



Introduction to NWB & DANDI

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BERKELEY LAB



CATALYST
NEURO

DARTMOUTH

Kitware

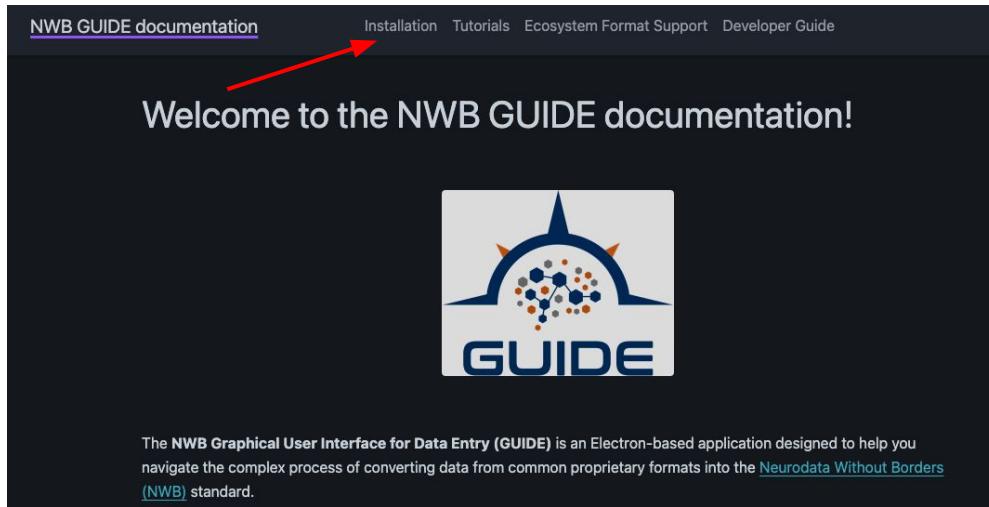
Schedule

10:15 - 10:45	Overview of NWB and DANDI
10:45 - 11:00	Q&A
11:00 - 12:15	NWB GUIDE (Interactive Tutorial) <ul style="list-style-type: none">• Easily convert data• Inspect NWB File• Explore NWB File
12:20	Group photo
12:30-13:30	Lunch
13:30 - 14:30	Advanced NWB conversion
14:30 - 15:30	Analysis tools in the NWB ecosystem

NWB GUIDE Tutorial

Installation

- ❑ <https://nwb-guide.readthedocs.io/en/v0.0.15/index.html>



The screenshot shows the NWB GUIDE documentation website. At the top, there is a dark header with the text "NWB GUIDE documentation" in white. Below the header, a red arrow points to the "Installation" link in a horizontal navigation bar. The main content area has a dark background with white text. It features a large "Welcome to the NWB GUIDE documentation!" message, followed by the NWB GUIDE logo, which consists of a blue sun-like shape with orange rays and a central cluster of orange and blue dots, with the word "GUIDE" in blue capital letters below it. At the bottom of the page, there is a paragraph of text describing the application.

The NWB Graphical User Interface for Data Entry (GUIDE) is an Electron-based application designed to help you navigate the complex process of converting data from common proprietary formats into the [Neurodata Without Borders \(NWB\)](#) standard.



Need for neurophysiology data standard and archive

- Data are expensive to collect
 - Money, time, animal use
- Sharing neurophysiology data within a lab and with collaborators is tedious
- Sharing scientific software is also difficult
- It is often easier to just collect new data and build new tools
- Difficult for labs to devote time and effort to sharing data and software



DANDI &



New NIH Data Management and Sharing Policy

For NIH projects starting Jan 25, 2023:

“Shared scientific data should be made accessible as soon as possible, and no later than the time of an associated publication, or the end of performance period, whichever comes first.” [1]

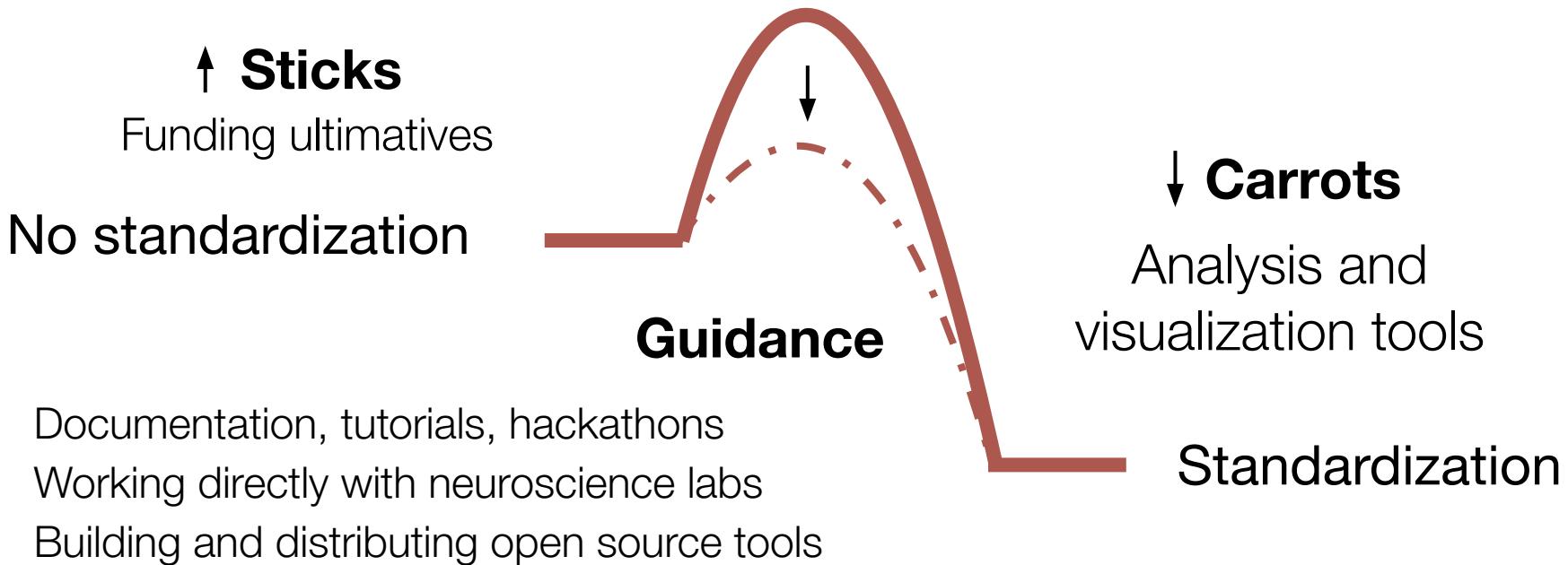
Applications must include Data Management and Sharing Plan, which indicates use of a data standard and archive [1]

“For BRAIN Initiative applications … applicants are required to share the data they collect using the BRAIN Initiative informatics infrastructure (both data archives and relevant data standards)” [2]

[1] <https://sharing.nih.gov/data-management-and-sharing-policy/sharing-scientific-data/data-sharing-approaches>

[2] <https://grants.nih.gov/grants/guide/notice-files/NOT-MH-19-010.html>

The energy barrier in data standardization



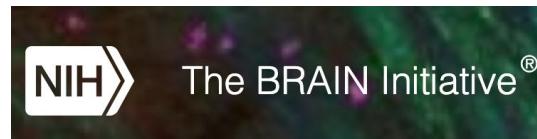
Neurodata Without Borders and the DANDI Archive



A standard for sharing, archiving, and analyzing neurophysiology and behavioral data

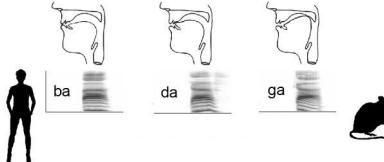
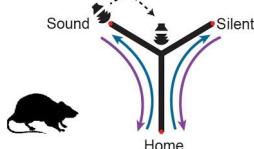


An archive for sharing and collaboration space for analyzing neurophysiology data

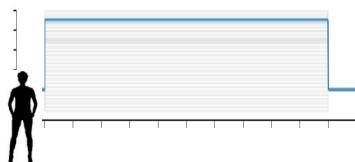


Challenge: Diversity of experiments and rate of innovation

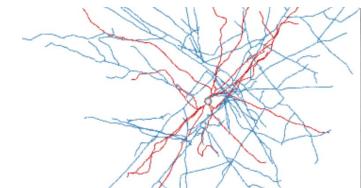
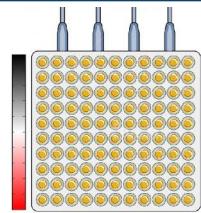
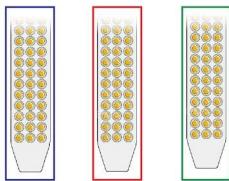
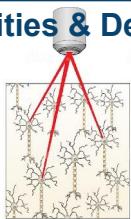
Species & Task



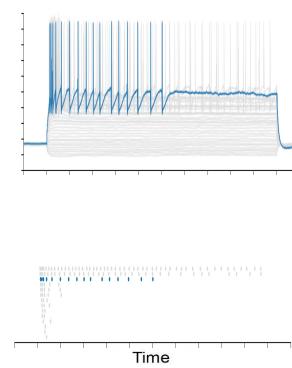
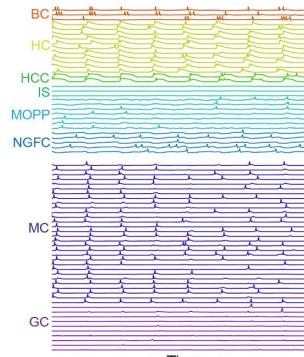
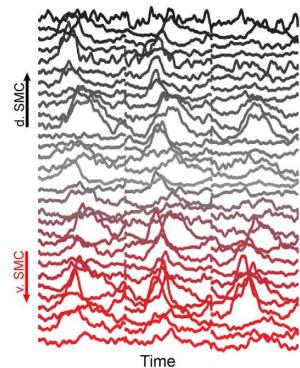
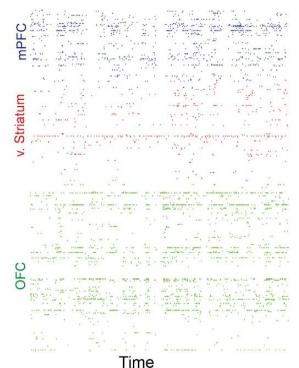
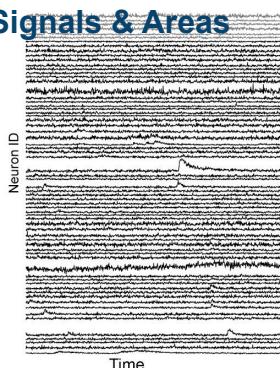
```
run Simulation  
(species == mouse,  
area == hippocampus,  
#neurons == N)  
while 1, t++  
do Vm(:,t) =  
NEURON(N, Vm(t-1))
```



