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

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The truth about many neuroimaging datasets

- They are **messy**
- Data organization/curation and processing is a time-consuming and error-prone process

How can we organize and process data in a consistent and reproducible manner, to avoid downstream headaches?

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

Capture

Take data as they are













- 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://	/digest neurobagel org/			
Capture	Organize	Process	Track	Extract
Take data as they are	Organize/curate imaging and non-imaging data	Use reproducible environments and parameters	Check data availability at the participant level	Get analysis-ready imaging-derived phenotypes (IDPs)
	tabular demographics	$FreeSurfer \land Y$	7.3.2 Image: Constraint of the second state of the seco	

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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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- 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

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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Legend

Directory File

scratch







...





nipoppy init

nipoppy reorg

nipoppy bidsify

nipoppy run

. . .

}

"bids_dir": "[[NIPOPPY_DATASET_ROOT]]",
"output_dir": "[[NIPOPPY_DPATH_PIPELINE_OUTPUT]]",
"analysis_level": "participant",





nipoppy init

nipoppy reorg

nipoppy bidsify

nipoppy run

nipoppy track

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	В	freesurfer	6.0.0	INCOMPLETE
02	В	freesurfer	7.4.1	INCOMPLETE





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participant_iu	session_iu	gm_vor	wm_vor	
001	A	399445	463167	
002	А	432054	422803	
002	В	432913	422634	



Nipoppy takeaways



- **Standardized organization** and workflow for both imaging and tabular data
- Flexible and reproducible processing pipelines
- Pipeline output tracking and imaging-derived phenotype (IDP) extraction
- Built-in support for **ongoing studies**
- Local, decentralized setup → facilitate multisite studies (see also: Neurobagel)

Thank you!

- Contact: michelle.wang6@mail.mcgill.ca
- Poster #2256 (June 26-27, 13:45-15:45)



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