Processing and analysis of NWB data

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Outline

- Overview of analysis and visualization tools
- Spotlights:
    - Neurosift
    - SpikeInterface
    - Optinist
    - PatchView

Analysis and visualization tools

https://nwb-overview.readthedocs.io/en/latest/tools/analysis_tools_home.html

Exploring NWB Files
NWB Widgets
Neurosift
NWB Explorer
HDF Tools

Extracellular Electrophysiology
SpikeInterface
CellExplorer
NEO

Optical Physiology
CaImAn
Suite2p
CIAtah
EXTRACT
CICADA
optinist

Intracellular Electrophysiology
PatchView

Behavior
DeepLabCut
SLEAP

Data analysis
pynapple
DataJoint

Neurosift

- Interactive visualizations of NWB data in the browser
- Streams NWB data directly from DANDI
- Integrated with the DANDI Web UI
- Supports many NWB data types (Issues welcome)

DANDI examples:

- [Ephys with position](#)
- [Ophys](#)
- [Simultaneous ephys and ophys](#)

Local: `neurosift view-nwb /path/to/file.nwb`

SpikeInterface

SpikeInterface is a Python module to analyze extracellular electrophysiology data.

With a few lines of code, SpikeInterface enables you to:

- Load electrophysiology data from a variety of formats

- Pre-process the recording

- Run several state-of-the-art spike sorters

- Post-process and curate the output

- Compute quality metrics

- Visualize the results

- Export to popular formats

NWB SpikeInterface tutorial [here](#)

SpikeInterface has containerized spike sorters

- Spike sorters can be difficult to install and can have conflicting dependencies

- We built and distributed Docker and Singularity containers for many common spike sorters:

Combinato	Kilosort (1, 2, 2.5, 3)	MountainSort (4, 5)	WaveClus
HDsort	pyKilosort	Spyking Circus	YASS
Ironclust	Klusta	Tri des clous	

- MATLAB-based sorters do not require a MATLAB software or license to run

- Easy to run:

```
>>> import spikeinterface.sorters as ss
>>> sorting_KS25 = ss.run_sorter("kilosort2_5", recording, docker_image=True)
```

- Tested on DANDI

CATALYST
NEURO

optinist

OptiNiSt(Optical Neuroimage Studio) is a GUI based workflow pipeline tools for processing two-photon calcium imaging data.

OptiNiSt helps researchers:

- try multiple data analysis methods
- visualize the results
- construct the data analysis pipelines
- OptiNiSt's data-saving format follows NWB standards.

OptiNiSt also supports reproducibility of scientific research, standardization of analysis protocols, and developments of novel analysis tools as plug-in.

optinist

ROI detection

Suite2p
CalmAn
LCCD

Postprocessing

Basic Neural Analysis(Event Trigger Average...)
Dimenstion Reduction(PCA...)
Neural Decoding(LDA...)
Neural Population Analysis(Correlation...)

