



# Assessing analytical variability with **Nipoppy**

**Michelle Wang**

NeuroDataScience-ORIGAMI Lab (JB Poline)

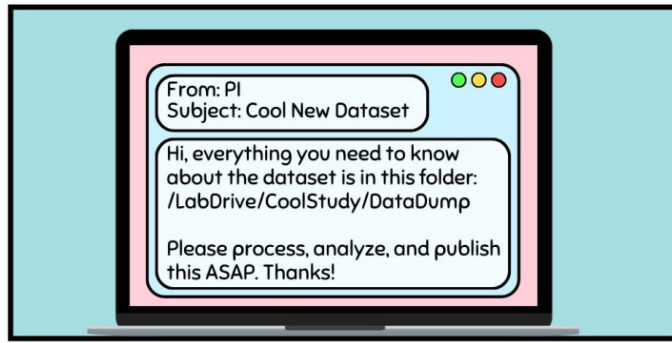
McGill University

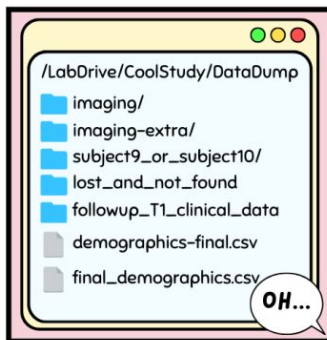
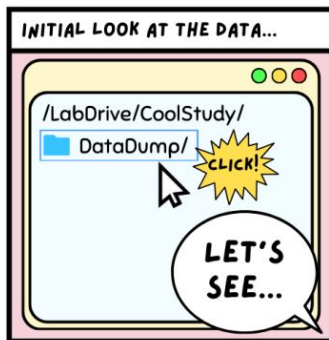
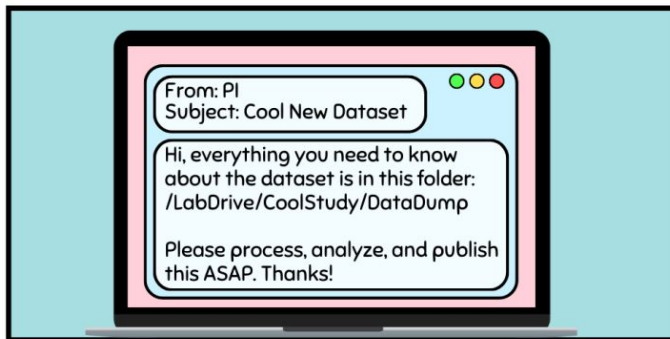
*2025 June 24*



ORIGAMI  
Lab



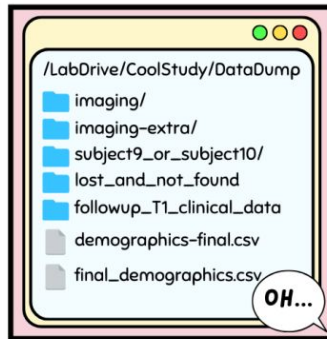
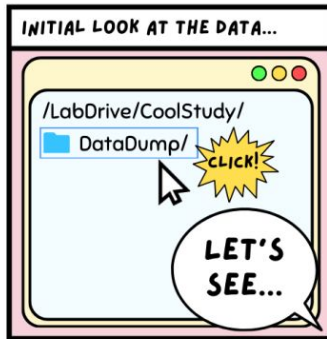
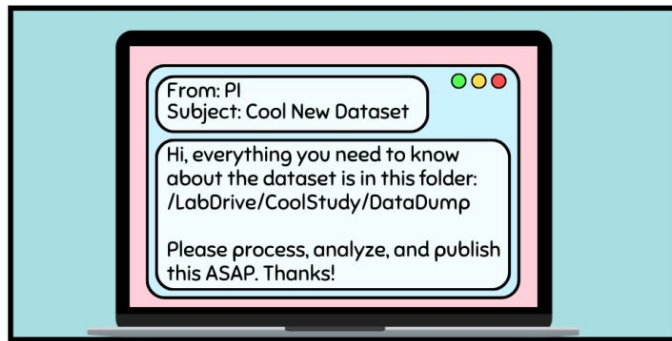




SUBJECT_ID	age	age (good)	Sex
001	21?	22	F
002_fixed	25	25	M
003		30	Male
004_T!	-1	26	0
004_T2	27	27	1
005	29	29	1
6	>18		997
007	26	999	F
008_bad	27	27	M
009	NA	26	F
010	25	25	

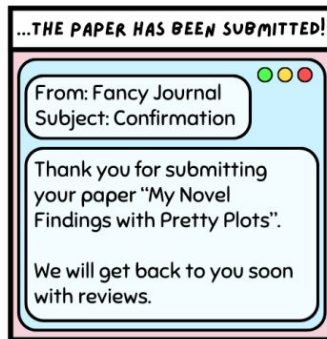
??





demographics-final.csv

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004_T!	-1	26	0
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008_bad	27	27	M
009	NA	26	F
010	25	25	??