Modalities & Devices



Signals & Areas

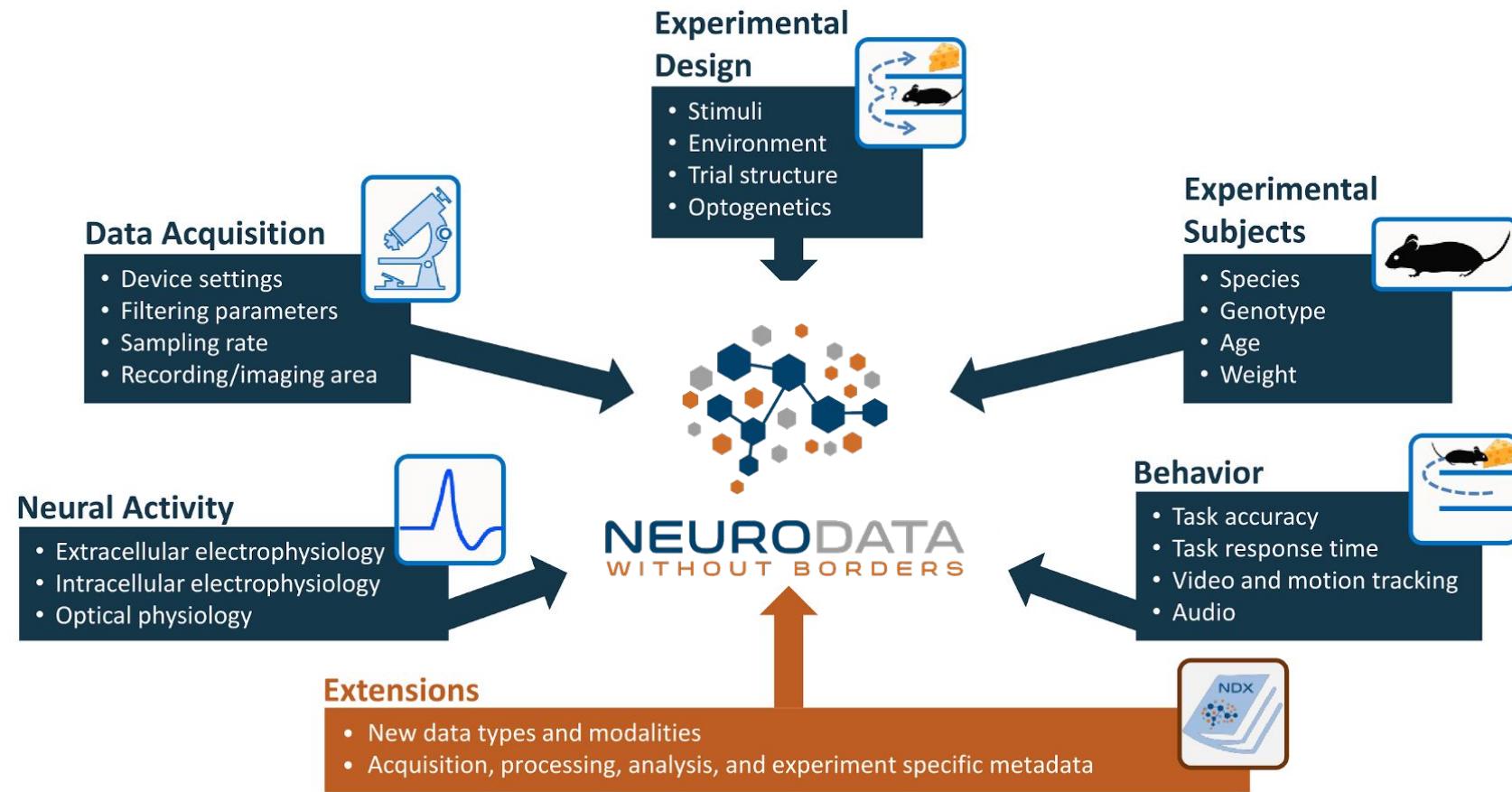


DANDI



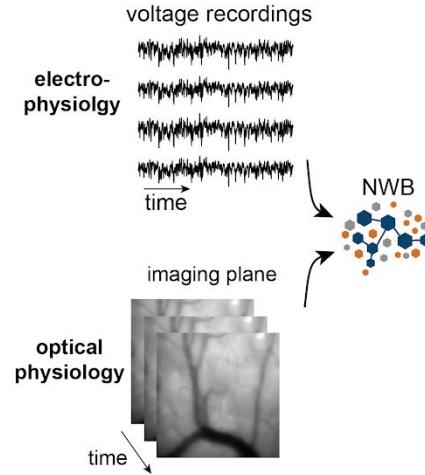
NEURODATA
WITHOUT BORDERS

NWB defines a unified data format for neurophysiology

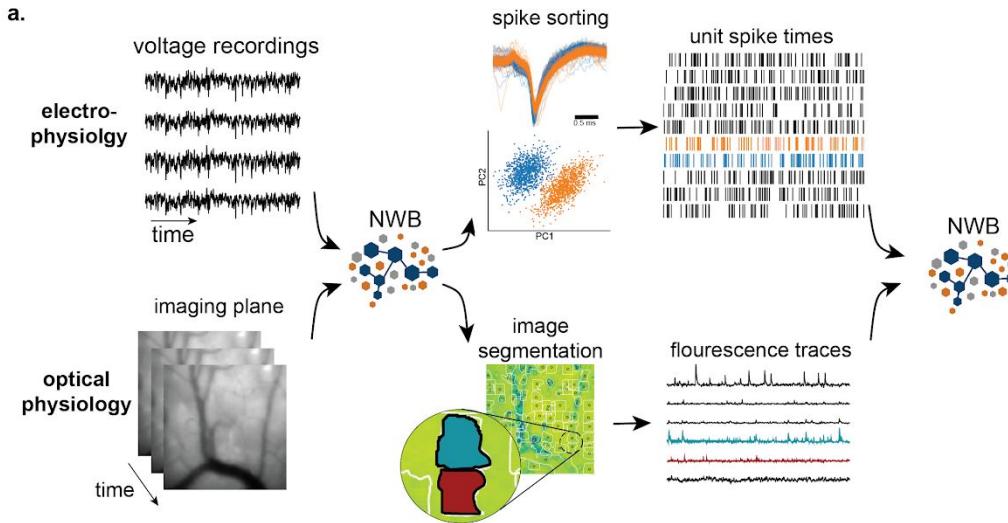


NWB enables unified storage of multimodal raw and processed data

a.

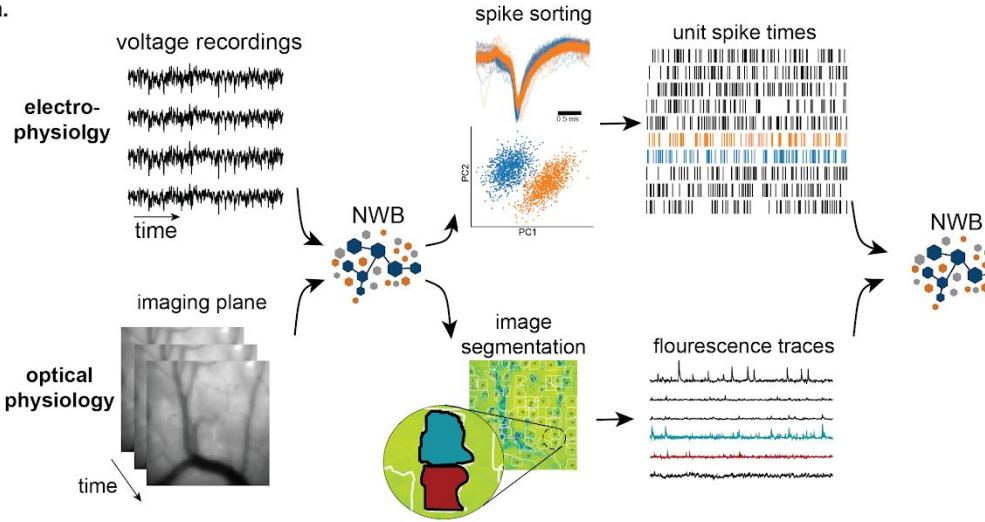


NWB enables unified storage of multimodal raw and processed data

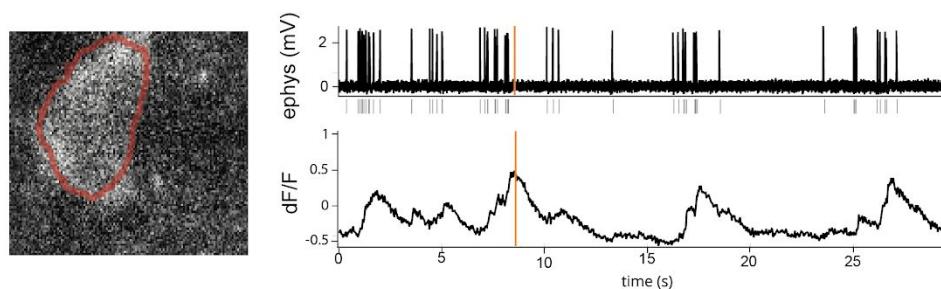


NWB enables unified storage of multimodal raw and processed data

a.



b.



NWB organizes your neurophysiology data and metadata



general

- subject (neurodata_type: Subject)
 - species : Mus musculus

- experimenter :
 - Ryan Ly
 - Ben Dichter

extracellular_ophys

electrodes :

id	x	y	z	location	...
0	1.1	0.5	0.1	SSp-II1	...
1	1.2	0.5	0.3	SSp-II1	...
2	1.3	0.5	0.5	SSp-II2/3	...

- acquisition
- processing
- units
- intervals

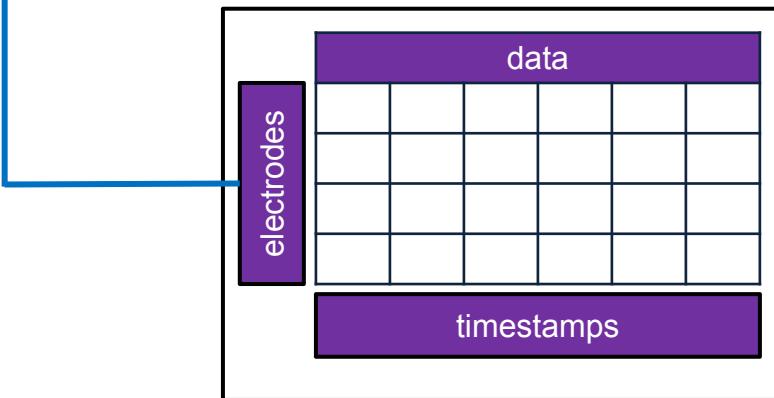
...

NWB organizes your neurophysiology data and metadata



- general
- acquisition

ElectricalSeries (neurodata_type: ElectricalSeries)



- Description
- Unit of measurement
- Conversion factor
- Channel conversion factor
- Offset
- Sampling rate

- processing
- units
- intervals

...

NWB organizes your neurophysiology data and metadata



- general
- acquisition
- processing

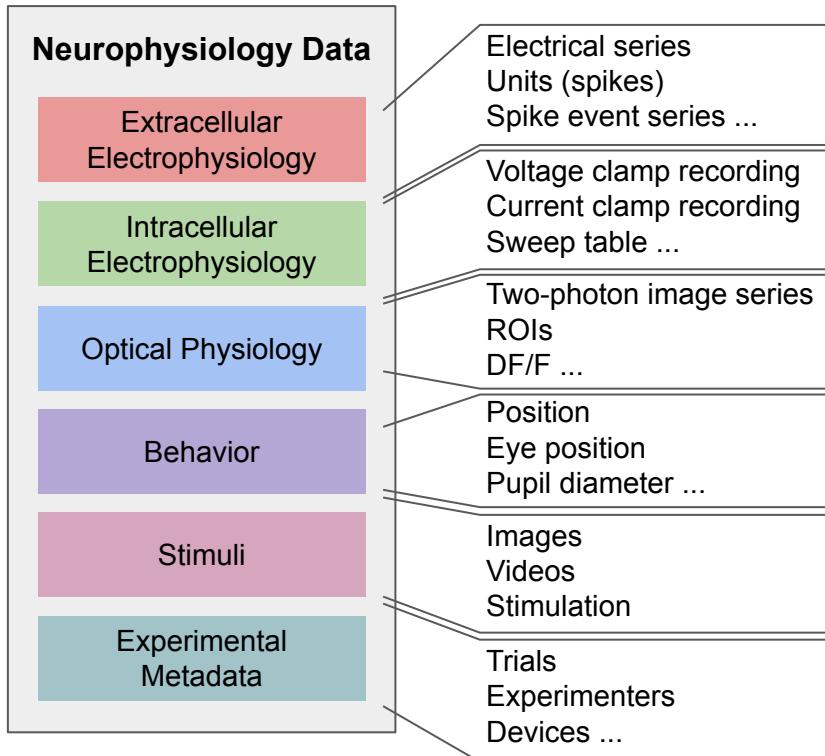
units (neurodata_type: Units)

id	spike_times	waveform_mean	waveform_sd	electrodes	...
0	[0.03, 0.14]	[0.01, 0.03, ...]	[0.04, 0.06, ...]	[0, 1, 2]	...
1	[0.6, 0.71, 0.82]	[0.12, 0.13, ...]	[0.06, 0.08, ...]	[3, 5, 6, 8]	...
2

- intervals

...

NWB provides structured neurodata types for most of neurophysiology data



NWB Extensions (NDX)

- NWB supports the **formal extension** of the data standard to define new data types and metadata
- Extensions are immediately usable and shared directly with the data
- [NDX Catalog](#): Catalog and tools for developing and publishing extensions
- [Extension proposals](#): Formal process for integration of extensions with NWB



NDX Catalog

Acquisition types

- ndx-miniscope
- ndx-simulation-output
- ndx-ecog
- ndx-fret
- ndx-nirs
- ndx-photometry
- ndx-ecg
- ndx-photostim

