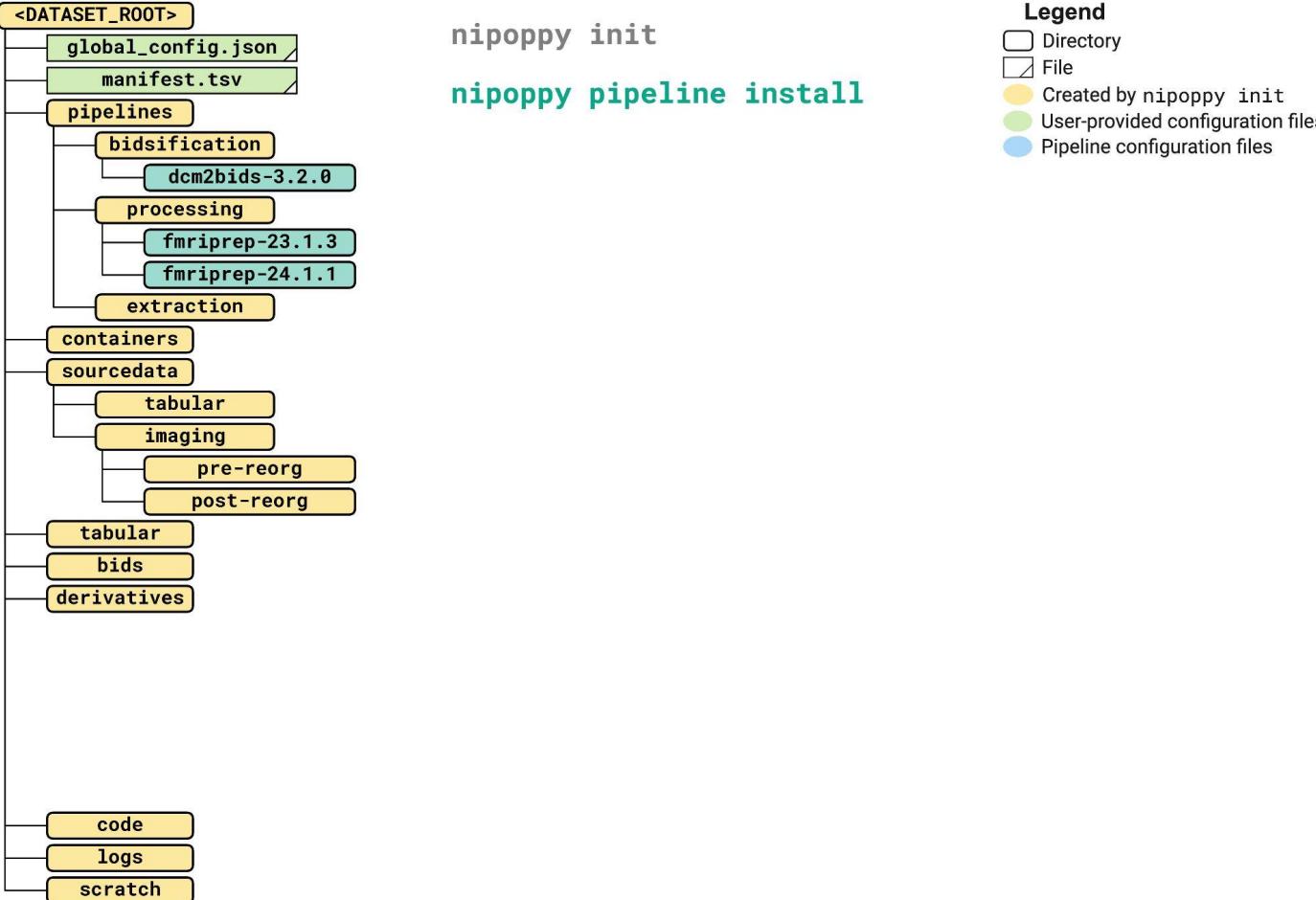
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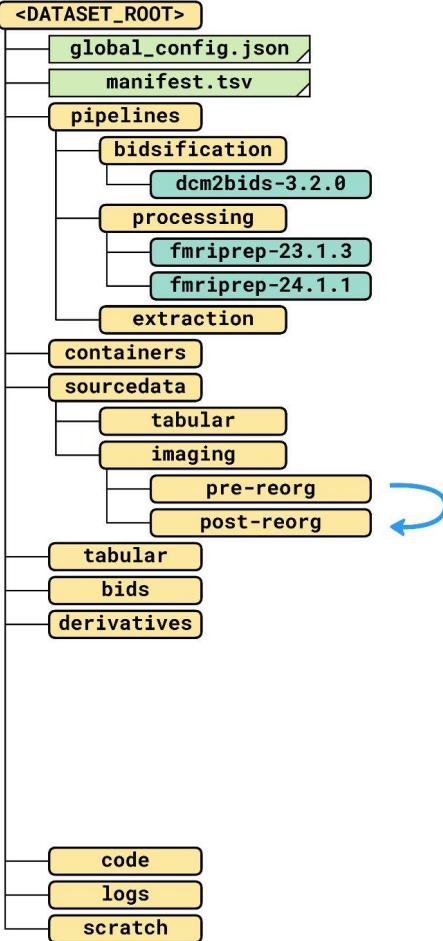
# A typical Nipoppyp workflow