# 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 **Nipoppy** framework

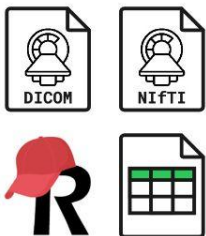
1. **Protocol** for best practices (FAIR principles) in organization/processing of neuroimaging-clinical datasets

# Introducing the **Nipoppy** framework

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

## Capture

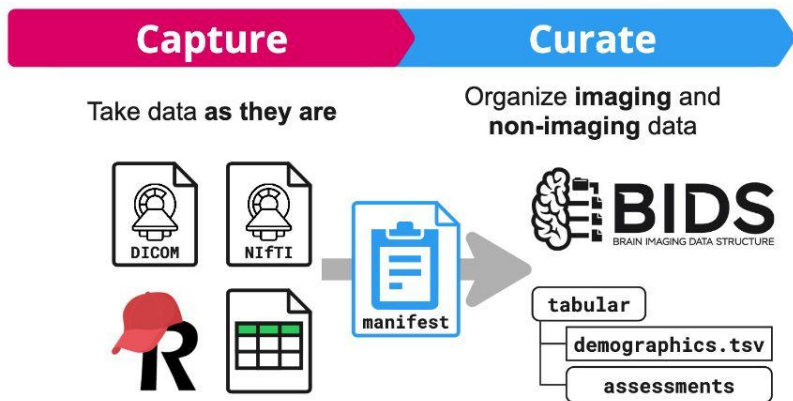
Take data **as they are**





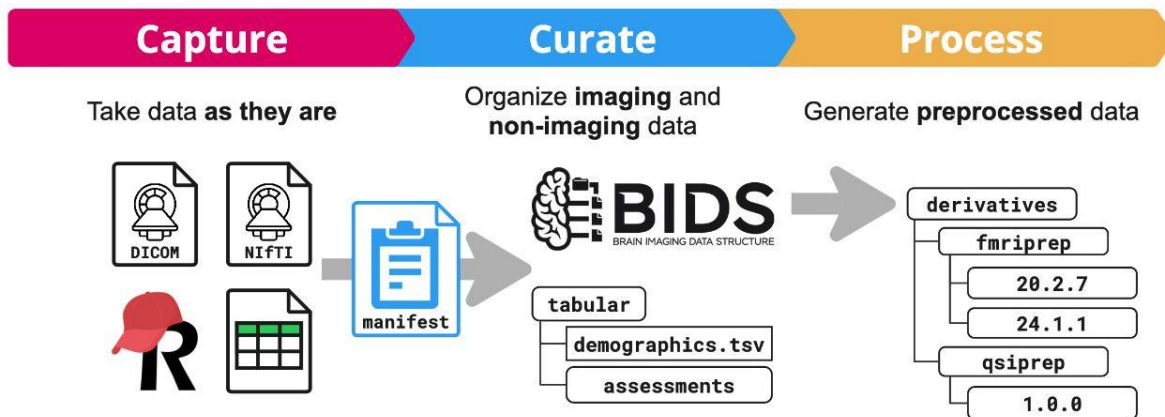
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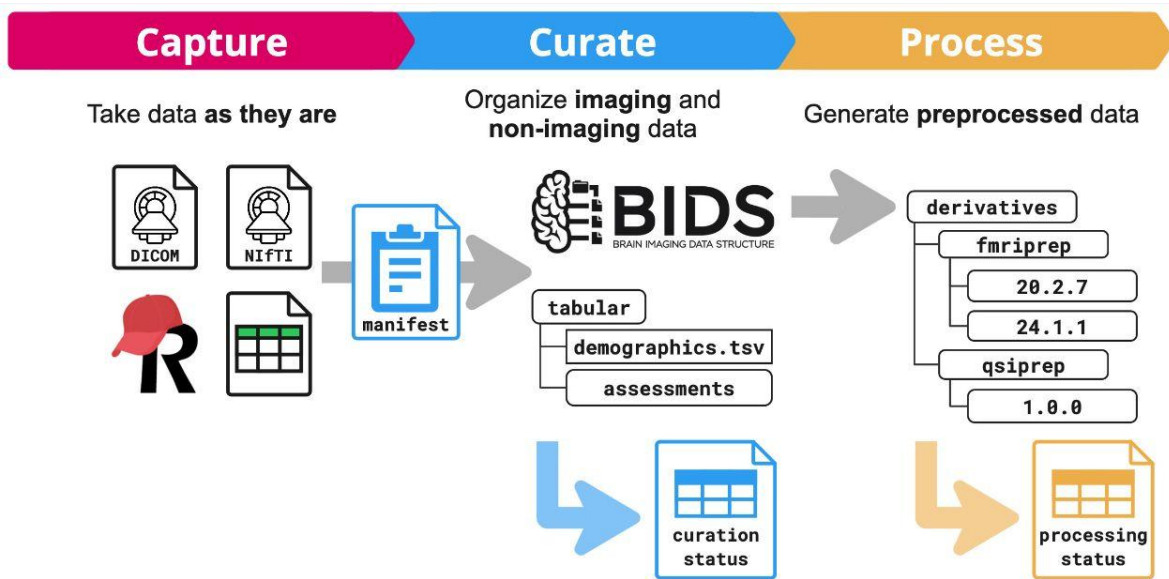
# Introducing the **Nipoppy** framework