Task types

- ndx-hierarchical-behavioral-data
- ndx-sound
- ndx-odor-metadata
- ndx-whisk

Processing

- ndx-extract

Lab-specific

- ndx-franklab-novela



DANDI

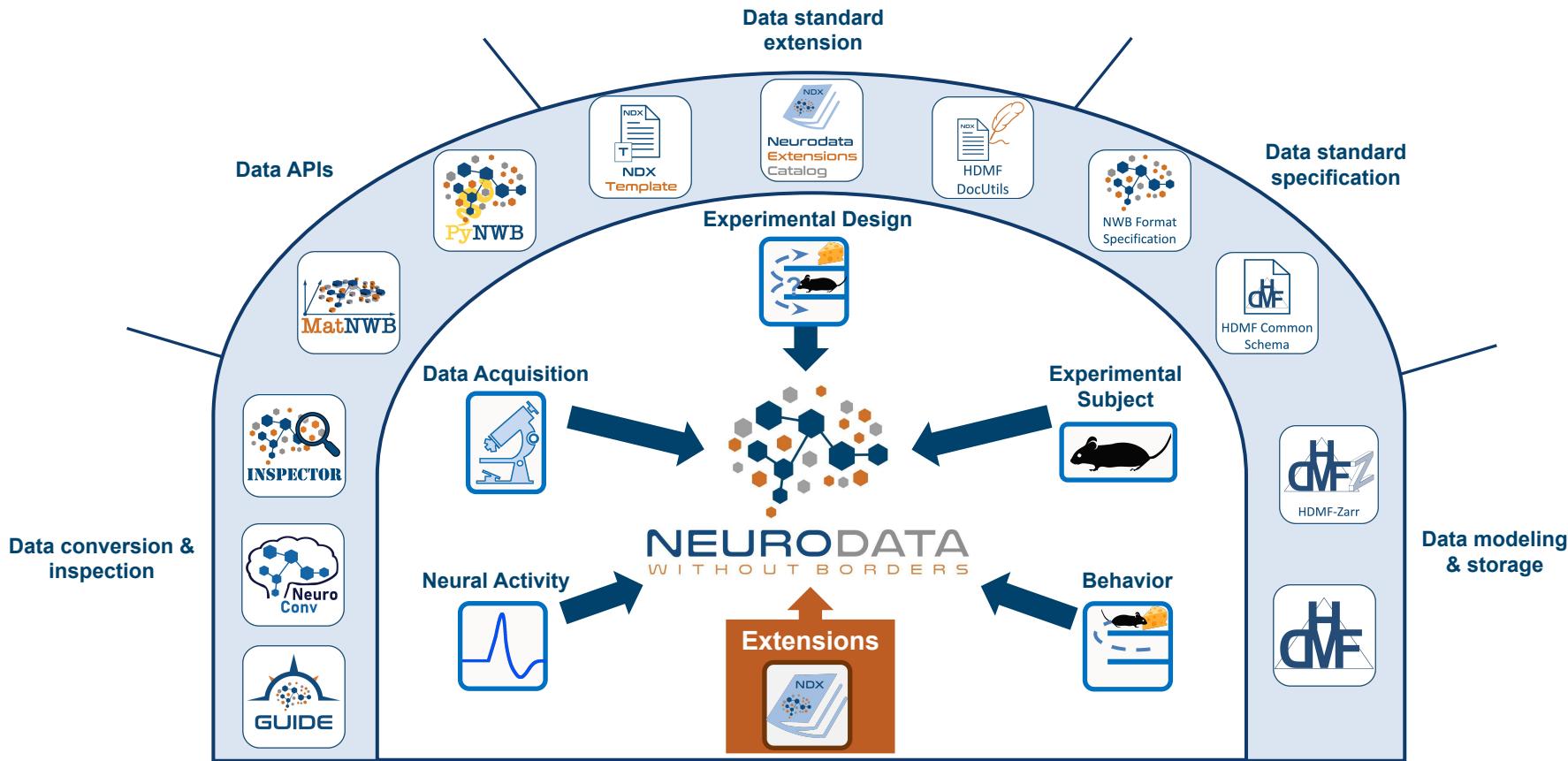


NWB Data Storage

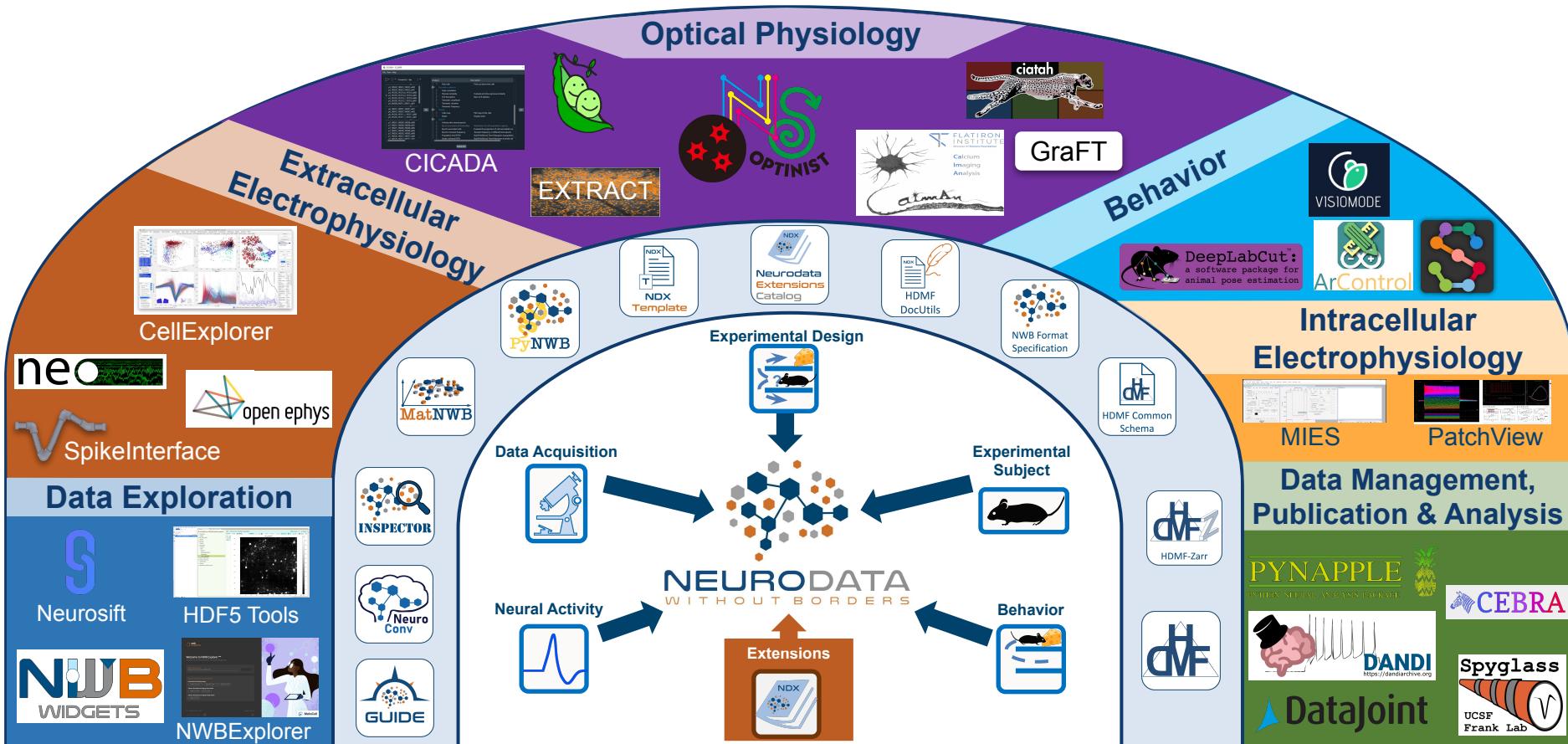
- NWB uses HDF5 as its main file storage backend:
 - Annotate complex data using Groups (like folders) Datasets (arrays) and Attributes in a single file
 - Supports advanced I/O features (e.g., lazy load, chunking, compression, links and references, parallel I/O, etc.)
 - Supported across platforms and languages (Matlab, Python, C/C++, Julia, R, Javascript...)
 - Targets long-term support
- NWB also supports Zarr
- We are working with the community to explore and support integration with other data management and storage technologies (e.g., DataJoint)



An ecosystem for neuroscience data standardization



A unified data standard and software ecosystem for neurophysiology



Tools Overview: <https://nwb-overview.readthedocs.io>

The screenshot shows the NWB Overview page with a dark background. The main navigation menu on the left includes sections for 'FOR USERS' (Intro to NWB, Converting neurophysiology data to NWB, Reading NWB Files, Extending NWB), 'FOR DEVELOPERS' (Accessing NWB Sources), and 'Analysis and Visualization Tools'. A large blue arrow points from this page to the 'Glossary of Core NWB Tools' page.

This page provides a quick overview of key software packages. It features sections for 'FOR USERS' and 'FOR DEVELOPERS'. Under 'FOR USERS', it lists 'Intro to NWB', 'Converting Data to NWB', 'Validating NWB Files', 'Extending NWB', and 'Core Development'. Under 'FOR DEVELOPERS', it lists 'Accessing NWB Sources'. The central content area contains sections for 'Read/Write NWB File APIs' (PyNWB and MatNWB), 'Converting Data to NWB' (NeuroConv), and 'Analysis and Visualization Tools'.

This page is a collection of tools cataloged for NWB users. It includes sections for 'FOR USERS' (Intro to NWB, Converting neurophysiology data to NWB, Extending NWB) and 'FOR DEVELOPERS' (Accessing NWB Sources). The central content area contains sections for 'Exploring NWB Files' (NWB Widgets, NWB Explorer, SpikeInterface, CellExplorer, EcoqVIS, CalmAn, suite2p, CIAtah, EXTRACT, MIES, DeepLabCut, pynapple), 'Analysis and Visualization Tools' (SpikeInterface, NWB Widgets, NWB Explorer, SpikeInterface, CellExplorer, EcoqVIS, CalmAn, suite2p, CIAtah, EXTRACT, MIES, DeepLabCut, pynapple), and 'Frequently Asked Questions'.

This page continues the catalog of tools. It includes sections for 'Analysis and Visualization Tools' (NWB Widgets, NWB Explorer, SpikeInterface, CellExplorer, EcoqVIS, CalmAn, suite2p, CIAtah, EXTRACT, MIES, DeepLabCut, pynapple), 'Exploring NWB Files' (NWB Widgets, NWB Explorer, SpikeInterface, CellExplorer, EcoqVIS, CalmAn, suite2p, CIAtah, EXTRACT, MIES, DeepLabCut, pynapple), and 'Extracellular Electrophysiology Physiology Tools' (SpikeInterface, NWB Widgets, NWB Explorer, SpikeInterface, CellExplorer, EcoqVIS, CalmAn, suite2p, CIAtah, EXTRACT, MIES, DeepLabCut, pynapple). The right side of the page contains detailed descriptions and links for each tool.

An Archive and Collaboration Space for Neurophysiology Projects



DANDI

PUBLIC DANDISETS

MY DANDISETS

ABOUT

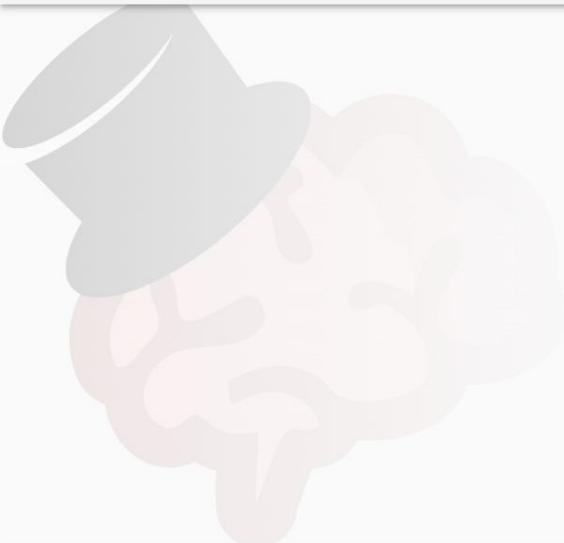
DOCUMENTATION

HELP

DANDIHUB

NEW DANDISSET

BD



The DANDI Archive

The BRAIN Initiative archive for publishing and sharing neurophysiology data including electrophysiology, optophysiology, and behavioral time-series, and images from immunostaining experiments.

Search Dandisets by name, description, identifier, or contributor name

554

dandisets

1431

users

725 TB

total data size

Contributing data to the DANDI Archive

- Stores neurophysiology data and associated behavioral data in NWB format
 - Validates NWB, checks for best practices, automatically extracts metadata
- Upload 100s of TBs for **FREE**
 - Talk to us if ≥ 10 TB
 - 5 TB per file max
 - Can handle all raw data for most experiments
 - AWS Open Data Sponsorship Program
- Open licenses: CC-0 or CC-BY
- Can upload data in embargo mode
- Create DOIs by “publishing” and re-publishing

[Link to Terms](#)

[Link to Policies](#)

DANDI Archive and FAIR Data

Data for: Neurons detect cognitive boundaries to structure episodic memories in humans (Zheng et al. 2022 Nat Neuro)

DOI

ID: 000207 | 0.220216.0323

Contact person

Contact Rutishauser, Ueli

Descriptive title (F)

Access

Dandiset

Citation

DOWNLOAD

CITE AS

FILES

METADATA

MANIFEST

Code for reusing data

Standardized metadata

Related resources

Code that reads and plots data deposited here

ID: Analysis code

Repo: github

Relation: dcterms:Describes

Detailed description

Keywords: human single neuron, hippocampus, episodic memory, cognitive boundaries, continuous experience, ROH consortium

Tags

Assets

Controlled vocabulary

Standards

Species

Homo sapiens - Human

Approach

electrophysiological approach

Data Standard

Neurodata Without Borders (NWB)

RRID:SCR_015242

Number Of Subjects

19

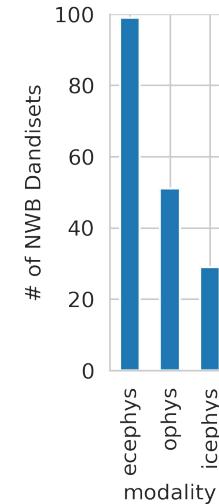
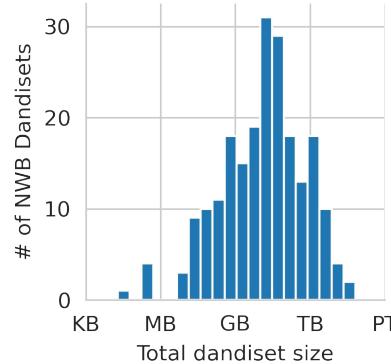
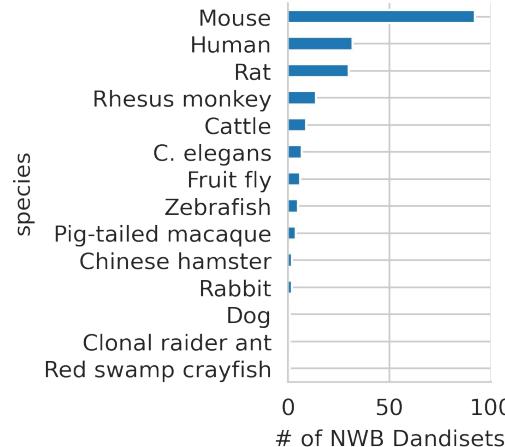
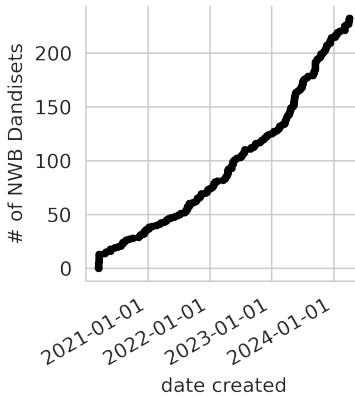
Variable Measured

Units

Measurement Technique

spike sorting technique

Neurophysiology datasets on DANDI



Highlights:

- **IBL - Brain Wide Map ([000409](#))**: 33.6 TB dataset from the International Brain Laboratory including Neuropixel electrophysiology, eye tracking, and behavioral monitoring for a visual decision making task
- **MICrONS Two Photon Functional Imaging ([000402](#))**: 1.3 TB of optical physiology data for a visual task. The functional data was co-registered with electron microscopy (EM) data.
- **Allen Institute OpenScope ([000036](#), [000037](#), [000488](#), [000535](#))**: Several studies from the Allen Institute Open Scope program that use optical physiology recordings of the visual cortex.



Neurosift: Explore NWB data in the browser

- Intelligent, interactive visualizations of NWB data
- Runs in browser- no need to install anything or run external services
- Streams data directly from the archive
- Integrated into the DANDI Archive website

The screenshot shows a list of four NWB files in the DANDI Archive:

File Name	Size
sub-CSHL047_ses-2d5f6d81-38c4-4bdc-ac3c-302ea4d5f46e-processed-only_behavior.nwb	628.1 MB
sub-CSHL047_ses-2d5f6d81-38c4-4bdc-ac3c-302ea4d5f46e_behavior+ecephys+image.nwb	109.7 GB
sub-CSHL047_ses-b52182e7-39f6-4914-9717-136db589706e-processed-only_behavior.nwb	473.7 MB
sub-CSHL047_ses-b52182e7-39f6-4914-9717-136db589706e_behavior+ecephys+image.nwb	53.6 GB

A context menu is open over the third file, showing options: "OPEN WITH" (with dropdown), "EXTERNAL SERVICES", "MetaCell/NWBExplorer", and "Neurosift".

Pagination controls at the bottom indicate page 1 of 1.

