Driving Collaboration in Calcium Imaging with NWB

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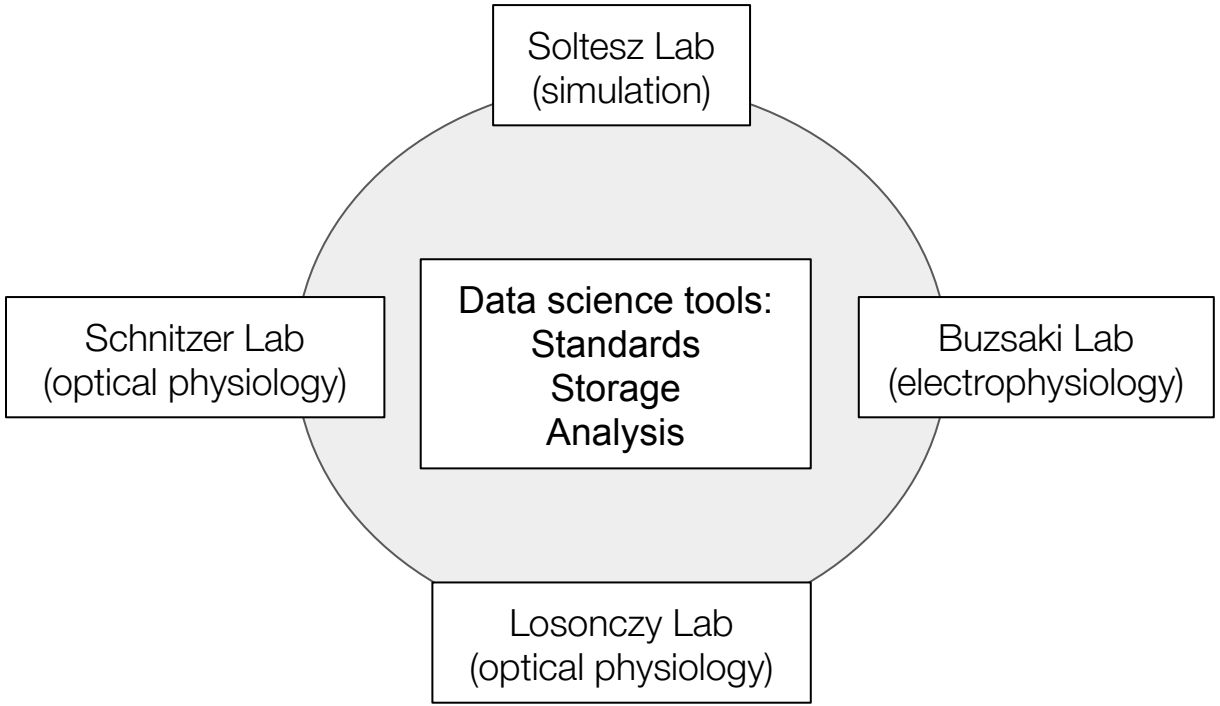
SIMONS FOUNDATION