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



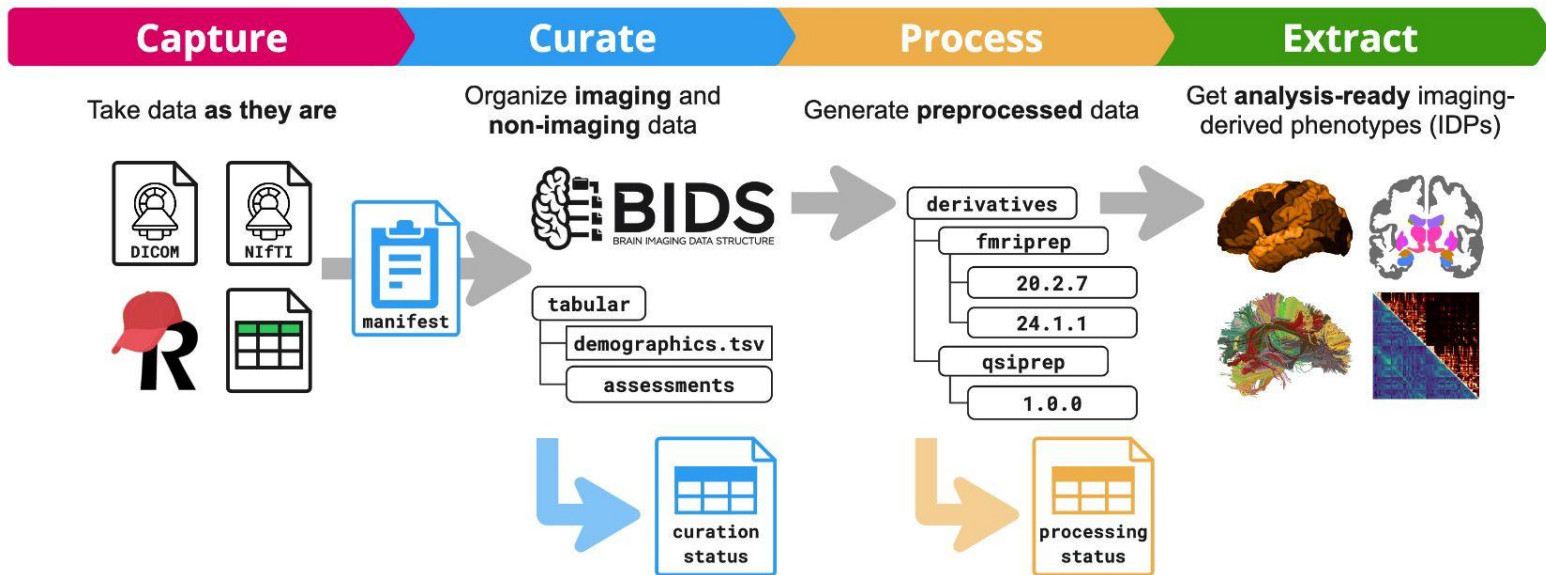
# Introducing the **Nipoppy** framework

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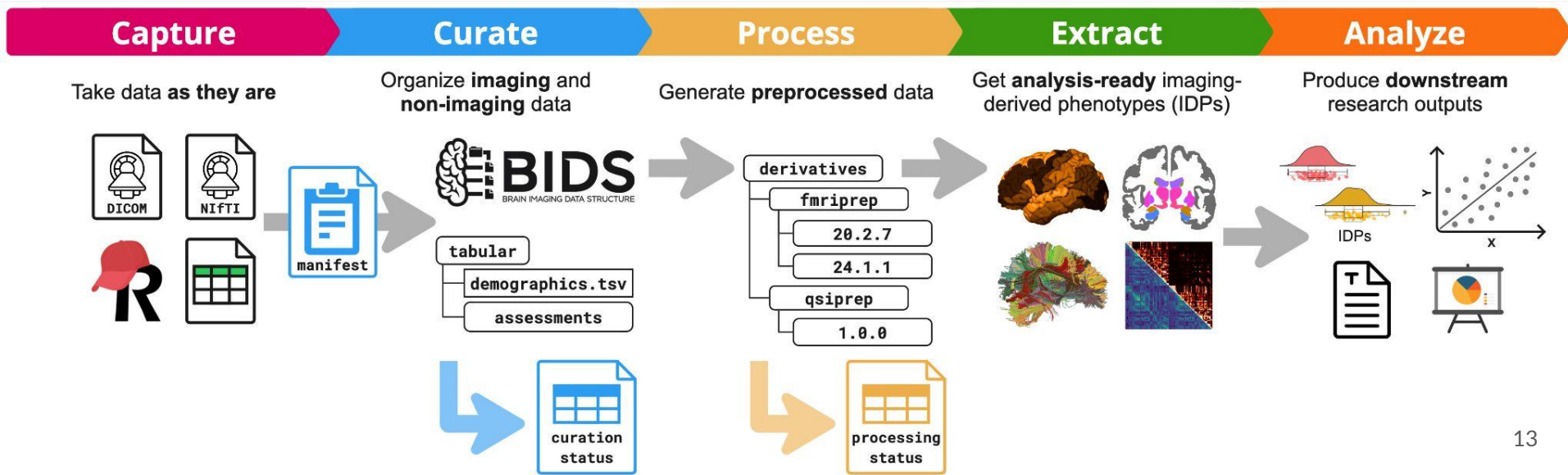
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# Introducing the **Nipoppy** framework