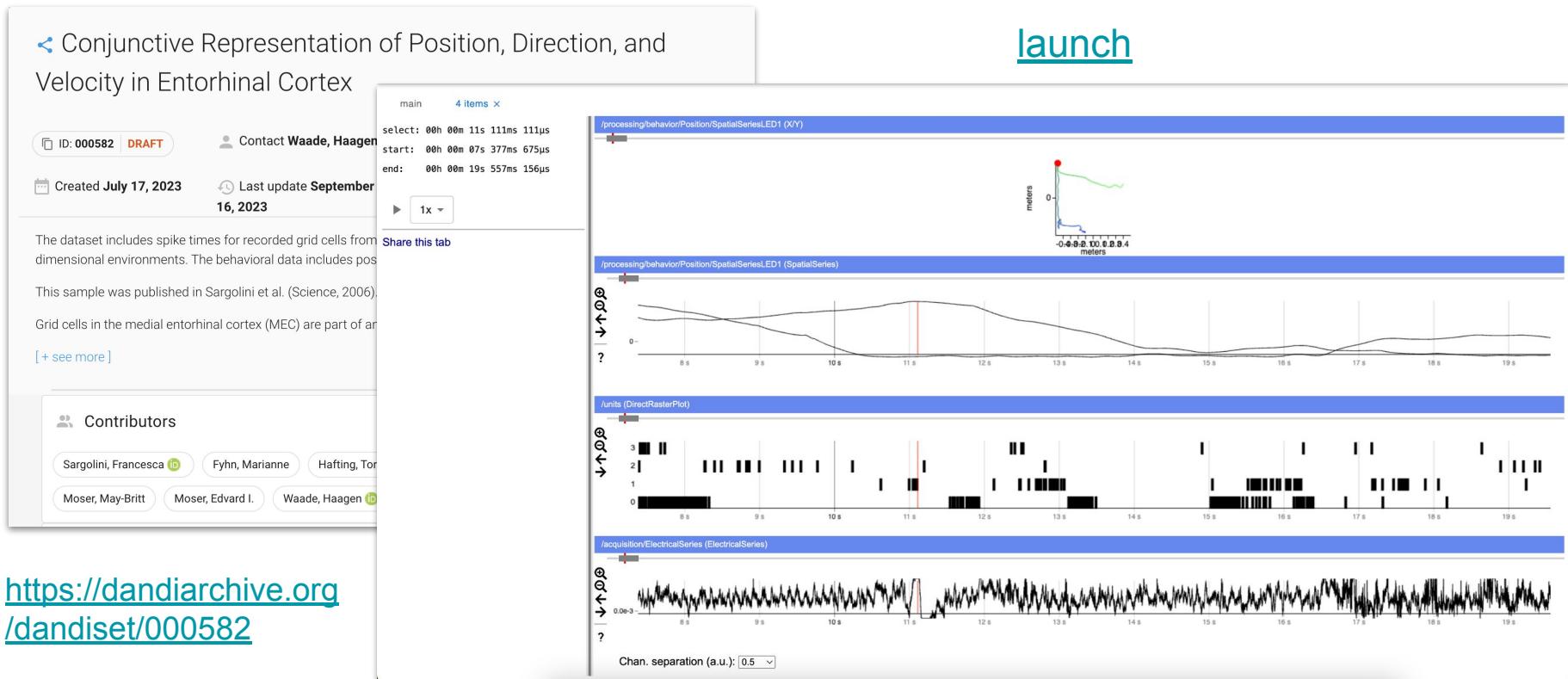


**Jeremy
Magland,
Flatiron**

Position tracking and trace views

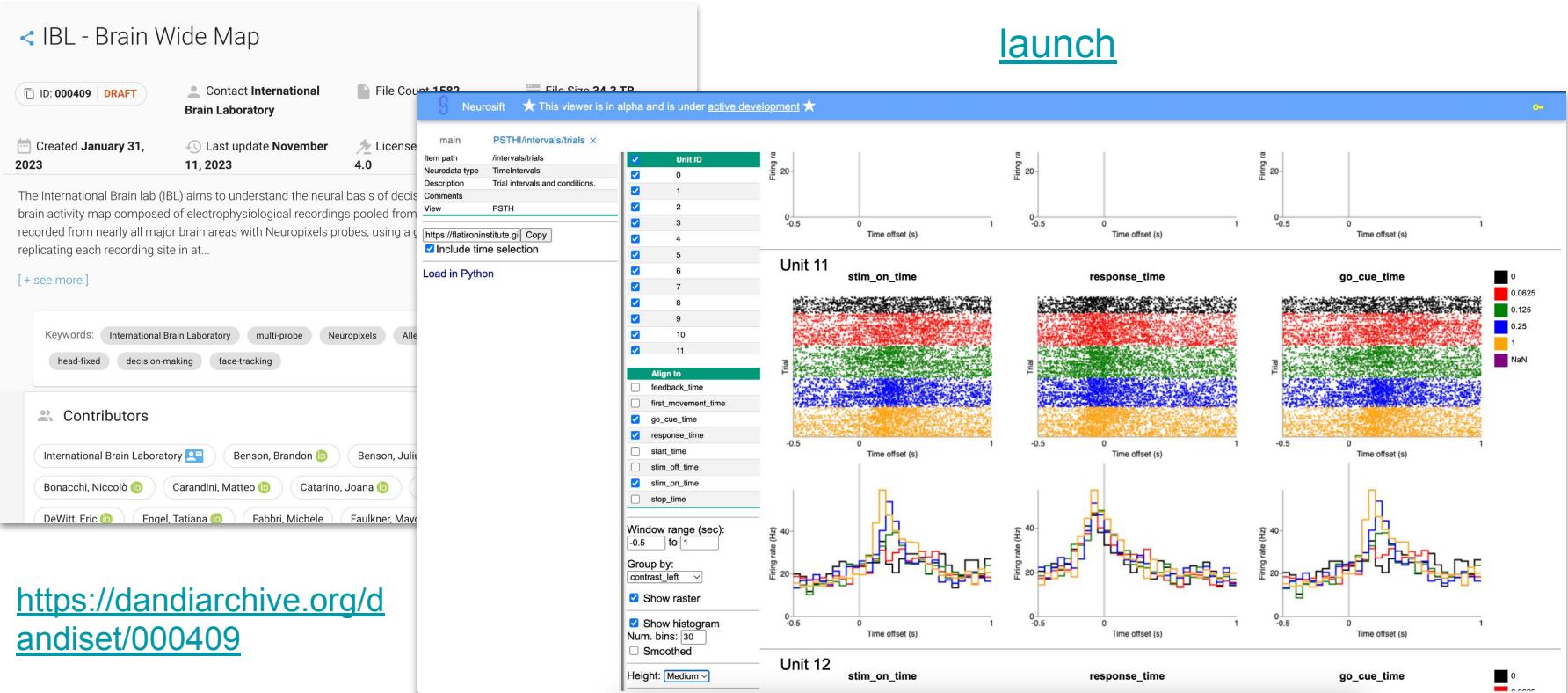
Conjunctive Representation of Position, Direction, and Velocity in Entorhinal Cortex

[launch](#)



[https://dandiarchive.org
/dandiset/000582](https://dandiarchive.org/dandiset/000582)

Peri-stimulus time histogram



<https://dandiarchive.org/dataset/000409>

Optical physiology segmentation

↳ Plitt & Giocomo (2021) Experience

Dependent Contextual Codes in the
Hippocampus. Nat Neuro

ID: 0.210819.1547 Contact Plitt, Mark

Created August 19, 2021 Last update August 19, 2021 License 4.0

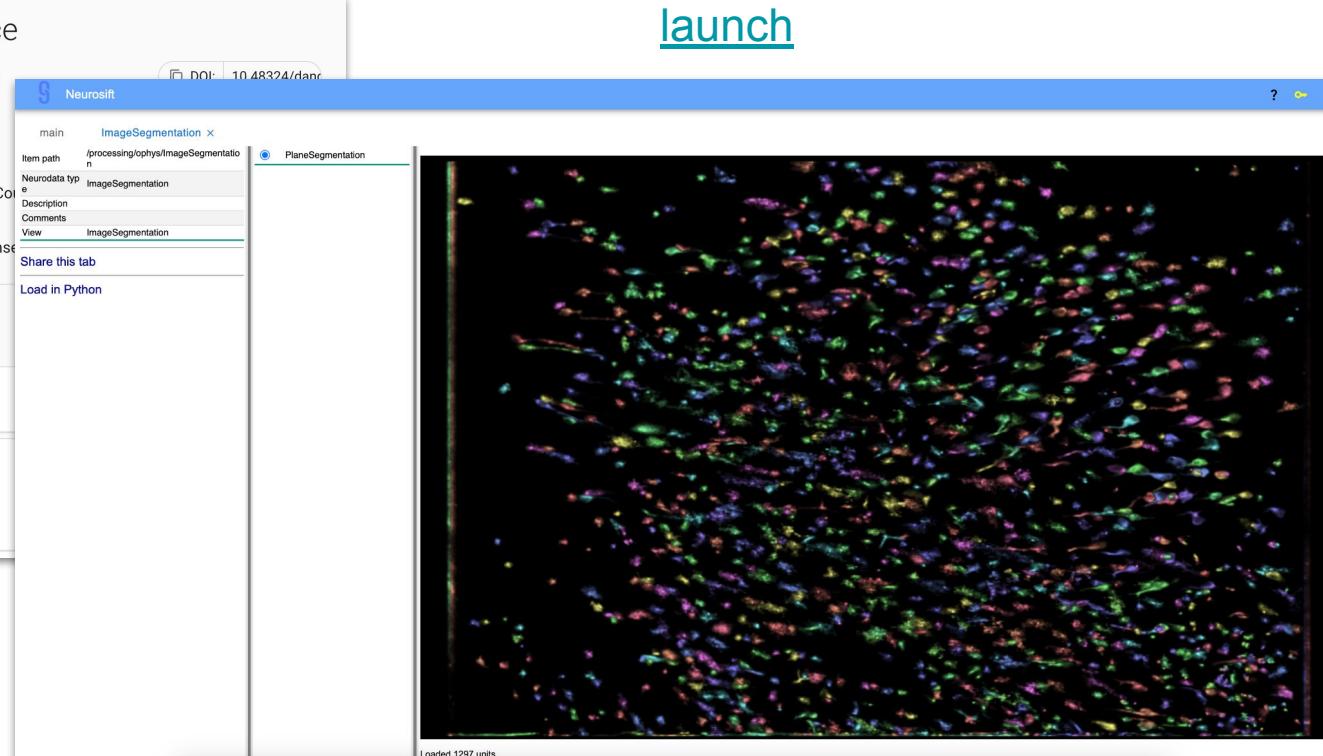
Data included in Plitt & Giocomo (2021) Nature Neuroscience

Subject matter: hippocampus

Contributors

Plitt, Mark Giocomo, Lisa M.

[https://dandiarchive.org/
dandiset/000054](https://dandiarchive.org/dandiset/000054)



Analyzing data on DANDI Hub

- DANDI Hub: a FREE cloud compute resource (<https://hub.dandiarchive.org>)
- Analyze datasets in Python, MATLAB, Julia, R, ...
- Fast access to stream and download DANDI data
- Different server options, including GPU
- Share analysis notebooks with the community



Publications reusing public NWB data

Publications:

1. Gala et al. 2021. Consistent cross-modal identification of cortical neurons with coupled autoencoders. *Nature Computational Science*.
 - a. Used DANDI:000020
2. Keshtkaran et al. 2022. A large-scale neural network training framework for generalized estimation of single-trial population dynamics. *Nature Methods*.
 - a. Used DANDI:000070, DANDI:000128, DANDI:000129
3. Schneider et al. 2023. Learnable latent embeddings for joint behavioural and neural analysis. *Nature*.
 - a. Used DANDI:000127 and several other public datasets
4. Easthope et al. 2023. Cortical control of posture in fine motor skills: evidence from inter-utterance rest position. *Frontiers in Human Neuroscience*.
 - a. Used NWB dataset shared on Figshare
5. Cai et al. 2023. FIOLA: an accelerated pipeline for fluorescence imaging online analysis. *Nature Methods*.
 - a. Used DANDI:000054
6. Patel et al. 2023. High-performance neural population dynamics modeling enabled by scalable computational infrastructure. *Journal of Open Source Software*.
 - a. Used DANDI:000128
7. Arbab et al. 2023. Investigating microglia-neuron crosstalk by characterizing microglial contamination in human and mouse patch-seq datasets. *iScience*.
 - a. Used DANDI:000020, DANDI:000209

Preprints:

8. Ye et al. 2021. Representation learning for neural population activity with Neural Data Transformers.
 - a. Used DANDI:000070
9. Nguyen et al. 2023. Fast Temporal Wavelet Graph Neural Networks. *arXiv*.
 - a. Used DANDI:000055
10. Azabou et al. 2023. A Unified, Scalable Framework for Neural Population Decoding.
 - a. Used DANDI:000688, DANDI:000070, DANDI:000128, DANDI:000129, and other public datasets
11. Bernaerts et al. 2023. Combined statistical-mechanistic modeling links ion channel genes to physiology of cortical neuron types.
 - a. Used DANDI:000008
12. Perkins et al. 2023. Simple decoding of behavior from a complicated neural manifold.
 - a. Used DANDI:000127, DANDI:000128, DANDI:000129, DANDI:000130, DANDI:000138, DANDI:000139, DANDI:000140
13. Vetter et al. 2023. Generating realistic neurophysiological time series with denoising diffusion probabilistic models.
 - a. Used DANDI:000055 and other public datasets

Styles of data reuse

1. **Showcase.** Demonstrate new analysis or software on various existing datasets
2. **Pilot.** Try an analysis on existing data before designing your own experiment
3. **Follow-up.** Explore questions that were left unanswered in the initial study
4. **Confirmative.** Find similar results in data from another lab
5. **Contrastive.** Show that your results are particular to your experiment preparation
6. **Aggregative.** Gain statistical power by combining data across labs
7. **Educational.** Train and inspire the next generation of scientists using real data

Questions?



DANDI

+



NEURODATA
WITHOUT BORDERS

Schedule

10:15 - 10:45	Overview of NWB and DANDI
10:45 - 11:00	Q&A
11:00 - 12:15	NWB GUIDE (Interactive Tutorial) <ul style="list-style-type: none">• Easily convert data• Inspect NWB File• Explore NWB File
12:20	Group photo
12:30-13:30	Lunch
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Converting to NWB



DANDI

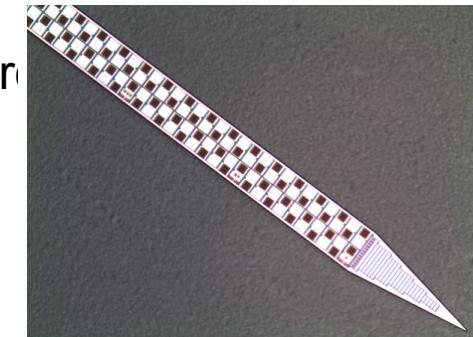
+



NEURODATA
WITHOUT BORDERS

Bottleneck: Converting to NWB

- Wrangling diverse data formats into one standard is still a bottleneck for many labs
- Standardizing neurophysiology data is challenging due to:
 - **Diversity** - many different proprietary formats
 - **Complexity** - experiments often use multiple data sources (each stream in a unique format)
 - **Volume** - terabyte (TB) scale and growing

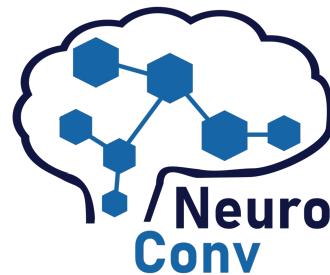


Neuropixels 1 probe
neuropixels.org

Converting data to NWB



No-code automated conversion
via graphical interface app
(some input data formats, beta)



Low-code automated
conversion for
common input data
formats



Custom code
using NWB APIs



DANDI



NWB GUIDE hands-on tutorial

To submit any feedback on the tutorial or your experience with the GUIDE, feel free to open an [issue](#) on our GitHub page.

If you do not see your data format listed on the Data Formats page or our [support table](#), please submit a request using this [form](#).