Saving Format

NWB

optinist: workflow
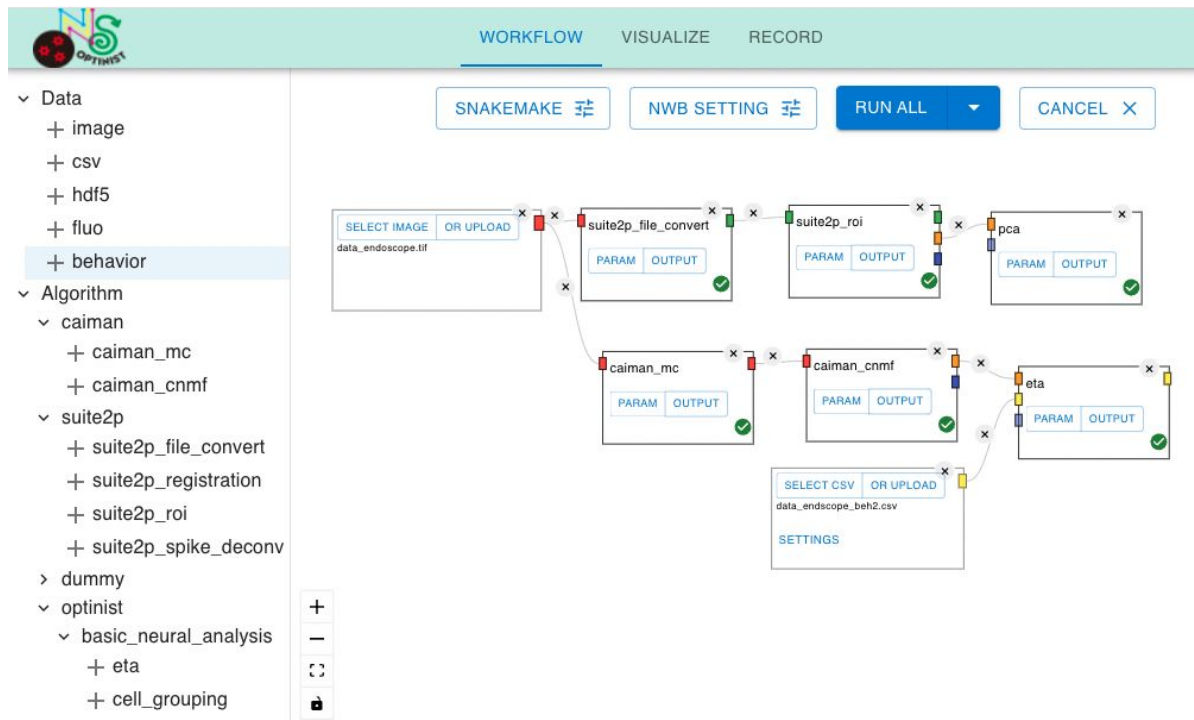
OptiNiSt allows you to make your analysis pipelines by graph style using nodes and edges on GUI. Parameters for each analysis are easily changeable.

optinist: visualize
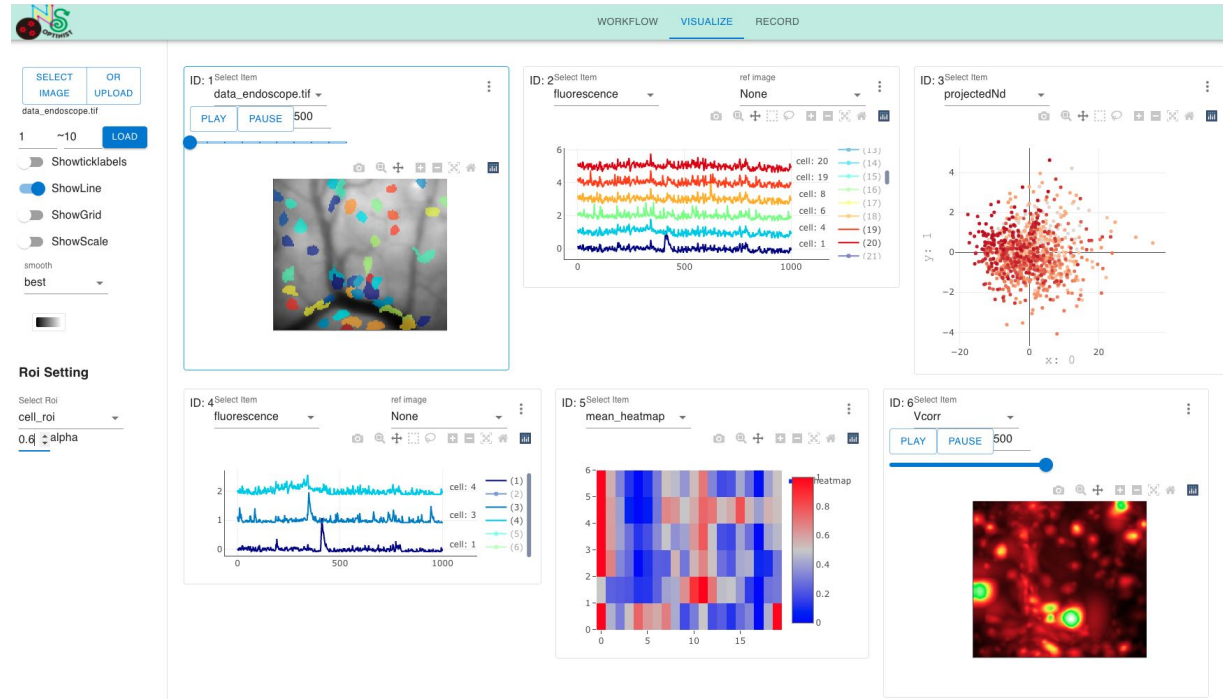
OptiNiSt allows you to visualize the analysis results with one click by plotly. It supports a variety of plotting styles.

optinist: record

OptiNiSt supports you in recording and reproducing workflow pipelines in an organized manner.