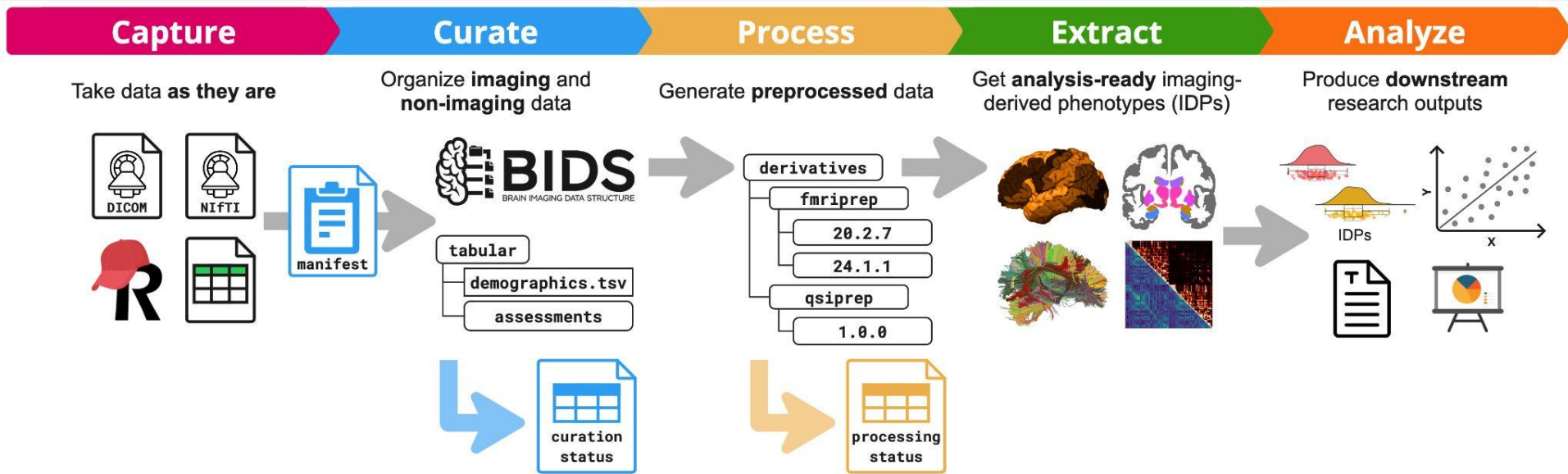
1. **Protocol** for best practices (FAIR principles) in organization/processing of neuroimaging-clinical datasets



# 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.nuro.ox.ac.uk/>)



# <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 ▾



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

**Capture**

**Curate**

**Process**

**Extract**

**Analyze**



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[\(https://dicom.nimg.org/\)](https://dicom.nimg.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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**Process**

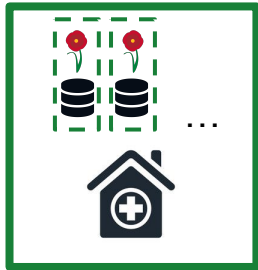
**Extract**

**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**

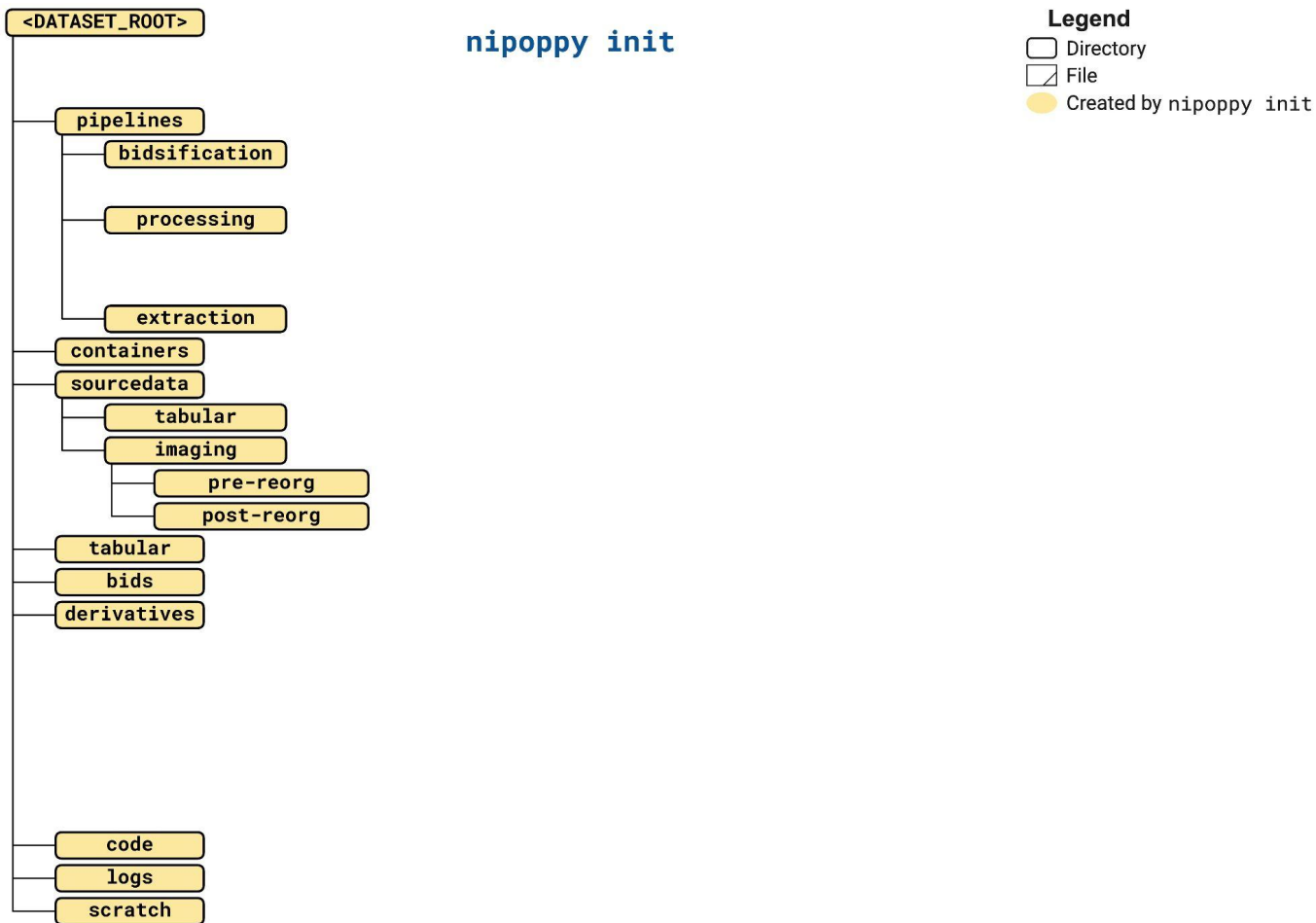
# Nipoppy for decentralized data management/processing