Schedule

10:15 - 10:45	Overview of NWB and DANDI
10:45 - 11:00	Q&A
11:00 - 12:15	Interactive Tutorials <ul style="list-style-type: none">➤ Easily convert data with NWB Guide➤ File validation (Inspector) and exploration (Neurosift) within NWB GUIDE
12:20	Group photo
12:30-13:30	Lunch
13:30 - 14:30	Advanced NWB conversion
14:30 - 15:30	Analysis tools in the NWB ecosystem

Hands-on session: Convert custom data using PyNWB

- You can use a Dandi hub instance or your local machine
- Navigate to <https://dandiarchive.org/>
- Start a Dandihub instance (Tiny or Base should be enough)
- git clone https://github.com/catalystneuro/stratneuro_2024
- Open folder stratneuro_2024/tutorial_pynwb
- Open **nwb_conversion_with_pynwb.ipynb**



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NEURODATA
WITHOUT BORDERS

Advanced NWB conversion with PyNWB and Neuroconv

NWB provides a robust and well designed schema for storage of multimodality neurophysiology data, and GUIDE can provide a direct way to convert simple experiments using the most popular acquisition systems, but:

- Some experiments might require custom data conversion
- Multimodality might require custom synchronization of signals
- NWB is flexible enough to allow for modality extensions
- The NWB schema might be a bit difficult to use for the first time



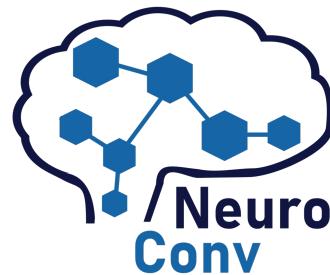
DANDI



Converting data to NWB



No-code automated conversion
via graphical interface app



Low-code automated
conversion for
common input data
formats



Custom code
using NWB APIs



DANDI



NeuroConv



Electrophysiology



Optical physiology



Behavior



```
from datetime import datetime
from dateutil import tz
from pathlib import Path
from neuroconv.converters import SpikeGLXConverterPipe

converter =
SpikeGLXConverterPipe(folder_path="spikeglx/Noise4Sam_g0")

metadata = converter.get_metadata()
session_start_time =
metadata["NWBfile"]["session_start_time"].replace(tzinfo=tz.gettz("US/Pacific"))
metadata["NWBfile"].update(session_start_time=session_start_time)

converter.run_conversion(nwbfile_path="my_spikeglx_session.nwb",
metadata=metadata)
```

A few lines of code...

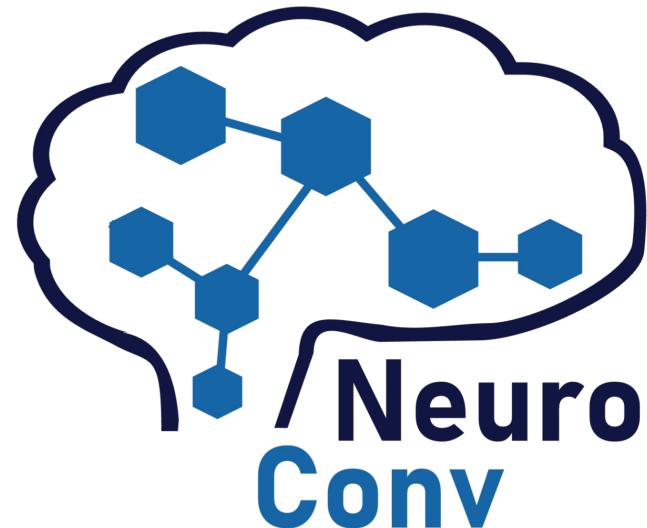


DANDI



Automated NWB conversions with NeuroConv

- Convert data to NWB with minimal time and effort
- Supports 44+ common neurophys data formats
- Automatically extracts format-specific metadata
- Seamlessly integrated data engineering
 - Converts on the TB scale
 - Can reduce file size by ~35%
 - Optimizes chunking for streaming from DANDI



Simple code to convert a SpikeGLX recording to NWB

```
from datetime import datetime
from dateutil import tz
from pathlib import Path
from neuroconv.converters import SpikeGLXConverterPipe

# Create a converter object with the path to your SpikeGLX data
converter = SpikeGLXConverterPipe(folder_path="spikeglx/Noise4Sam_g0")

# For data provenance, we add time zone information of the acquisition to the metadata
metadata = converter.get_metadata()
session_start_time = metadata["NWBFile"]["session_start_time"].replace(tzinfo=tz.gettz("US/Pacific"))
metadata["NWBFile"].update(session_start_time=session_start_time)

# Choose a path for saving the NWB file and run the conversion
converter.run_conversion(nwbfile_path="my_spikeglx_session.nwb", metadata=metadata)
```

Demo code for all supported data types in [NeuroConv Conversion Gallery](#)

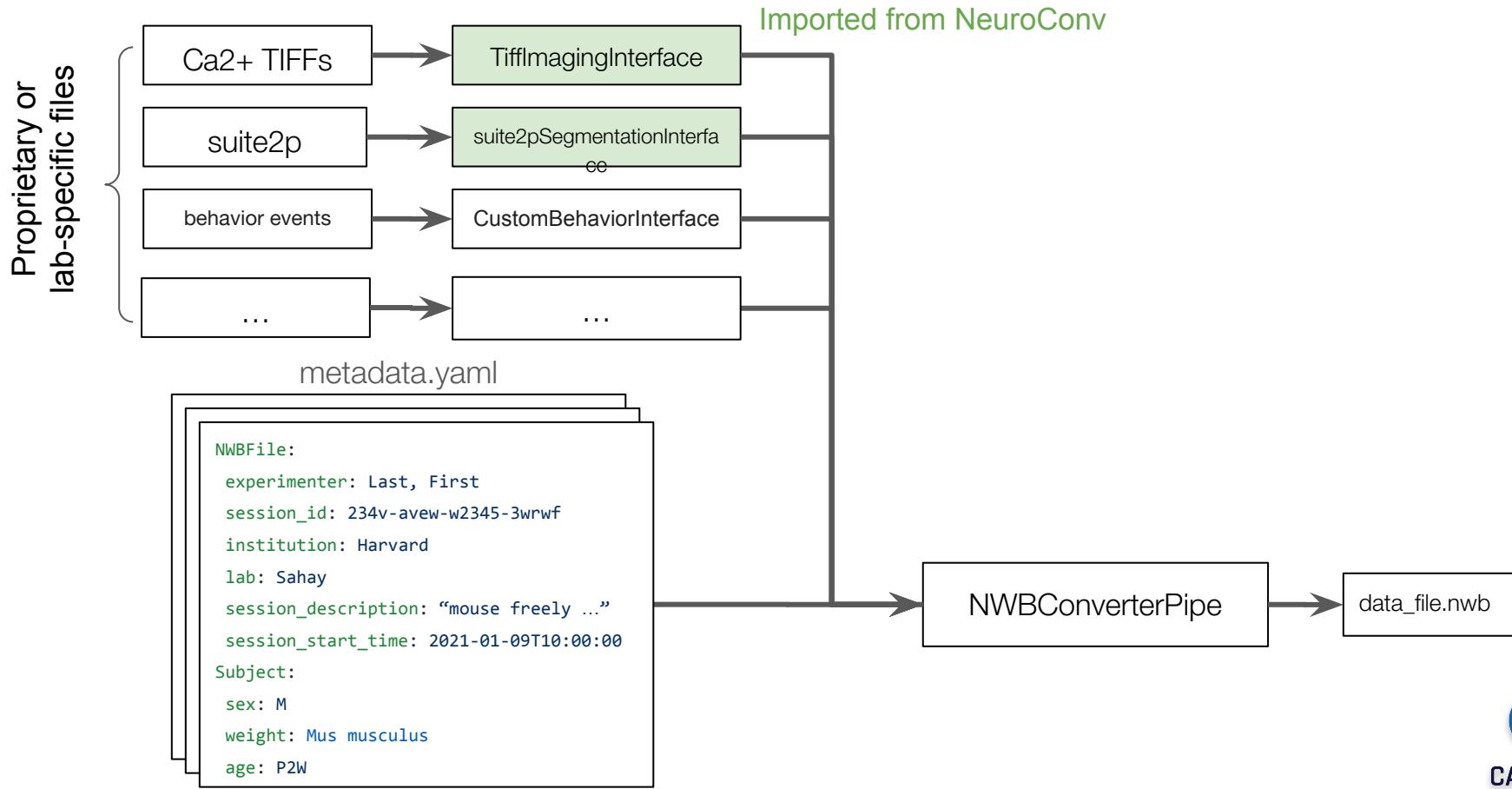


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NEURODATA
WITHOUT BORDERS

Strategy: Modularize by data stream





NeuroConv supports 44 common input formats

Extracellular electrophysiology

Recording

- AlphaOmega
- Axona
- Biocam
- Blackrock
- EDF
- Intan
- MaxOne
- MCSRaw
- MERec
- Neuralynx
- NeuroScope
- OpenEphys
- Plexon
- Spike2
- Spikegadgets
- SpikeGLX
- TDT

Sorting

- Blackrock
- Cell Explorer
- KiloSort
- Neuralynx
- NeuroScope
- Phy
- Plexon

Intracellular electrophysiology

- ABF

Optical physiology

Imaging

- Bruker
- HDF5
- Micro-Manager
- Miniscope
- Scanbox
- ScanImage
- Tiff

Segmentation

- Caiman
- CNMFE
- EXTRACT
- Suite2P

Behavior

- Audio
- DeepLabCut
- FicTrac
- LightningPose
- SLEAP
- Videos

Text for Trials Table

- CSV
- Excel



DANDI



NEURODATA
WITHOUT BORDERS

Use NWB APIs to write (and read) NWB data

- Most useful for converting custom data
- Also trial times, responses, and properties
- APIs support:
 - Iteratively reading and writing data
 - Custom chunking
 - Custom compression
 - Writing data in NWB extensions
- Lots of documentation and tutorials!



github.com/NeurodataWithoutBorders/matnwb

PyNWB tutorials



PyNWB stable Search docs

GETTING STARTED
Installing PyNWB

Tutorials

- General tutorials
- Domain-specific tutorials
- Advanced I/O

Citing PyNWB

RESOURCES
Validating NWB files
Exporting NWB files
API Documentation

FOR DEVELOPERS
Installing PyNWB for Developers
Software Architecture
How to Update Requirements Files
Software Process

Read the Docs v: stable

[/ Tutorials](#) Edit on GitHub

Tutorials

General tutorials



NWB File Basics



Adding/Removing Containers from an NWB File



Annotating Time Intervals



Exploratory Data Analysis with NWB



Extending NWB



Object IDs in NWB



Reading and Exploring an NWB File

Domain-specific tutorials



Extracellular Electrophysiology



Calcium Imaging Data



Intracellular Electrophysiology



Query Intracellular Electrophysiology Metadata

MatNWB tutorials

Intro to MatNWB

[Basic File Reading](#) | a demo showcase for basic visualization from a DANDI dataset.

[Extracellular Electrophysiology](#) | [YouTube walkthrough](#)

[Calcium Imaging](#) | [YouTube walkthrough](#)

[Intracellular Electrophysiology](#)

[Behavior](#)

[Optogenetics](#)

[Dynamic tables](#)

[Images](#)

[Advanced data write](#) | [YouTube walkthrough](#)

[Using Dynamically Loaded Filters](#)

[Remote read](#)

[Scratch Space](#)



DANDI



NEURODATA
WITHOUT BORDERS

Hands-on session: Convert custom data using PyNWB

- You can use a Dandi hub instance or your local machine
- Navigate to <https://dandiarchive.org/>
- Start a Dandihub instance (Base should be enough)
- git clone https://github.com/catalystneuro/stratneuro_2024
- Open folder stratneuro_2024/tutorial_pynwb
- Open **nwb_conversion_with_pynwb.ipynb**



DANDI

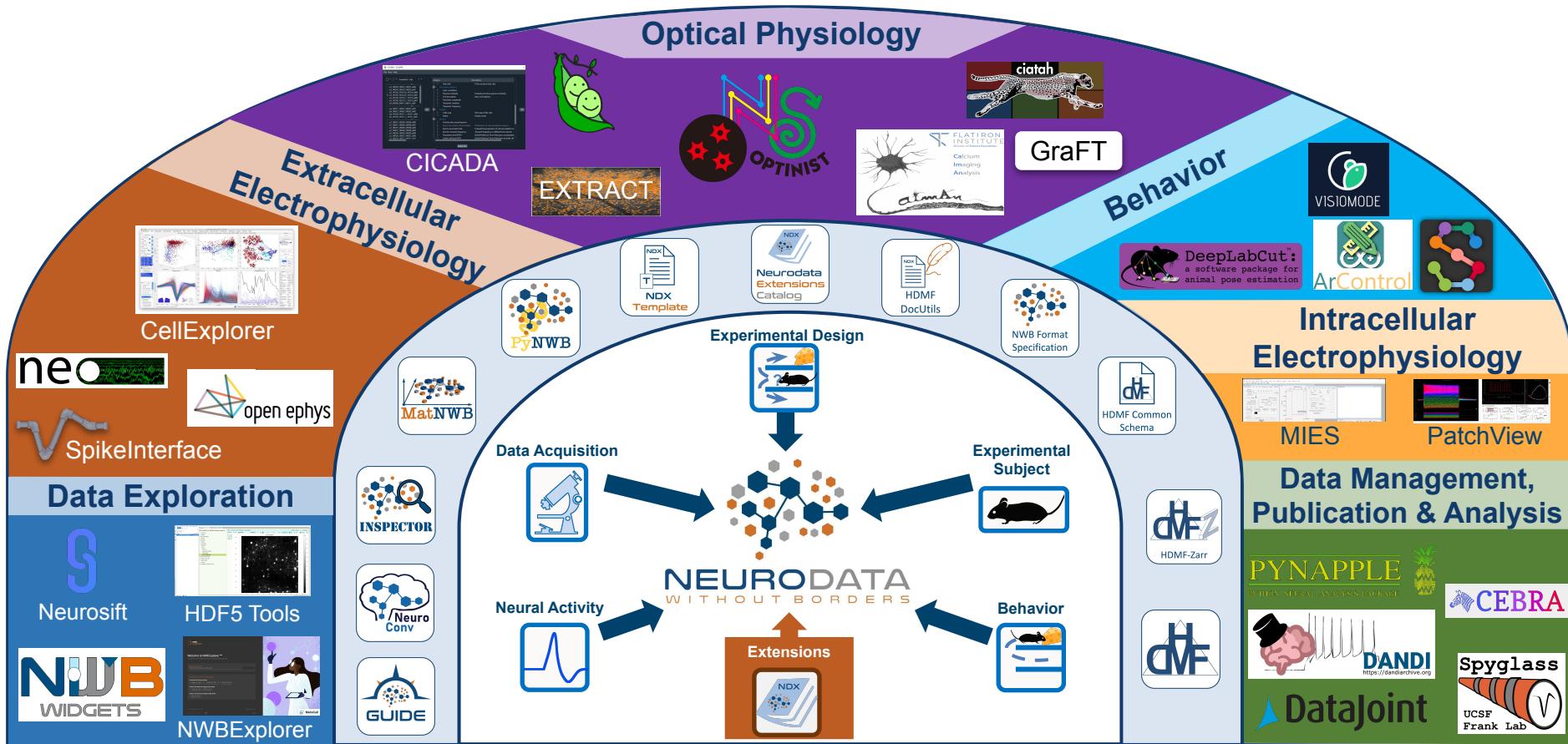


NEURODATA
WITHOUT BORDERS

Schedule

10:15 - 10:45	Overview of NWB and DANDI
10:45 - 11:00	Q&A
11:00 - 12:15	Interactive Tutorials <ul style="list-style-type: none">➤ Easily convert data with NWB Guide➤ File validation (Inspector) and exploration (Neurosift) within NWB GUIDE
12:20	Group photo
12:30-13:30	Lunch
13:30 - 14:30	Advance NWB conversion
14:30 - 15:30	Analysis tools in the NWB ecosystem

Data Analysis within NWB ecosystem





Neurosift - Explore NWB data in the browser

- Intelligent, interactive visualizations of NWB data
- Runs in browser- no need to install anything or run external services
- Streams data directly from the archive
- Integrated into the DANDI Archive website

The screenshot shows a list of four NWB files in the DANDI Archive:

- sub-CSHL047_ses-2d5f6d81-38c4-4bdc-ac3c-302ea4d5f46e-processed-only_behavior.nwb (628.1 MB)
- sub-CSHL047_ses-2d5f6d81-38c4-4bdc-ac3c-302ea4d5f46e_behavior+ecephys+image.nwb (109.7 GB)
- sub-CSHL047_ses-b52182e7-39f6-4914-9717-136db589706e-processed-only_behavior.nwb (473.7 MB)
- sub-CSHL047_ses-b52182e7-39f6-4914-9717-136db589706e_behavior+ecephys+image.nwb (53.6 GB)

A context menu is open over the third file, listing "EXTERNAL SERVICES" and "Neurosift".