BERKELEY LAB

NEURODATA WITHOUT BORDERS

Stanford University

Facilitating collaboration within a U19

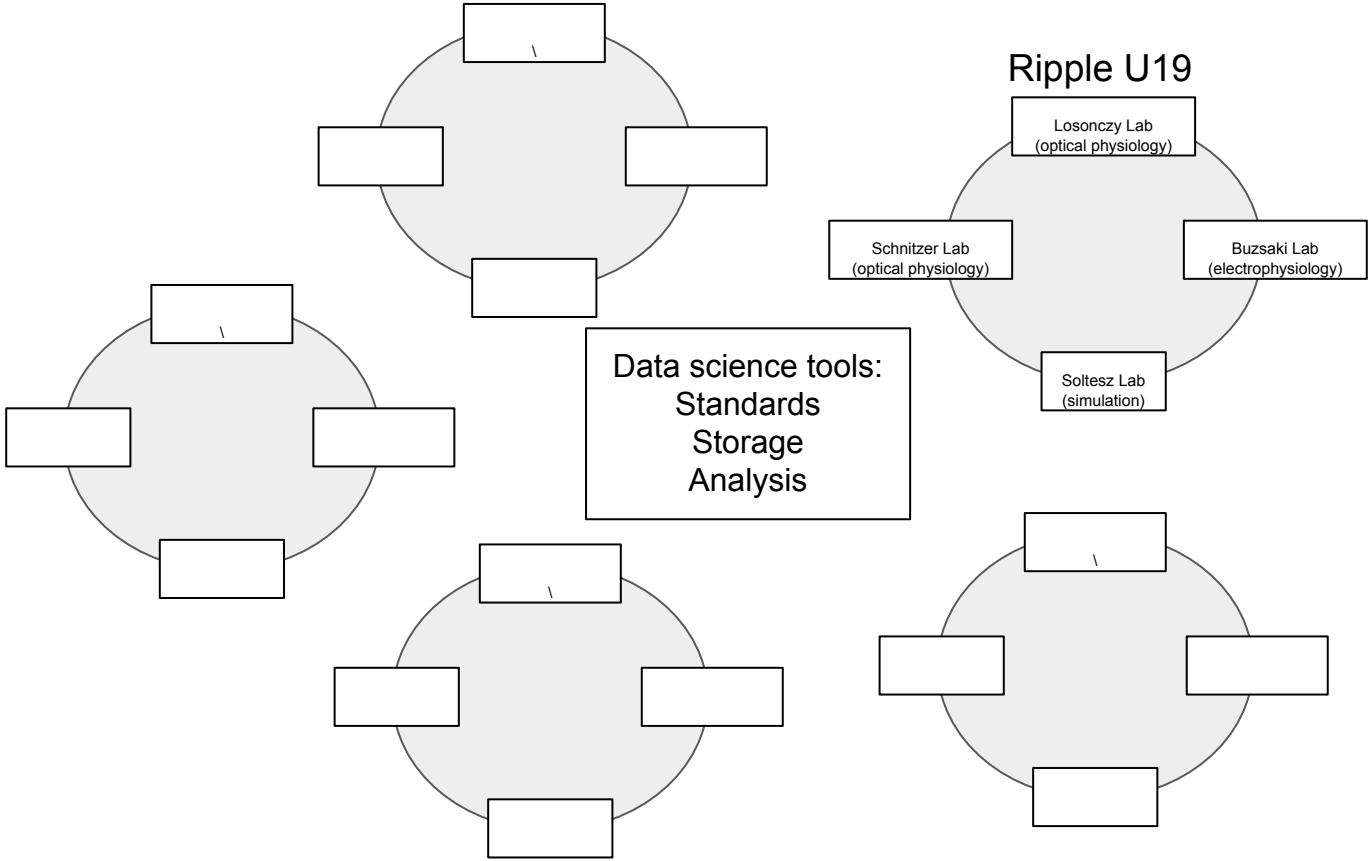


Challenges:

- Different imaging modalities
- Different programming languages
- Different regions

Microcosm of data sharing in systems neuroscience

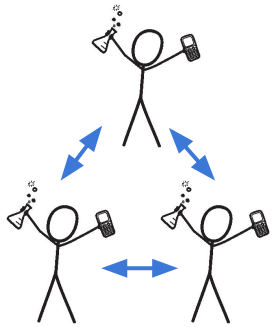
The same problems at a larger scale



Neurophysiology Data

- Extracellular Electrophysiology
- Intracellular Electrophysiology
- Optical Physiology
- Behavior
- Stimuli
- Experimental Metadata