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

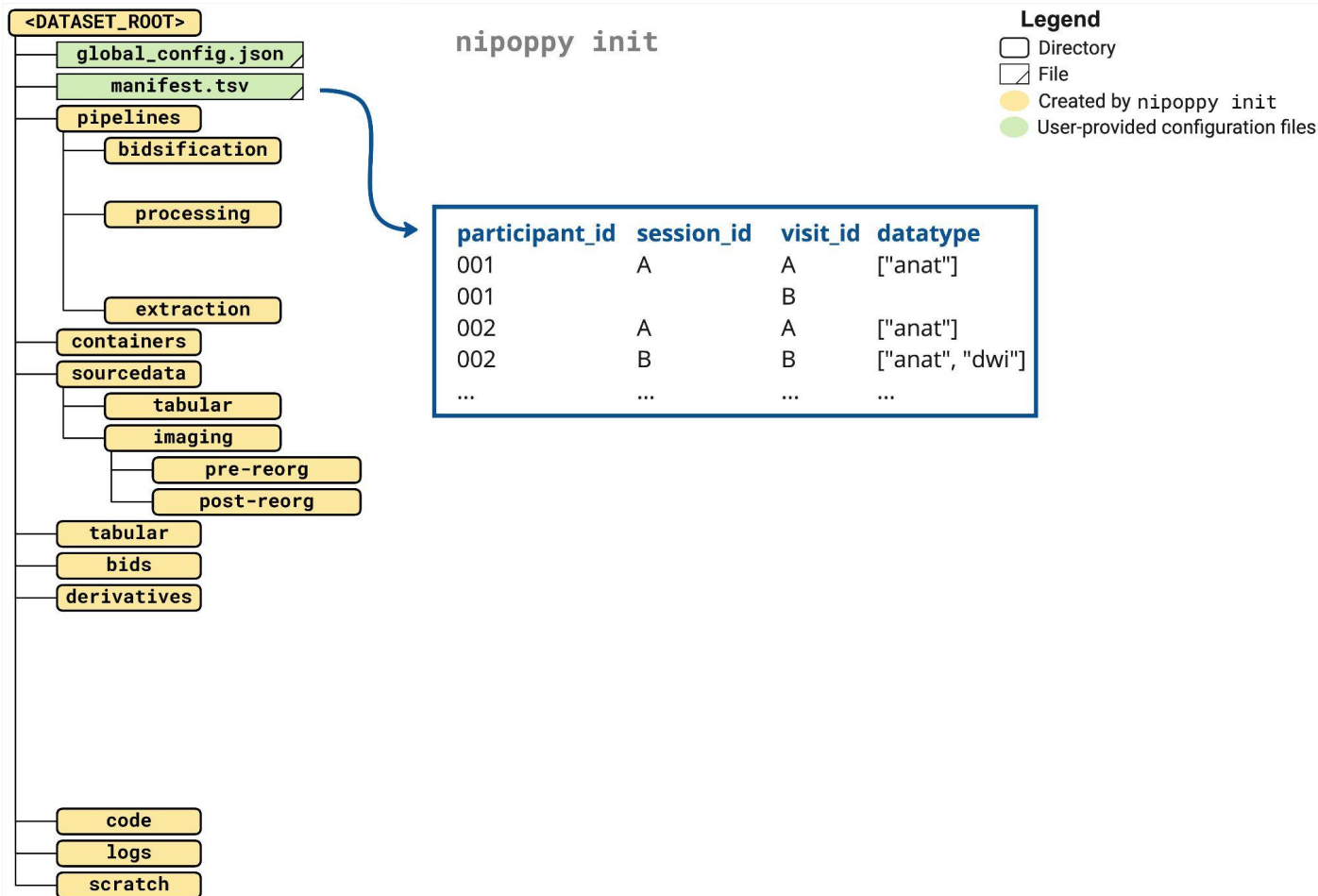


# A typical **Nipoppy** workflow

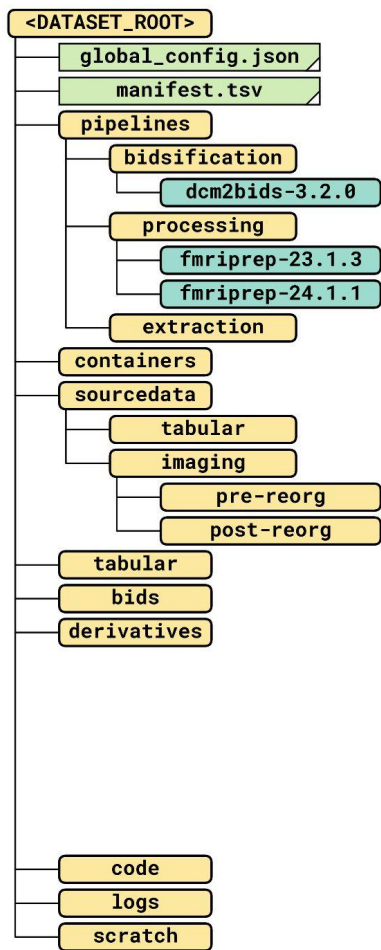
# A typical **Nipoppy** workflow



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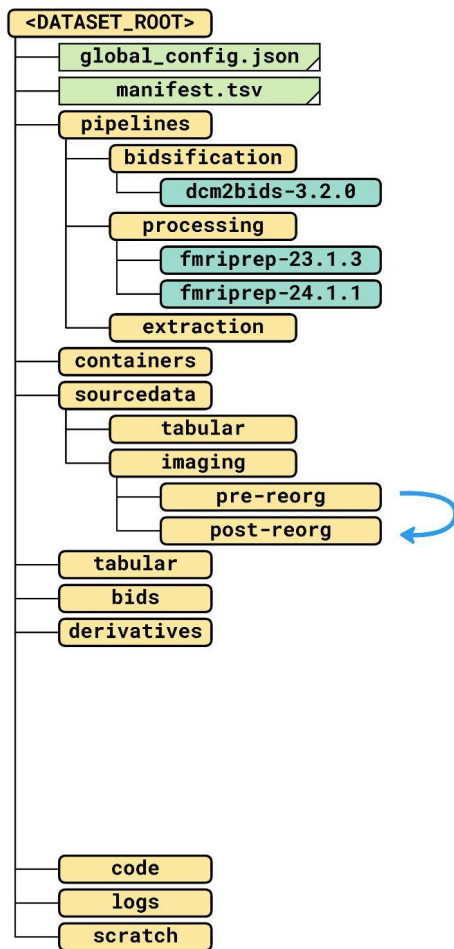
nipoppy init