Pagination controls at the bottom show page 1 of 1.

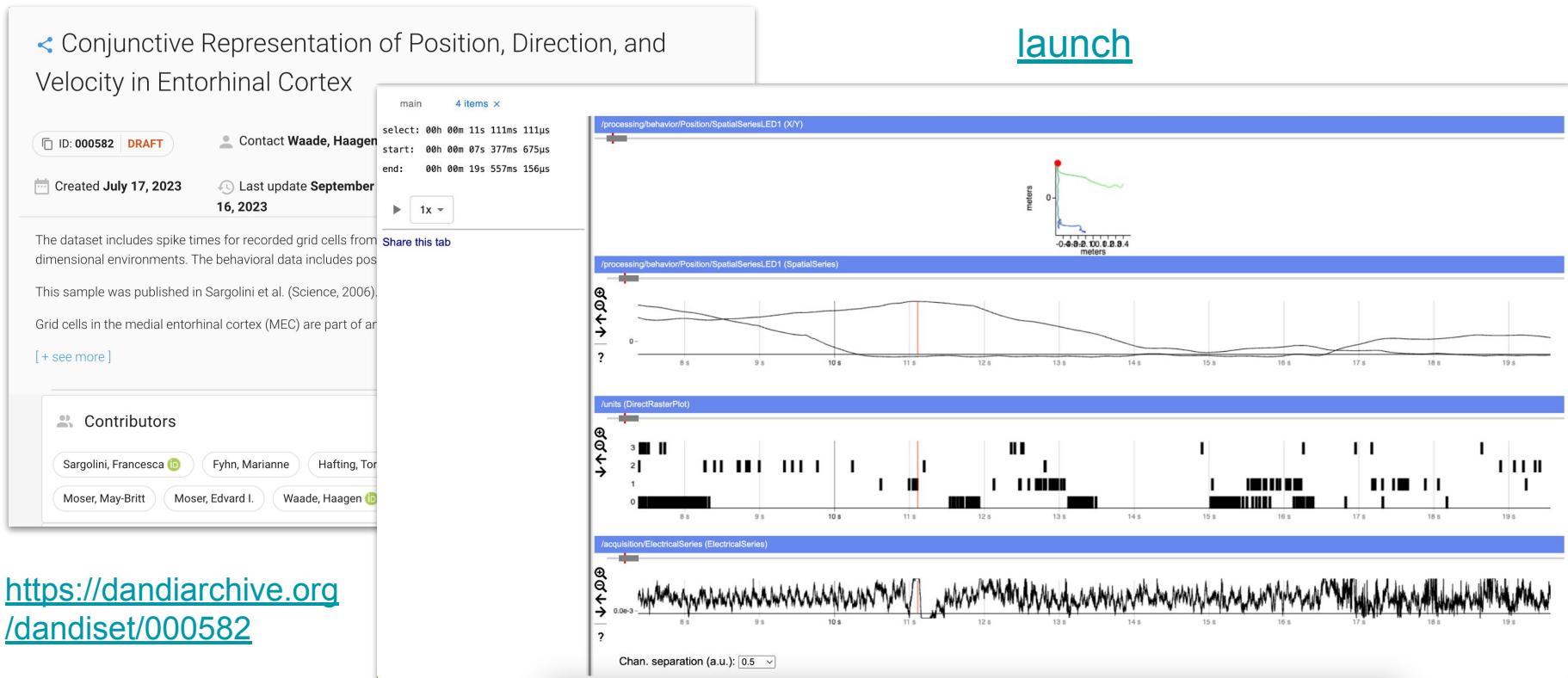


**Jeremy
Magland,
Flatiron**

Neurosift - Position tracking and trace views

Conjunctive Representation of Position, Direction, and Velocity in Entorhinal Cortex

[launch](#)



[https://dandiarchive.org
/dandiset/000582](https://dandiarchive.org/dandiset/000582)

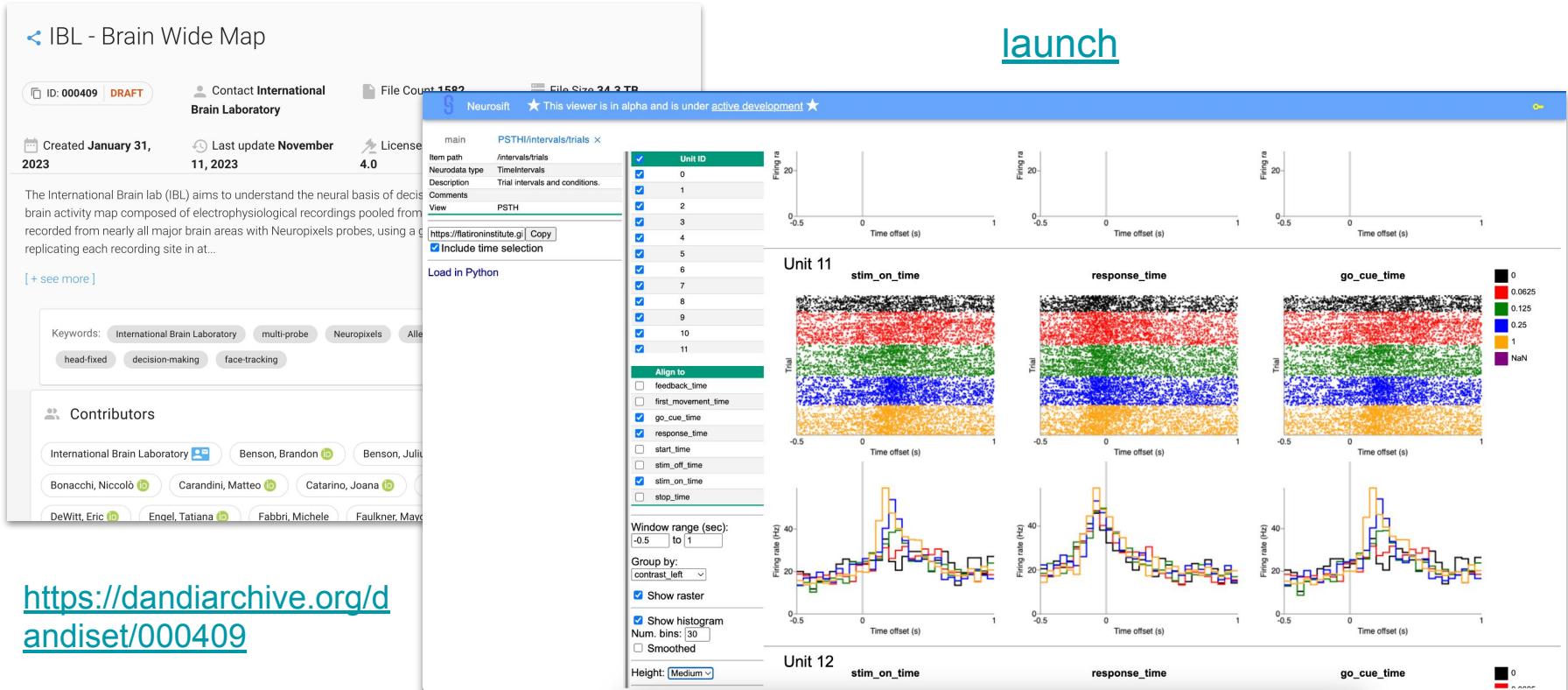


DANDI &



NEURODATA
WITHOUT BORDERS

Neurosift - Peri-stimulus time histogram



<https://dandiarchive.org/dandiset/000409>

Dendro - Analyse neurophys data in the cloud

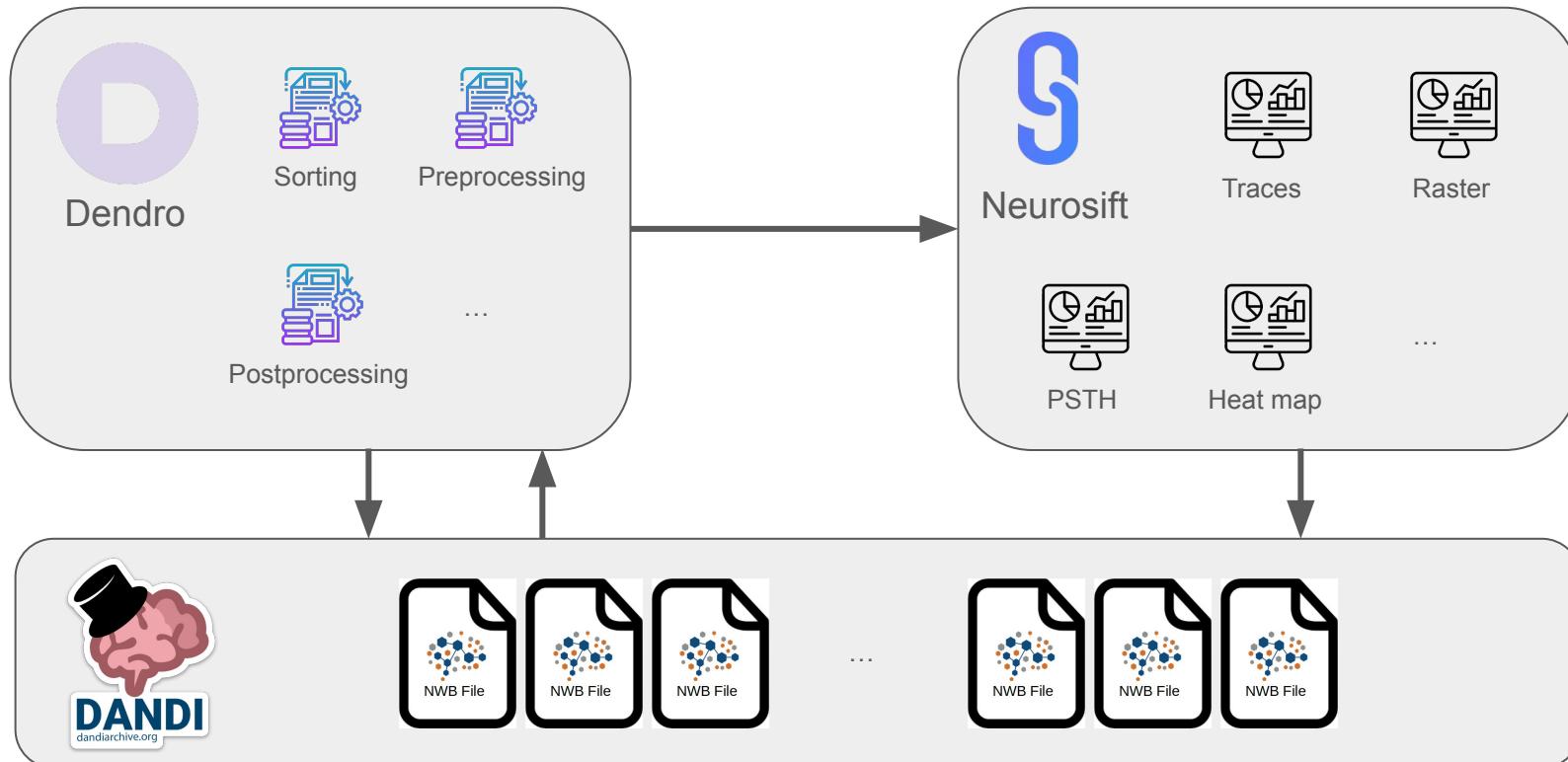
Dendro is an open source web application that aims at:

- Facilitating the usage of complex neurodata processing algorithms
- Promoting reusability of experimental data
- Promoting reproducibility of results with full data processing provenance

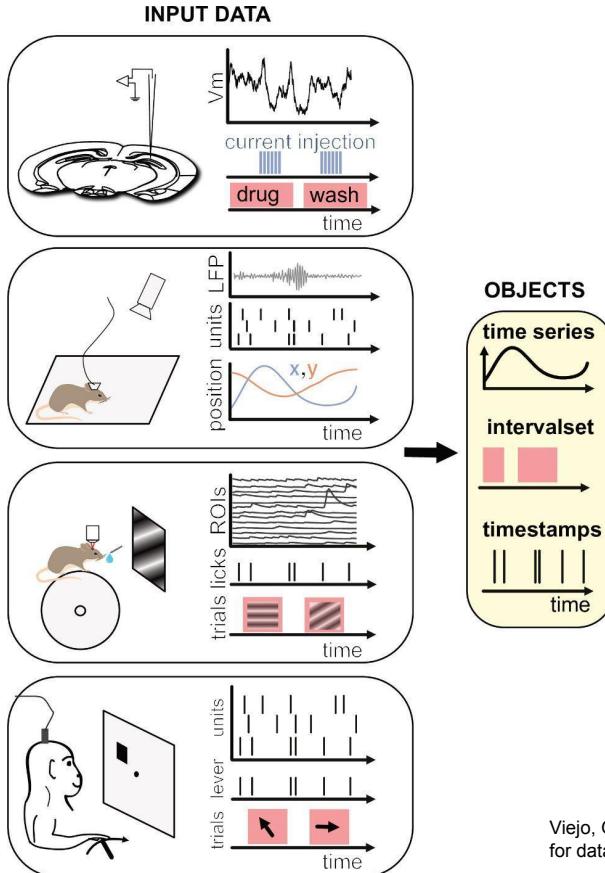
<https://dendro.vercel.app>

<https://flatironinstitute.github.io/dendro-docs/>

Cloud Ecosystem: NWB + DANDI + Dendro + Neurosift



Pynapple



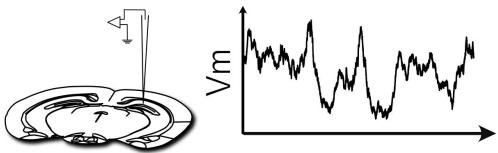
Viejo, G., Levenstein, D., Carrasco, S. S., Mehrotra, D., Mahallati, S., Vite, G. R., ... & Peyrache, A. (2023). Pynapple, a toolbox for data analysis in neuroscience. *eLife*, 12, RP85786.