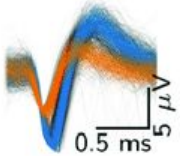
NEURODATA WITHOUT BORDERS

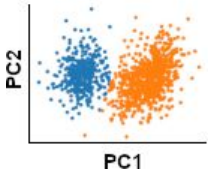


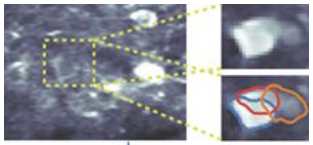
DANDI

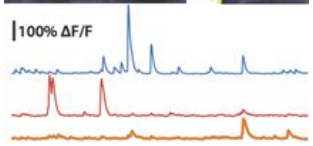
figshare

- Sharing and Archiving
- Analysis and Visualization









Ecosystem around NWB Standard

Analysis and visualization: utilizes rules

I/O tools (PyNWB, MatNWB): rule enforcement

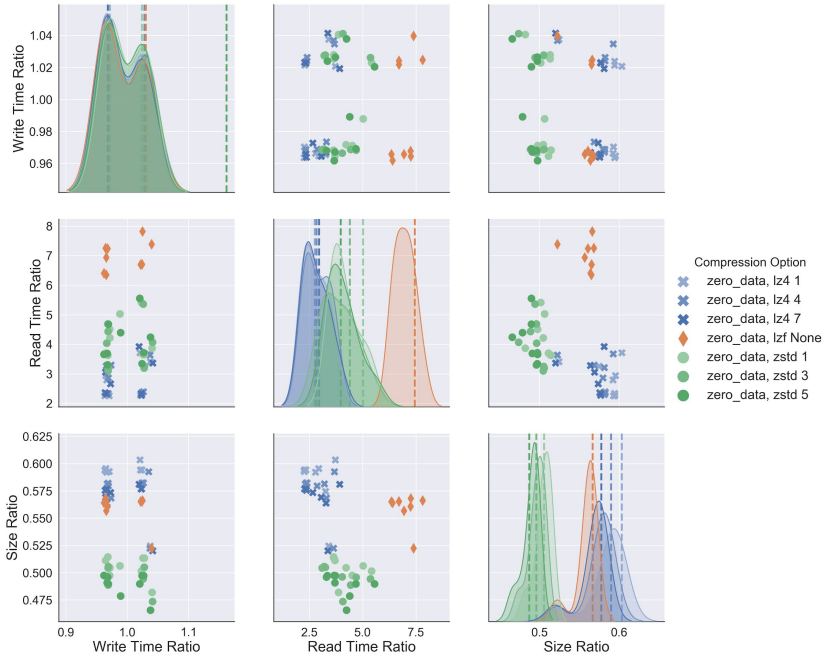
NWB schema: data storage rules

Standards: NWB for Calcium Imaging

- Standard for acquired images as well as processed intermediates (motion correction, ROIs, DF/F, deconvolved spikes)
    - Support for 3D imaging, including 3D ROIs
- Flexible: supports multiple channels, planes, segmentation schemes, etc.
    - Add new data types through extensions
- Interchangeable APIs supported in python and MATLAB
- NWBWidgets: Interactive visualization of data objects

Storage: Compression

- Data size becoming major bottleneck
  - Esp. SCAPE microscopy, at 2GB/sec
- Advanced HDF5 I/O features allow for chunking and compression
- Optimization between size, write time, read time portability
- Light preprocessing can make a big difference