PatchView

PatchView is a GUI tool to perform data analysis and visualization on multi channel whole-cell recording (multi-patch) data, including:

- firing pattern analysis
- mini-event analysis
- synaptic connection detection
- morphological analysis

and more.
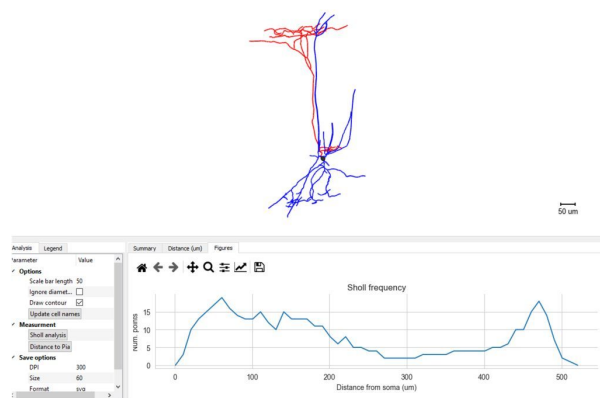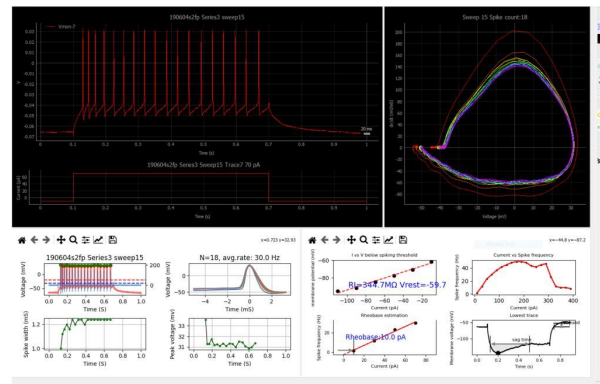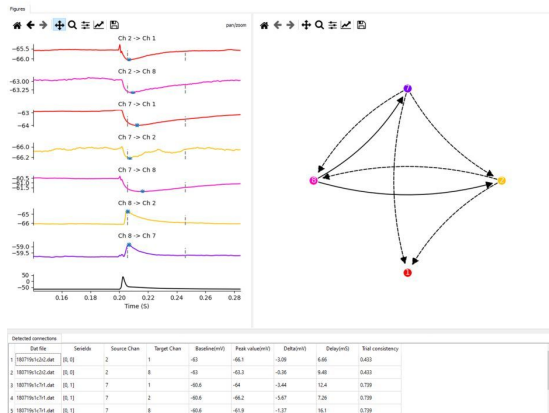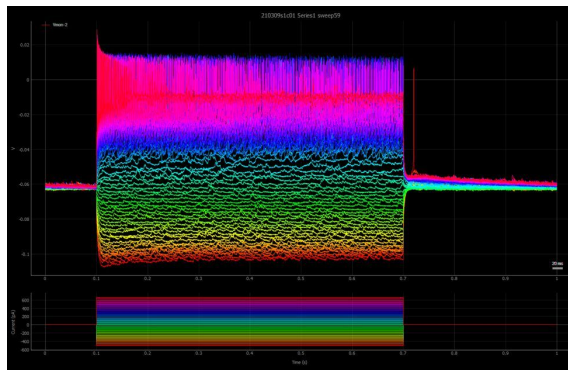
The NWB ecosystem and the future of tool integration

- Many diverse analysis and visualization tools in NWB ecosystem

- Helps adoption of NWB, reuse of open data, adoption of tool

- "NWB adoption" usually entails reading and/or writing NWB files, and demonstrating feature in tutorials

- In the future, could include DANDI integration

- Currently, there are levels of support

    - How flexibly can it read an NWB file?

    - How much control does the user have in the metadata?

    - How well does the output file follow best practices?

- We should make it easier for tools developers to integrate into the NWB ecosystem