DANDI



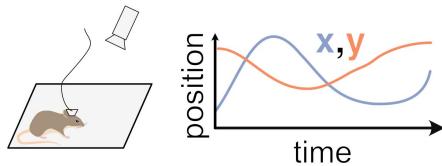
NEURODATA
WITHOUT BORDERS



Tsd: 1-dimension

```
In [11]: tsd = nap.Tsd(t=t, d=d)

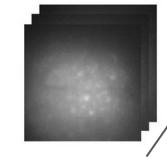
In [12]: tsd
Out[12]:
Time (s)
-----
0.0      0.397043
1.0      1.55294
2.0      0.455892
3.0      -1.17359
4.0      -0.110113
...
95.0     -0.573408
96.0     -0.0110915
97.0     -1.58027
98.0     0.998846
99.0     0.542692
dtype: float64, shape: (100, )
```



TsdFrame: 2-dimensions

```
In [20]: tsdframe = nap.TsdFrame(t=t, d=d,
...:             columns = ['x', 'y'])

In [21]: tsdframe
Out[21]:
Time (s)      x        y
-----
0.0      -0.029719  -0.273102
1.0       0.181754   3.25403
2.0      -0.495068  -0.524877
3.0      -1.20696   -0.033936
4.0      -0.664662   2.20862
...
95.0      0.942969   0.180585
96.0      2.15161    0.661736
97.0      0.751956  -1.72922
98.0     -1.45054    1.52954
99.0      0.199145   0.582944
dtype: float64, shape: (100, 2)
```



TsdTensor: n-dimensions

```
In [34]: tsdtensor = nap.TsdTensor(t=t, d=d)

In [35]: tsdtensor
Out[35]:
Time (s)
-----
0.0      [[-0.87 ... -0.87] ...]
1.0      [[1.14 ... 1.14] ...]
2.0      [[0.25 ... 0.25] ...]
3.0      [[1.29 ... 1.29] ...]
4.0      [[-0.91 ... -0.91] ...]
...
95.0     [[-2.01 ... -2.01] ...]
96.0     [[-0.08 ... -0.08] ...]
97.0     [[0.53 ... 0.53] ...]
98.0     [[-0.62 ... -0.62] ...]
99.0     [[-0.55 ... -0.55] ...]
dtype: float64, shape: (100, 15, 15)
```

Numpy array

```
In [15]: tsd.index.values  
Out[15]:  
array([ 0.,  1.,  2.,  3.,
```

```
In [16]: tsd.values  
Out[16]:  
array([ 0.39704278,  1.55294416,
```

```
In [11]: tsd = nap.Tsd(t=t, d=d)  
  
In [12]: tsd  
Out[12]:  
Time (s)  
-----  
0.0      0.397043  
1.0      1.55294  
2.0      0.455892  
3.0     -1.17359  
4.0     -0.110113  
...  
95.0     -0.573408  
96.0     -0.0110915  
97.0     -1.58027  
98.0      0.998846  
99.0      0.542692  
dtype: float64, shape: (100, )
```

Numpy array

```
In [15]: tsd.index.values  
Out[15]:  
array([ 0.,  1.,  2.,  3.,
```

```
In [16]: tsd.values  
Out[16]:  
array([ 0.39704278,  1.55294416,
```

```
In [11]: tsd = nap.Tsd(t=t, d=d)  
  
In [12]: tsd  
Out[12]:  
Time (s)  
-----  
0.0      0.397043  
1.0      1.552944  
2.0      0.455892  
3.0     -1.17359  
4.0     -0.110113  
...  
95.0     -0.573408  
96.0     -0.0110915  
97.0     -1.58027  
98.0      0.998846  
99.0      0.542692  
dtype: float64, shape: (100, )
```

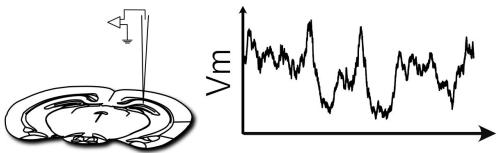
Numpy functions

np.mean

np.add

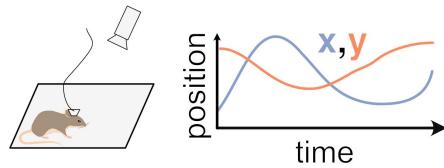
np.min

...



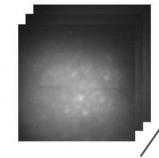
Tsd: 1-dimension

```
In [11]: tsd = nap.Tsd(t=t, d=d)
```



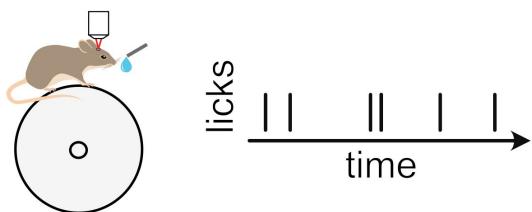
TsdFrame: 2-dimensions

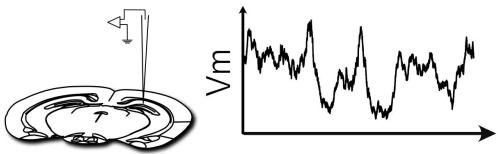
```
In [20]: tsdframe = nap.TsdFrame(t=t, d=d,
...:     columns = ['x', 'y'])
```



TsdTensor: n-dimensions

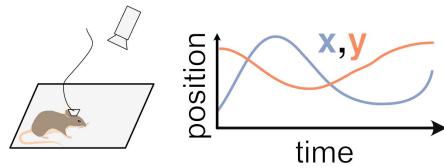
```
In [34]: tsdtensor = nap.TsdTensor(t=t, d=d)
```





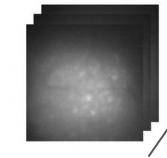
Tsd: 1-dimension

```
In [11]: tsd = nap.Tsd(t=t, d=d)
```



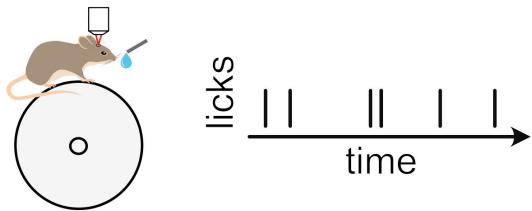
TsdFrame: 2-dimensions

```
In [20]: tsdframe = nap.TsdFrame(t=t, d=d,
...:     columns = ['x', 'y'])
```



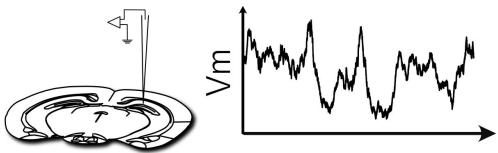
TsdTensor: n-dimensions

```
In [34]: tsdtensor = nap.TsdTensor(t=t, d=d)
```



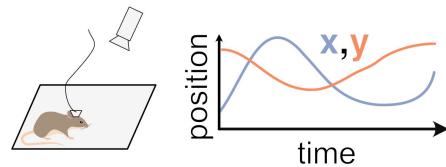
Ts: Timestamps

```
In [6]: nap.Ts(t)
Out[6]:
Time (s)
33.539693925
43.282779525
72.041005727
92.79257003
93.164316742
shape: 5
```



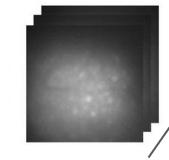
Tsd: 1-dimension

```
In [11]: tsd = nap.Tsd(t=t, d=d)
```



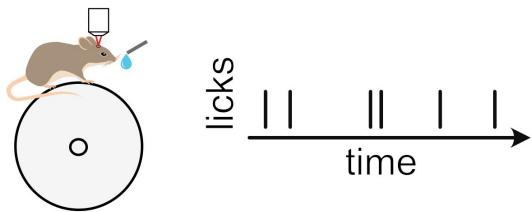
TsdFrame: 2-dimensions

```
In [20]: tsdframe = nap.TsdFrame(t=t, d=d,
...:     columns = ['x', 'y'])
```



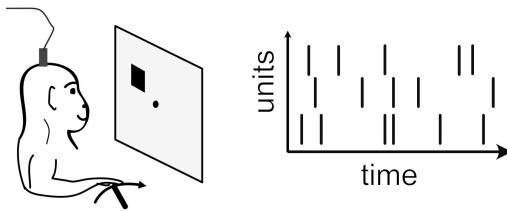
TsdTensor: n-dimensions

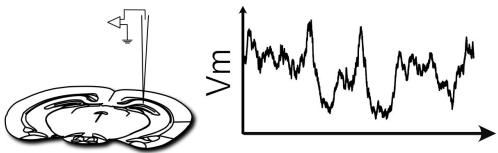
```
In [34]: tsdtensor = nap.TsdTensor(t=t, d=d)
```



Ts: Timestamps

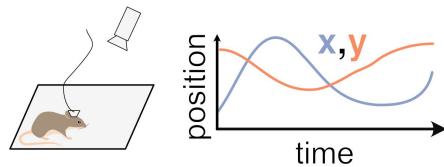
```
In [6]: nap.Ts(t)
Out[6]:
Time (s)
33.539693925
43.282779525
72.041005727
92.79257003
93.164316742
shape: 5
```





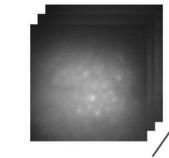
Tsd: 1-dimension

```
In [11]: tsd = nap.Tsd(t=t, d=d)
```



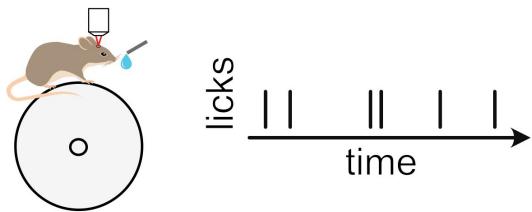
TsdFrame: 2-dimensions

```
In [20]: tsdframe = nap.TsdFrame(t=t, d=d,
...:     columns = ['x', 'y'])
```



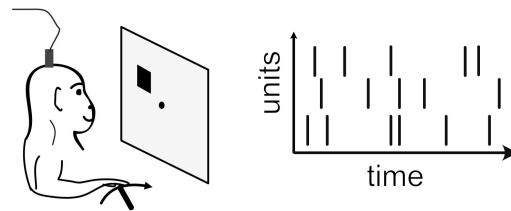
TsdTensor: n-dimensions

```
In [34]: tsdtensor = nap.TsdTensor(t=t, d=d)
```



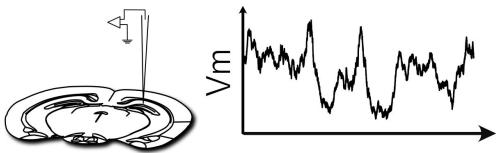
Ts: Timestamps

```
In [6]: nap.Ts(t)
Out[6]:
Time (s)
33.539693925
43.282779525
72.041005727
92.79257003
93.164316742
shape: 5
```



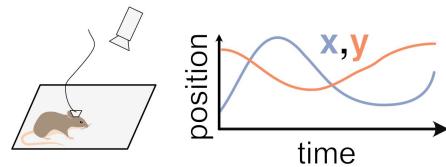
TsGroup: group of timestamps

```
In [18]: nap.TsGroup(data=data)
Out[18]:
Index      rate
0        10.02
1         5.01
2         2.06
```



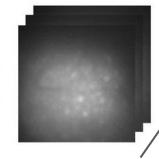
Tsd: 1-dimension

```
In [11]: tsd = nap.Tsd(t=t, d=d)
```



TsdFrame: 2-dimensions

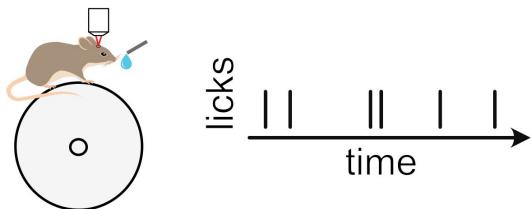
```
In [20]: tsdframe = nap.TsdFrame(t=t, d=d,
...:     columns = ['x', 'y'])
```



 FLATIRON
INSTITUTE

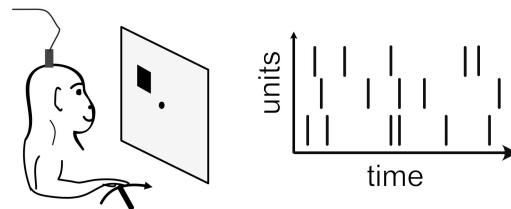
TsdTensor: n-dimensions

```
In [34]: tsdtensor = nap.TsdTensor(t=t, d=d)
```



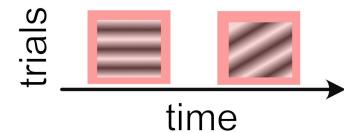
Ts: Timestamps

```
In [6]: nap.Ts(t)
```

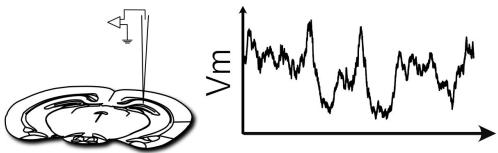


TsGroup: group of timestamps

```
In [18]: nap.TsGroup(data=data)
```

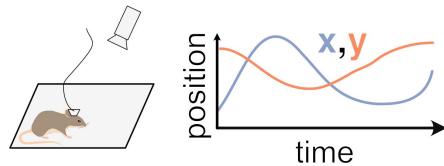


IntervalSet: set of epochs



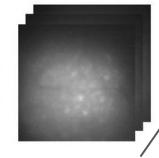
Tsd: 1-dimension

```
In [11]: tsd = nap.Tsd(t=t, d=d)
```



TsdFrame: 2-dimensions

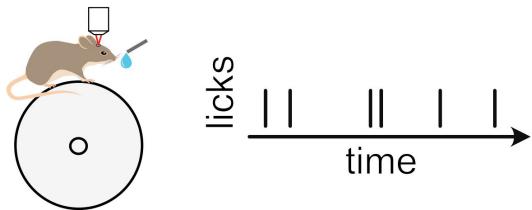
```
In [20]: tsdframe = nap.TsdFrame(t=t, d=d,
...: columns = ['x', 'y'])
```