# A typical Nipoppyp workflow



# A typical Nipoppyp workflow



nipoppyp init

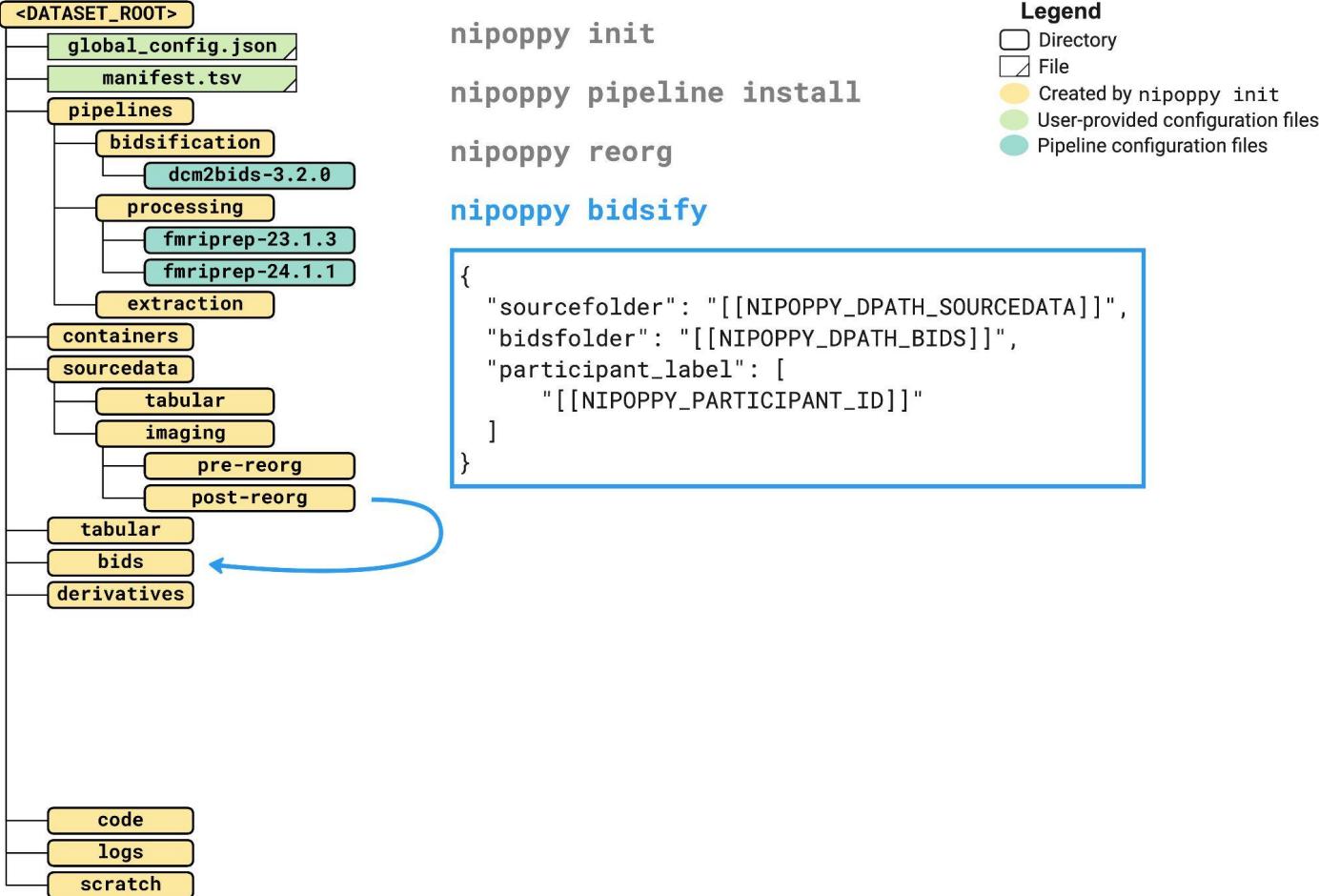
nipoppyp pipeline install

nipoppyp reorg

## Legend

- Directory
- File
- Created by nipoppyp init
- User-provided configuration files
- Pipeline configuration files

# A typical Nipoppyp workflow



`nipoppyp init`

`nipoppyp pipeline install`

`nipoppyp reorg`

`nipoppyp bidsify`

```
{  
    "sourcefolder": "[[NIPOPPY_DPATH_SOURCEDATA]]",  
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        "[[NIPOPPY_PARTICIPANT_ID]]"  
    ]  
}
```