Need to think about lossy compression like PCA

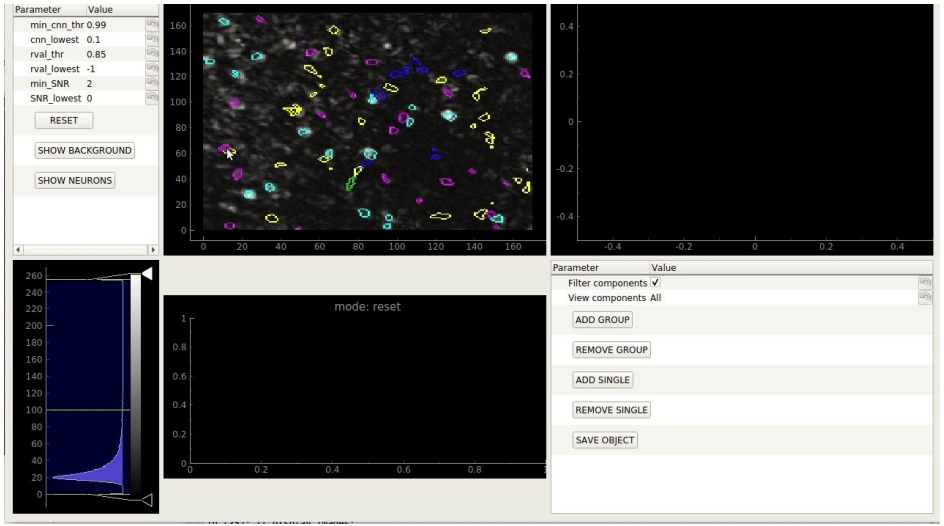
Storage: DANDI Archive

Working with DANDI team to host data publicly

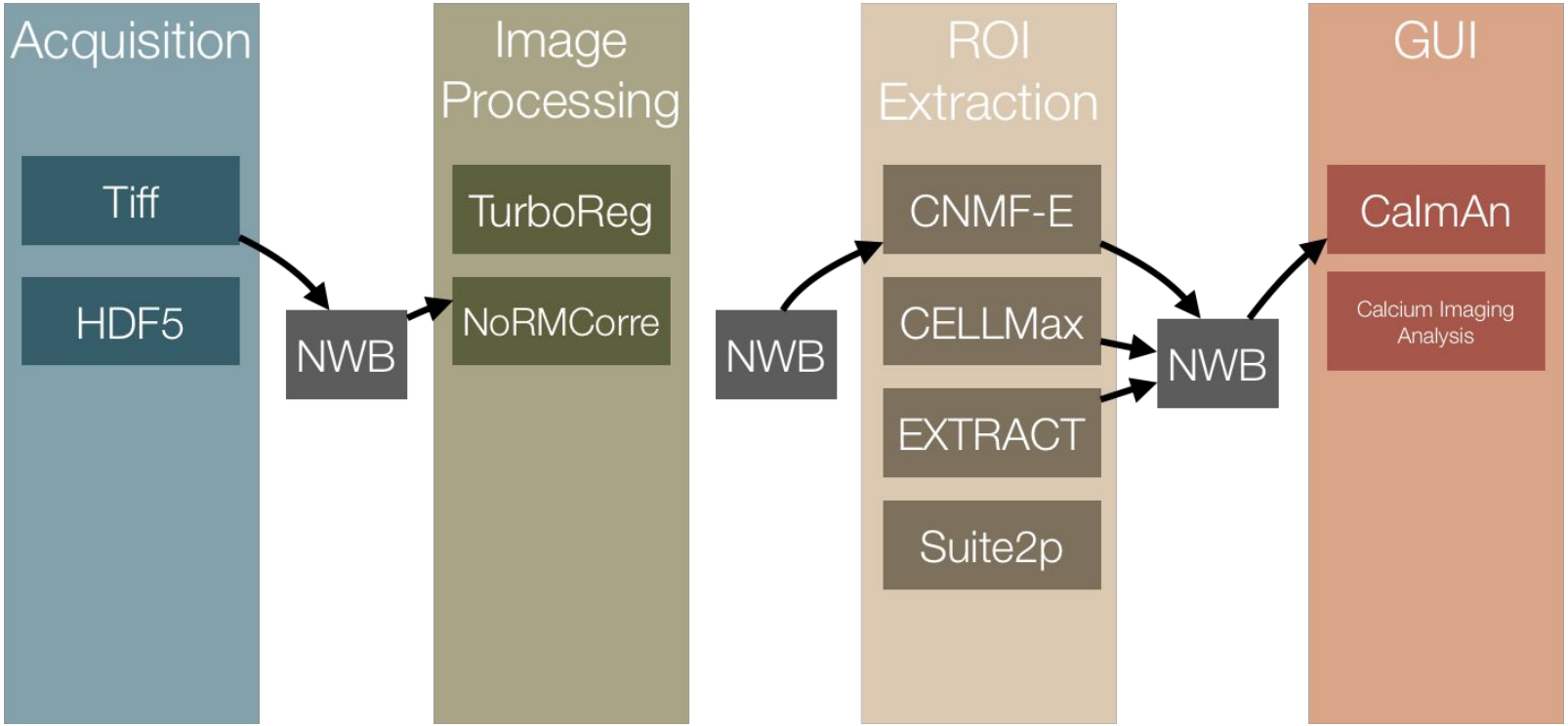
- Infrastructure to support large data files
- Meta-data that facilitates searching
- Integrate visualization for exploration