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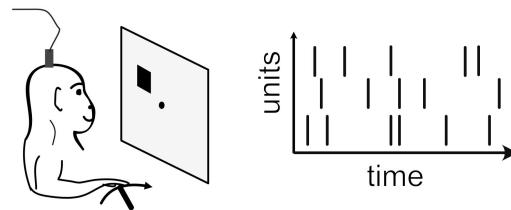
TsdTensor: n-dimensions

```
In [34]: tsdtensor = nap.TsdTensor(t=t, d=d)
```



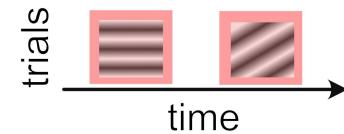
Ts: Timestamps

```
In [6]: nap.Ts(t)
```



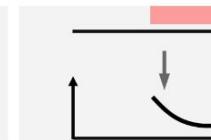
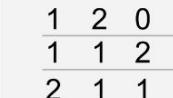
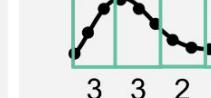
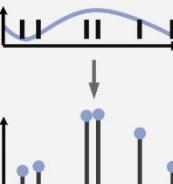
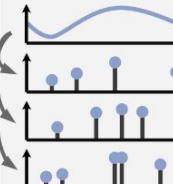
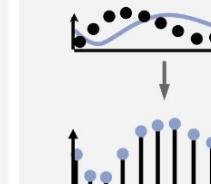
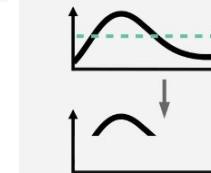
TsGroup: group of timestamps

```
In [18]: nap.TsGroup(data=data)
```

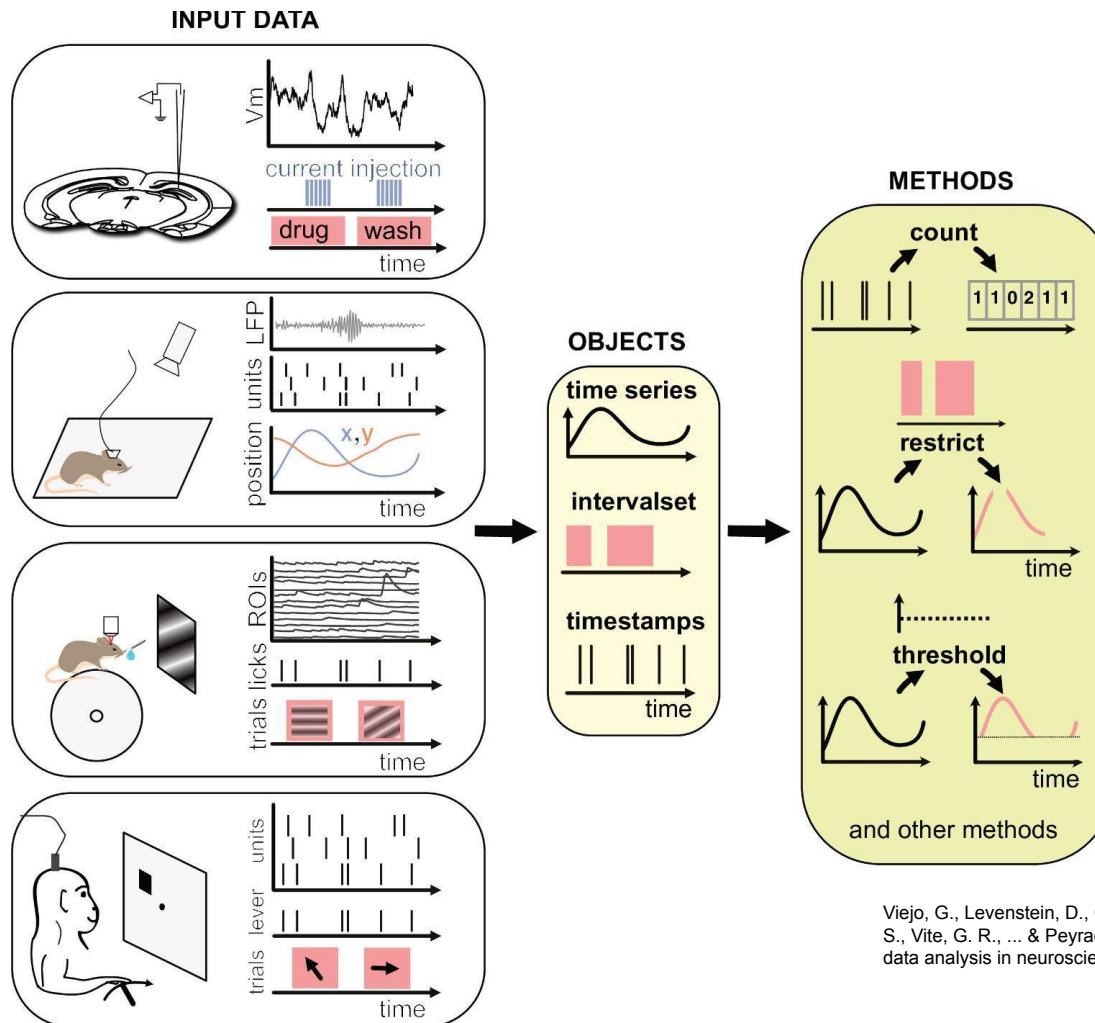


IntervalSet: set of epochs

```
In [23]: nap.IntervalSet(
...: start=start,
...: end = end)
Out[23]:
start    end
0        0.0    1.0
1        3.0    5.0
2        9.0   12.0
```

objects	timestamps	timestamps group	timestamped data	timestamped data frame
methods				
<code>restrict(IntervalSet)</code>				
<code>count(bin_size)</code>				
<code>value_from(Tsd)</code>				
<code>threshold(value)</code>				

Viejo, G., Levenstein, D., Carrasco, S. S., Mehrotra, D., Mahallati, S., Vite, G. R., ... & Peyrache, A. (2023). Pynapple, a toolbox for data analysis in neuroscience. *eLife*, 12, RP85786.



Viejo, G., Levenstein, D., Carrasco, S. S., Mehrotra, D., Mahallati, S., Vite, G. R., ... & Peyrache, A. (2023). Pynapple, a toolbox for data analysis in neuroscience. *eLife*, 12, RP85786.

NWB interface

```
In [1]: 1 import pynapple as nap  
2  
3 nwb = nap.load_file("A2929-200711.nwb")
```

```
In [2]: 1 nwb
```

A2929-200711.nwb

Keys	Type
position_time_support	IntervalSet
epochs	IntervalSet
z	Tsd
y	Tsd
x	Tsd
rz	Tsd
ry	Tsd
rx	Tsd

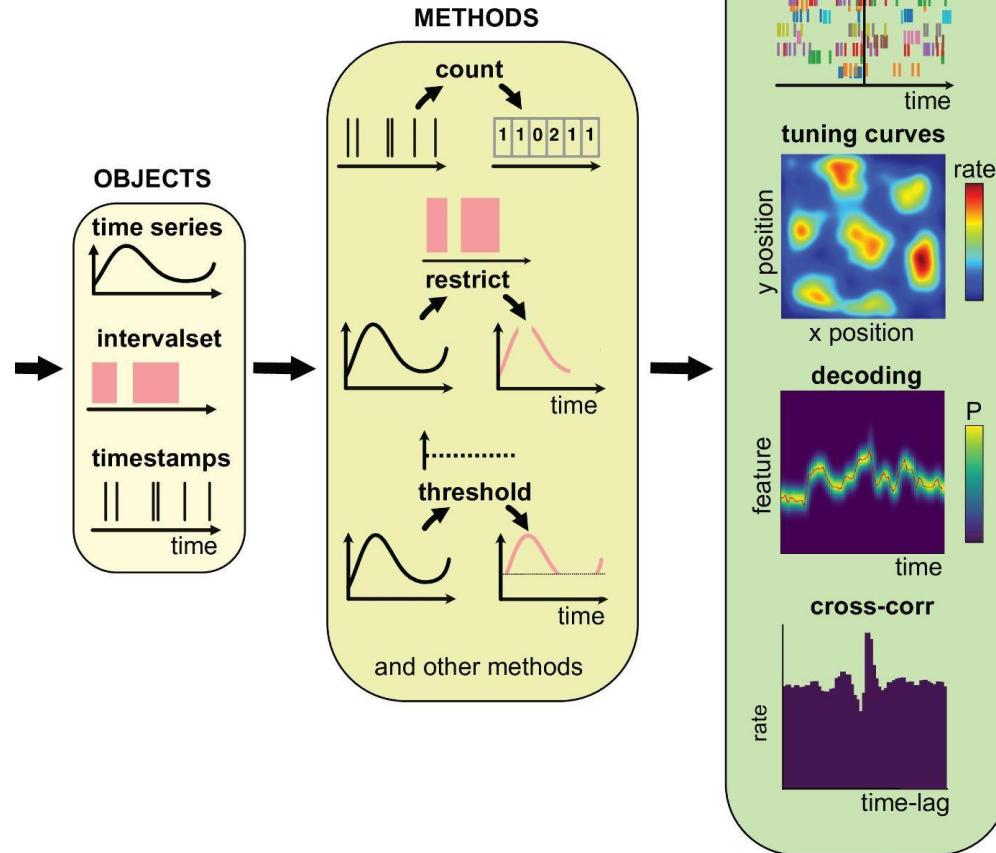
```
In [3]: 1 nwb["position_time_support"]
```

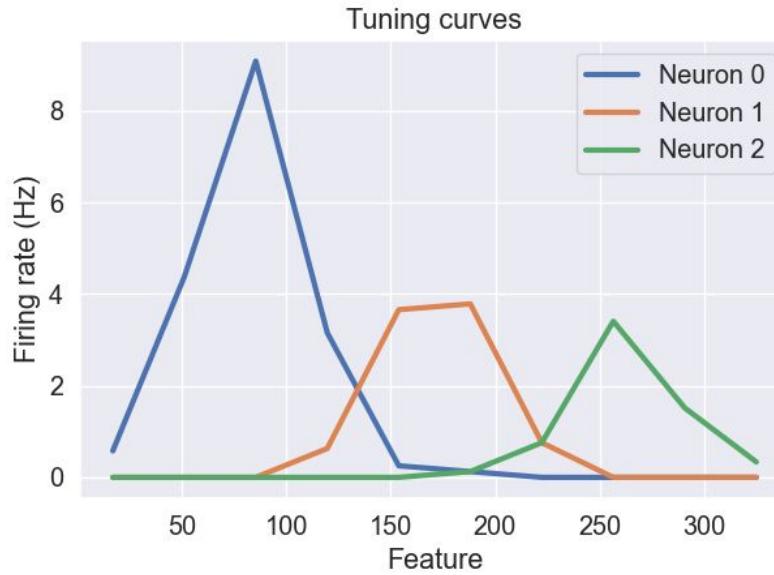
Out[3]:

	start	end
0	670.6407	1199.99495



NEURODATA
WITHOUT BORDERS





```
tuning_curve = nap.compute_1d_tuning_curves(
    spikes,
    feature,
    nb_bins=10,
    ep=ep)
```

Hands-on session: NWB data analysis in the cloud

- Open folder stratneuro_2024/tutorial_nwb_analysis/
- Open **nwb_stream_analysis.ipynb**
- We will stream and run data analysis in remote NWB files



DANDI



NEURODATA
WITHOUT BORDERS



CATALYST
NEURO

Want help?



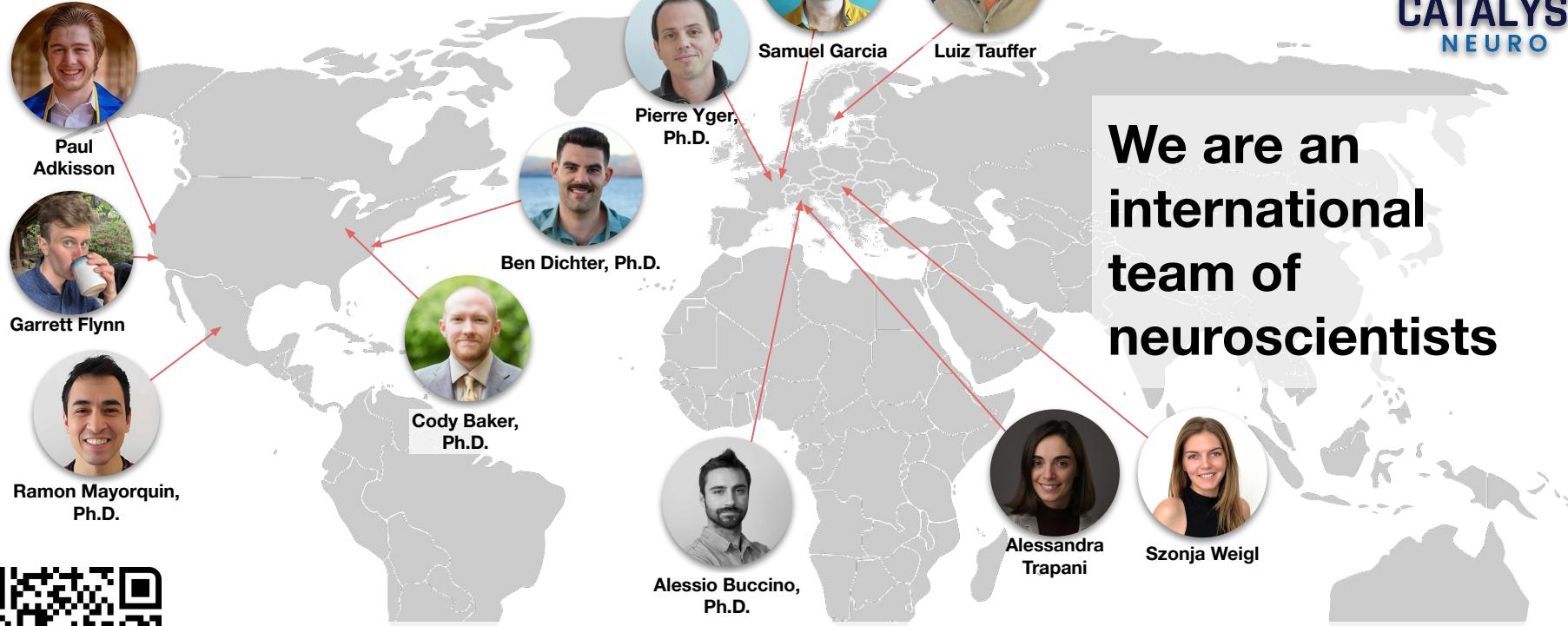
Paul
Adkisson



Garrett Flynn



Ramon Mayorquin,
Ph.D.



We are an
international
team of
neuroscientists

We use data and software engineering to connect
neurophysiology data producers, tool builders, and users

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