## Legend

Directory

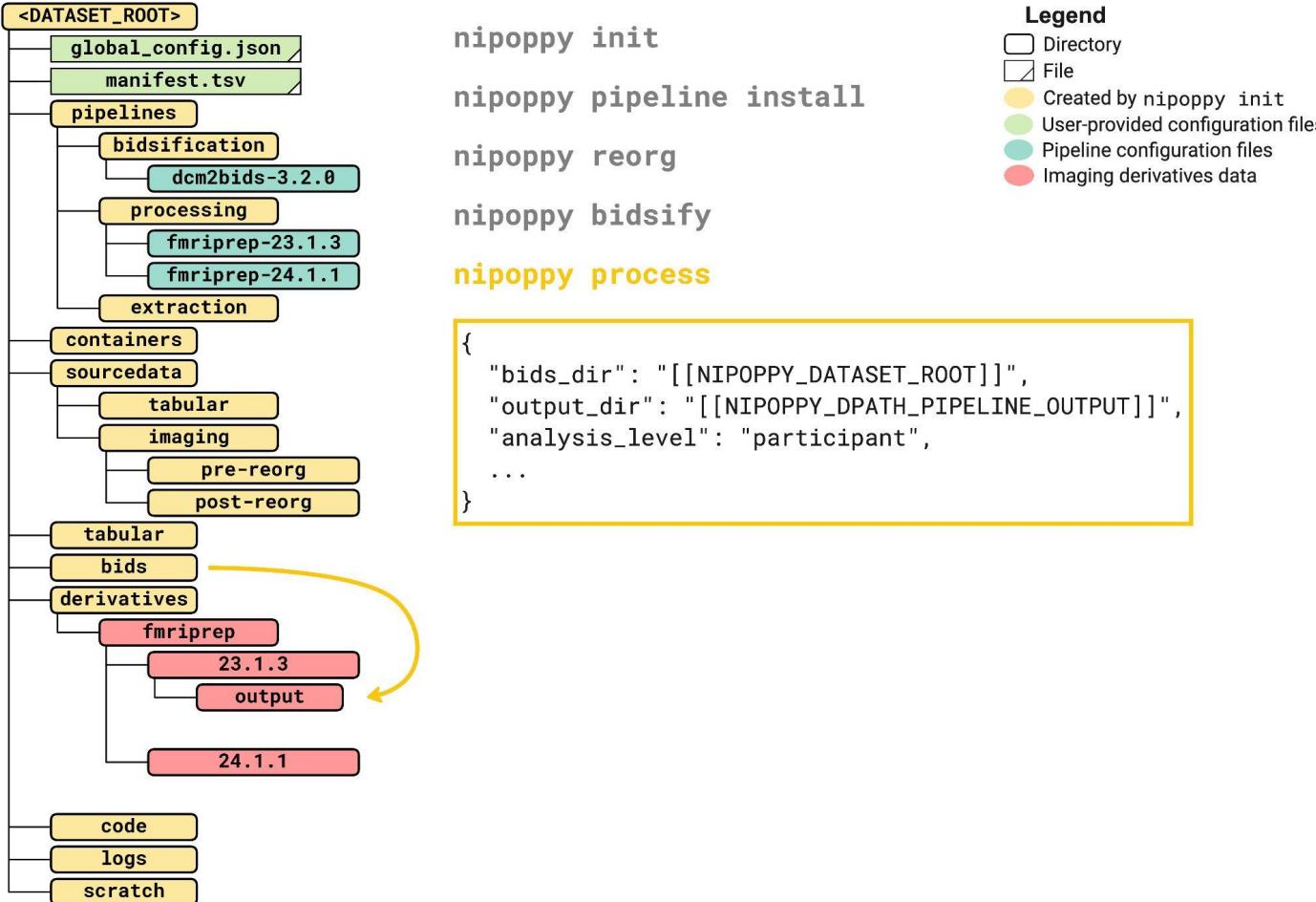
File

Created by nipoppyp init

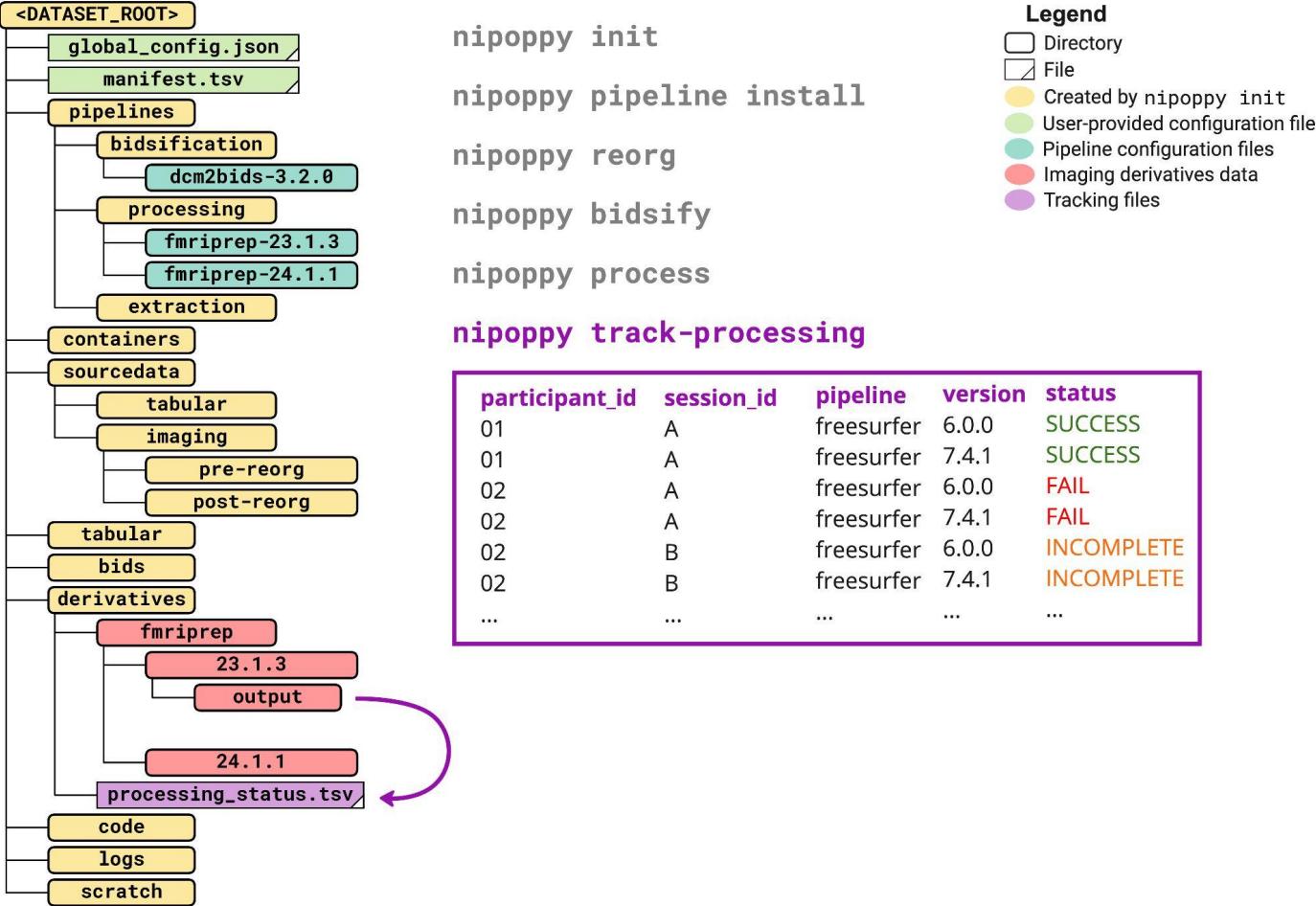
User-provided configuration files

Pipeline configuration files

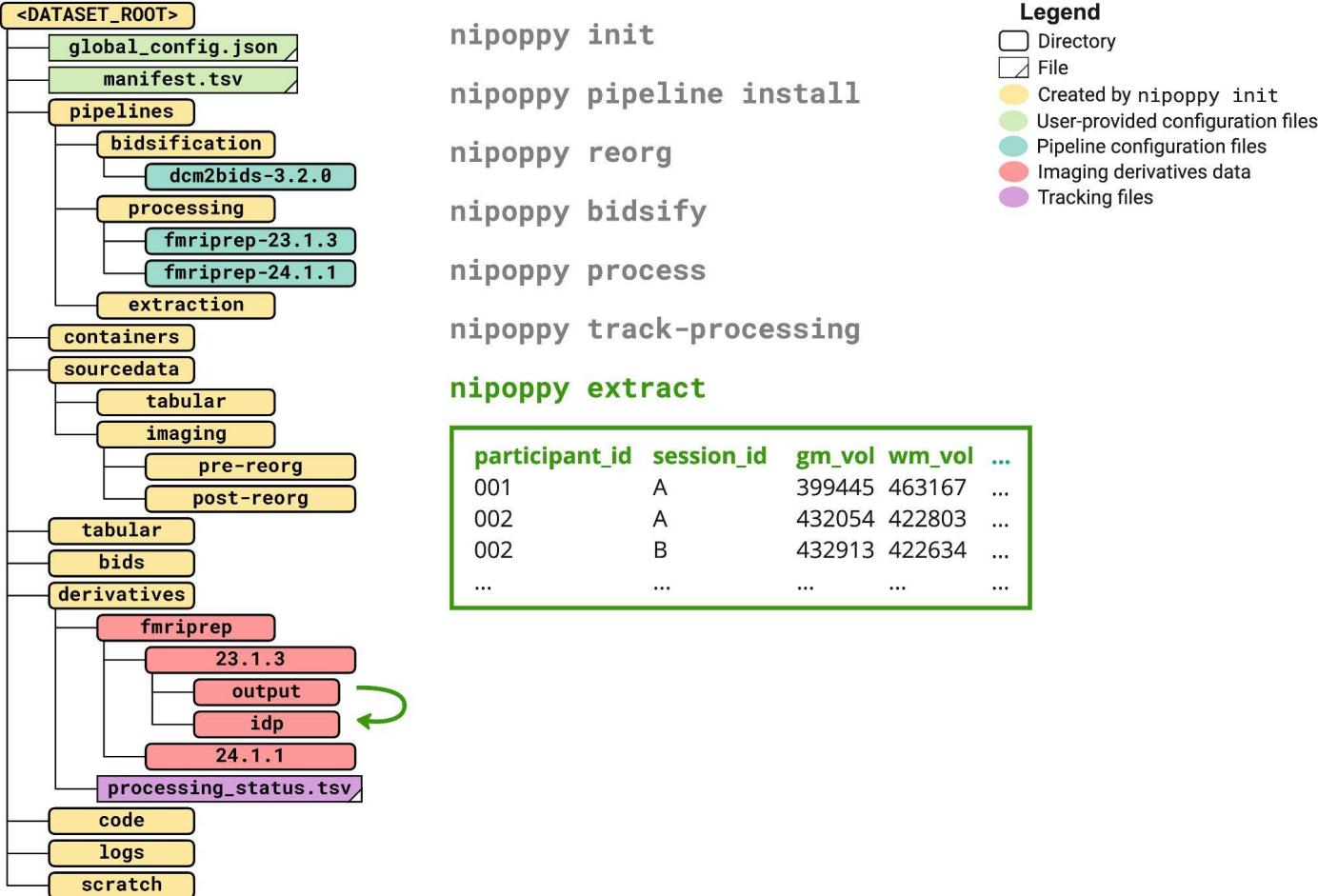
# A typical Nipoppyp workflow



# A typical Nipoppyp workflow



# A typical Nipoppyp workflow



nipoppyp init  
nipoppyp pipeline install  
nipoppyp reorg  
nipoppyp bidsify  
nipoppyp process  
nipoppyp track-processing  
**nipoppyp extract**

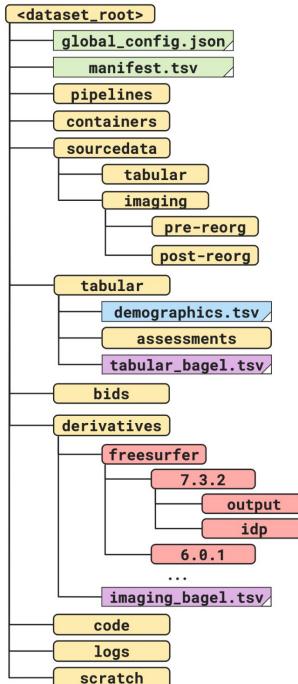
participant_id	session_id	gm_vol	wm_vol	...
001	A	399445	463167	...
002	A	432054	422803	...
002	B	432913	422634	...
...	...	...	...	...