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

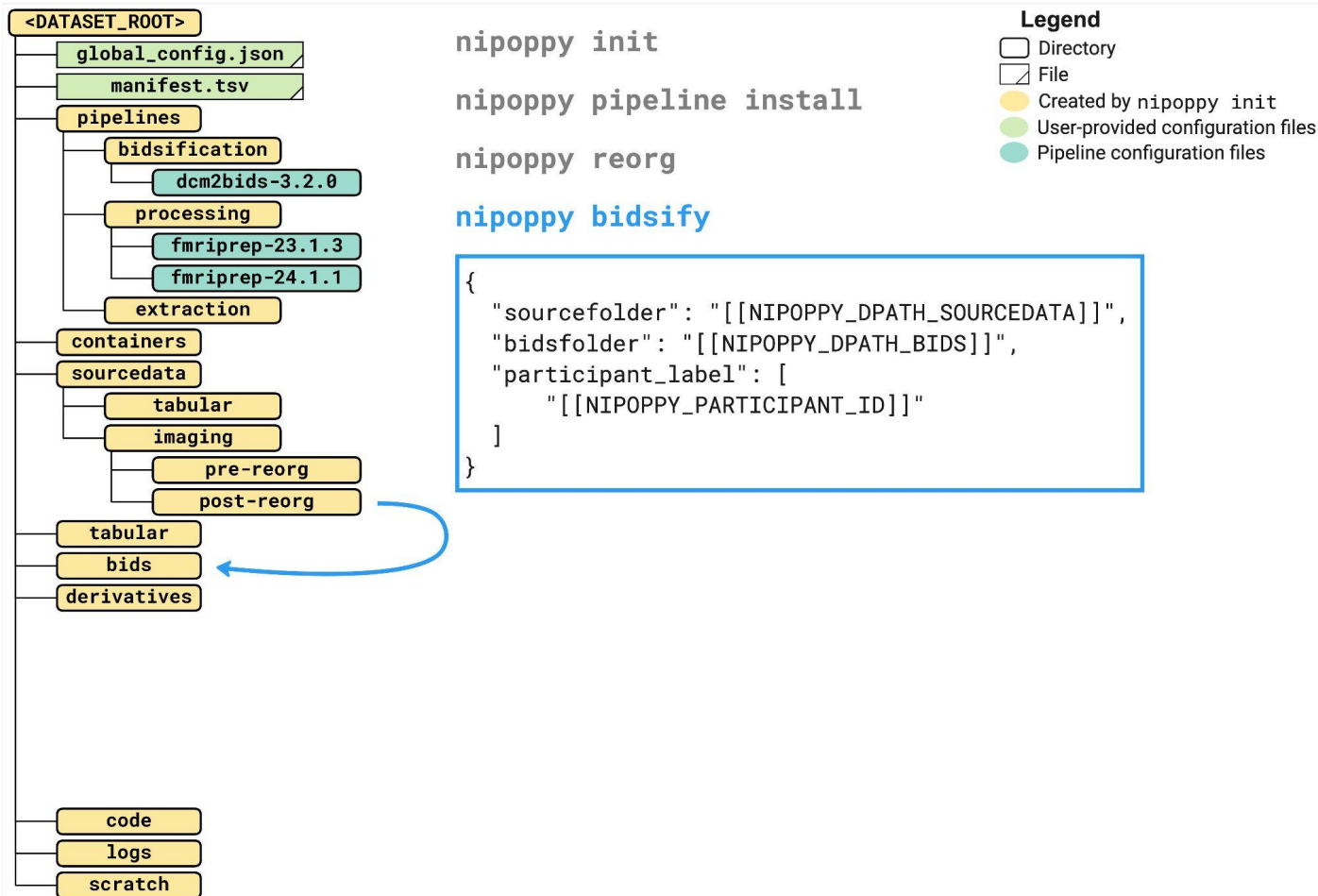
● Created by nipoppy init

● User-provided configuration files

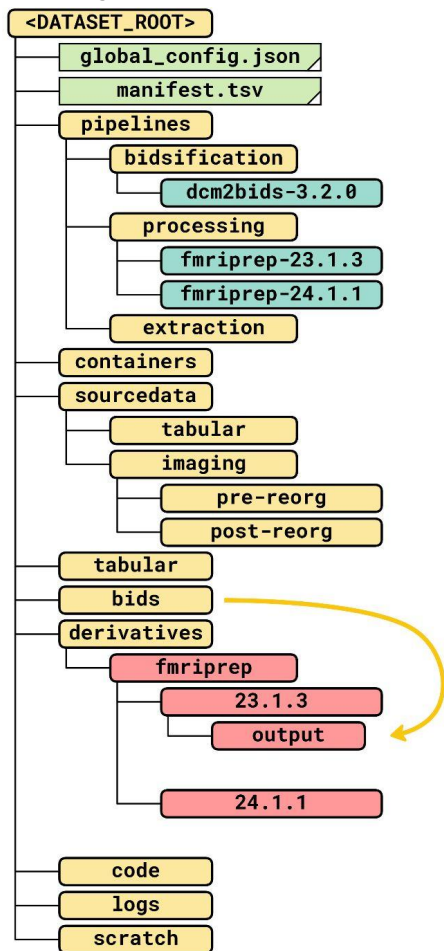
● Pipeline configuration files



# 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

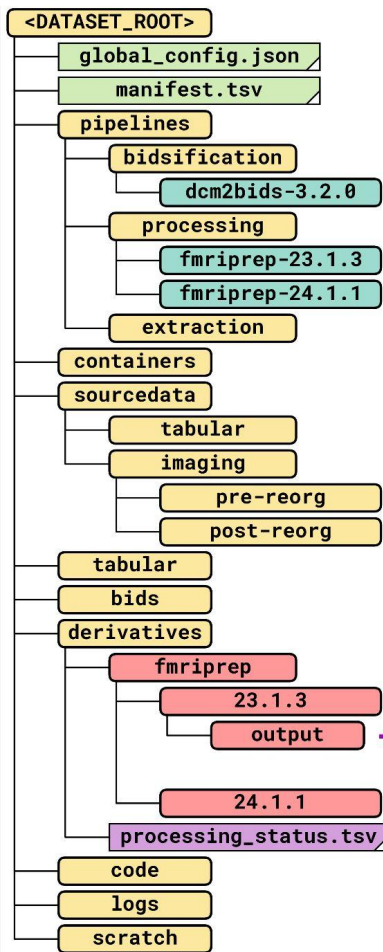
○ Created by nipoppy init

○ 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