Analysis: NWB Integration with CaImAn

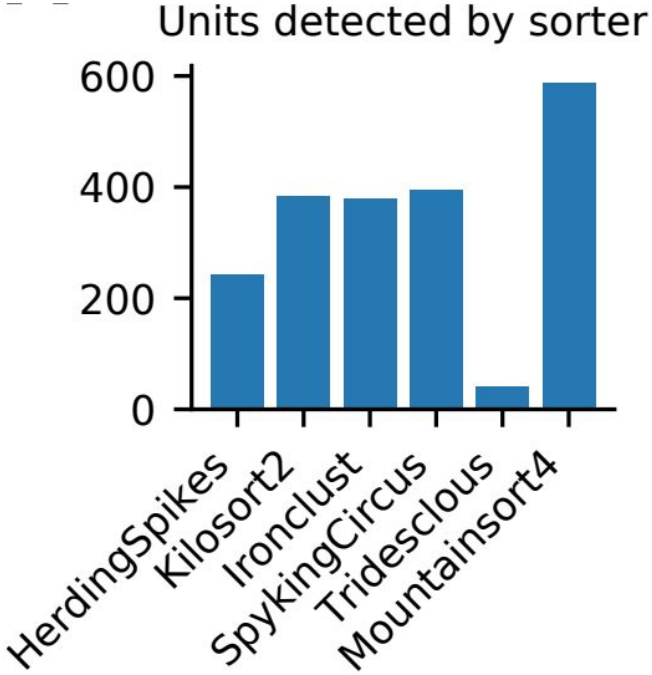
- Calcium Imaging Analysis (CaImAn) is a popular pipeline for analysis of large-scale calcium imaging data
- We have worked with the CaImAn team to integrate with NWB
- Reads and writes acquired and processed data
- Imports into new QC GUI

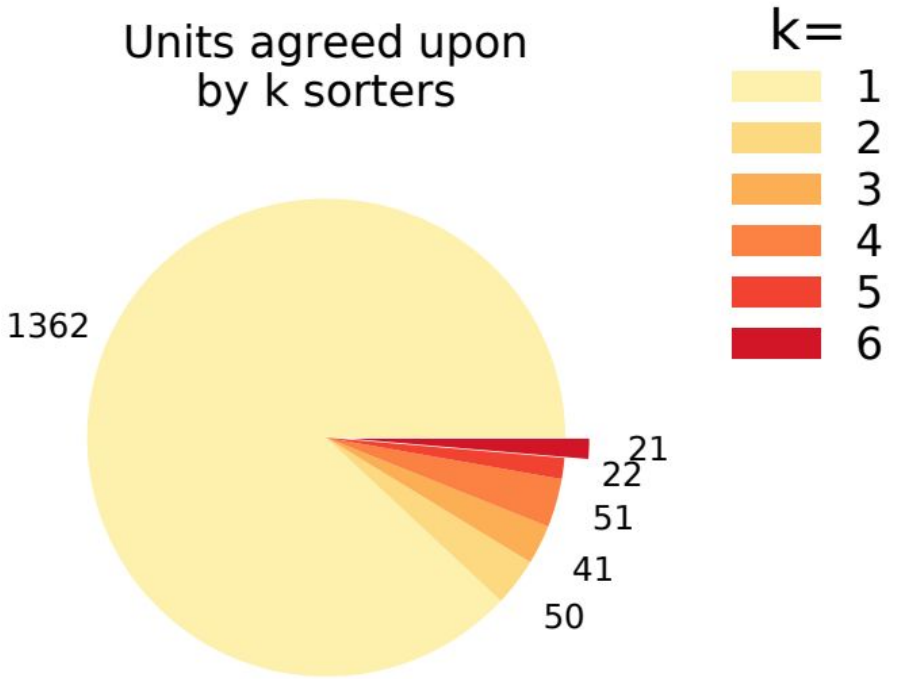


Generalizing NWB support for optical physiology



Comparing spike sorters





Alessio P. Buccino, Cole L. Hurwitz, et al. *bioRxiv*. 2019.

Questions

- How can we decide what meta-data is essential across tools?
- What is the best way to connect tools, through a data format or through a common API?
- Can we come to an agreement about the phases of analysis and how different tools fit into them?
- How should we compare across tools?