# Nipoppo takeaways

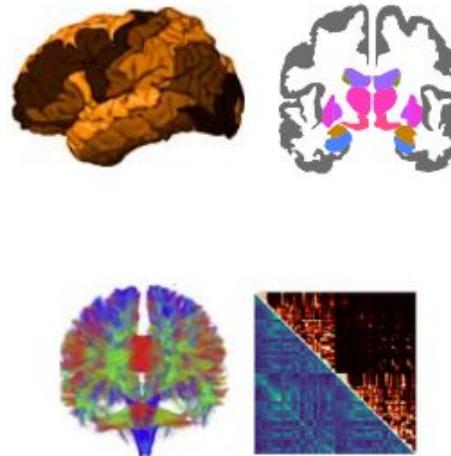
Framework combining **existing tools**



## Local data management



## Reproducible MRI processing and IDP extraction

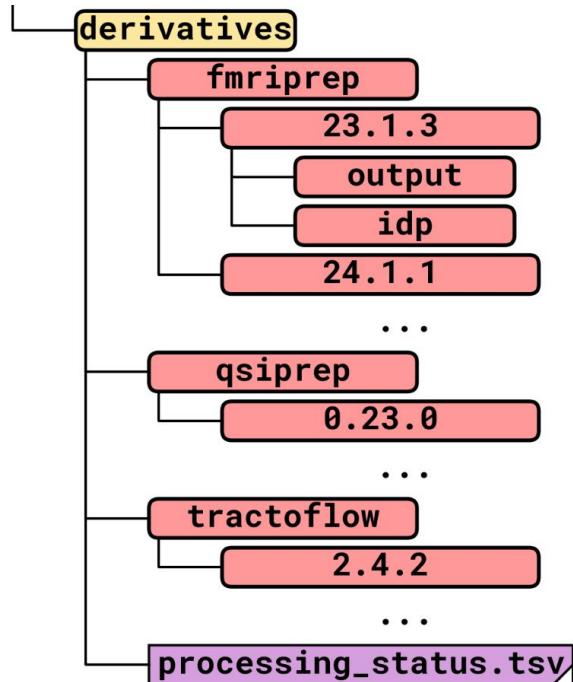


## Progress tracking



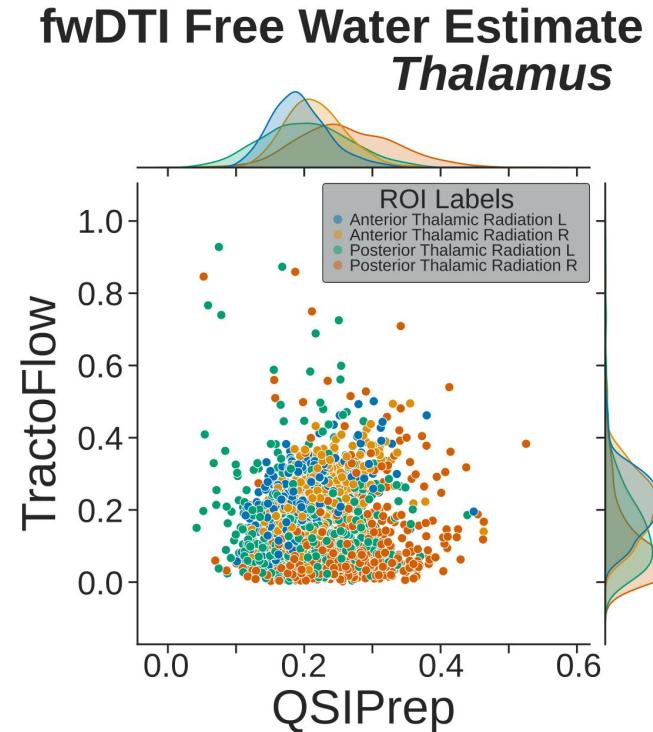
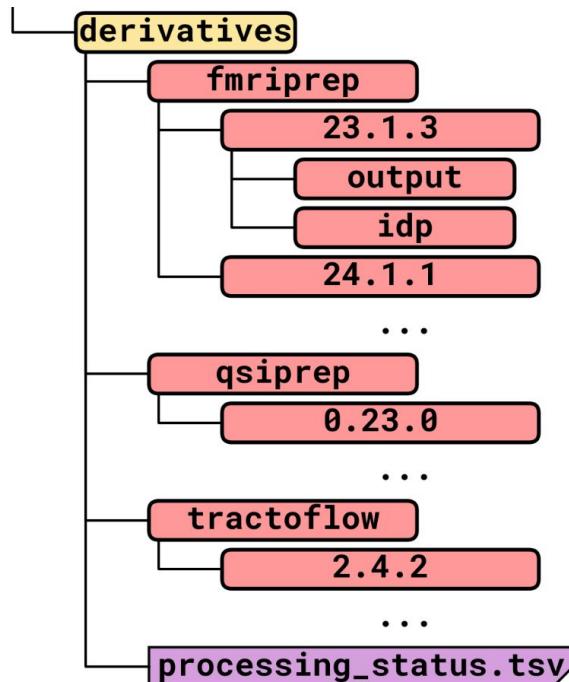
# NipoppY for analytical flexibility studies

- Running different pipelines/versions
- Runtime parameters stored in JSON files



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**Demo! But before...**

# Thank you!



Michelle  
Wang



Mathieu  
Dugré



Brent  
McPherson



Nikhil  
Bhagwat



Arman  
Jahanpour



Sebastian  
Urchs



Alyssa  
Dai



Julia  
Pfarr



Jean-Baptiste  
Poline



ORIGAMI  
Lab



**neuro**  
Montreal Neurological  
Institute-Hospital

CIHR IRSC  
Canadian Institutes of  
Health Research  
Instituts de recherche  
en santé du Canada

Québec  
Fonds de recherche – Nature et technologies  
Fonds de recherche – Santé  
Fonds de recherche – Société et culture

PARKINSON  
QUÉBEC

UNIQUE  
CENTRE

NIH  
National Institutes  
of Health

THE MICHAEL J. FOX FOUNDATION  
FOR PARKINSON'S RESEARCH



**McGill**  
UNIVERSITY

Chan  
Zuckerberg  
Initiative

HBHL  
NEUROHUB

P  
QUEBEC  
PARKINSON  
NETWORK

Brain  
Canada  
Foundation