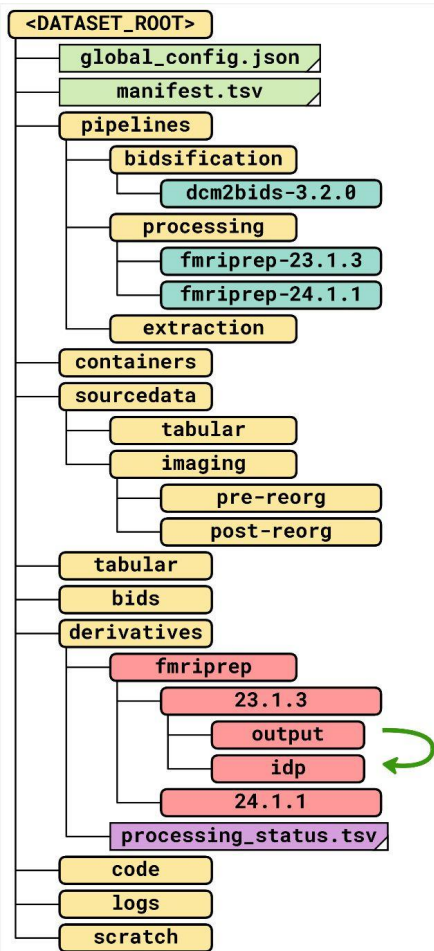
nipoppy track-processing

## Legend

- Directory
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- Created by nipoppy init
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- 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

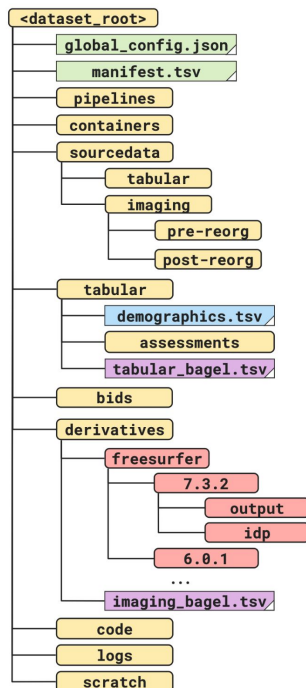
- Directory
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# Nipoppy takeaways

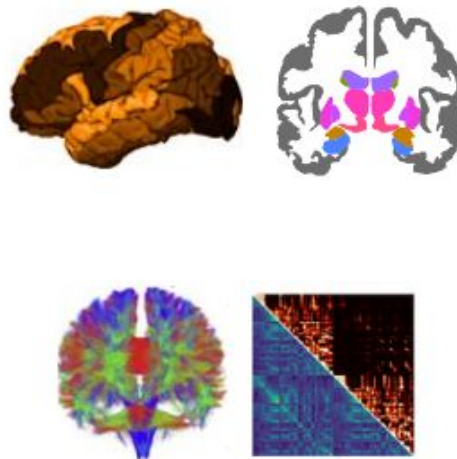
Framework combining **existing tools**



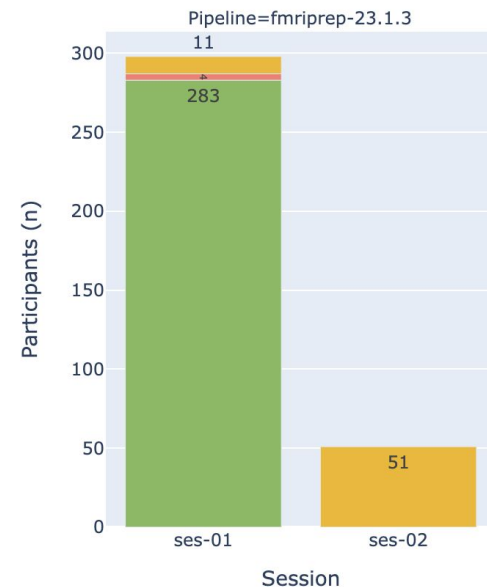
## Local data management



## Reproducible MRI processing and IDP extraction

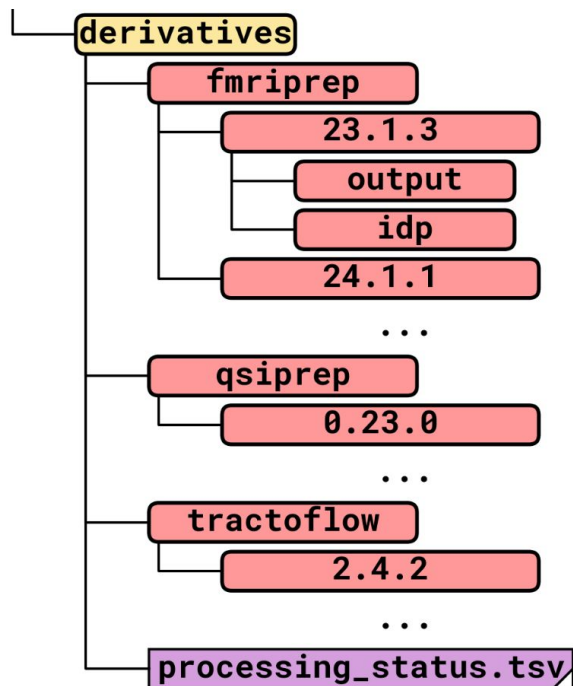


## Progress tracking



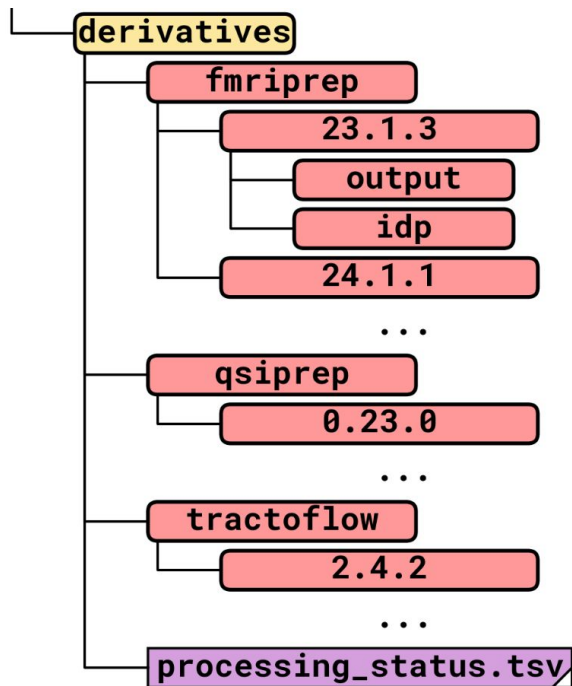
# Nipoppy for analytical flexibility studies

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

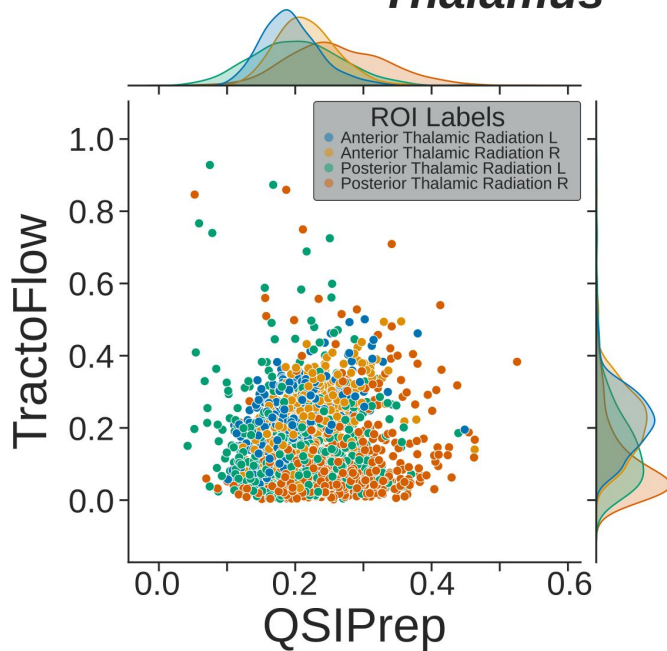


# Nipoppy for analytical flexibility studies

- Running different pipelines/versions
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## fwDTI Free Water Estimate *Thalamus*



**Demo! But before...**



# Thank you!



Michelle Wang



Mathieu Dugré



Brent McPherson



Nikhil Bhagwat



Arman Jahanpour



Sebastian Urchs



Alyssa Dai



Julia Pfarr



Jean-Baptiste Poline

