

Calcium Imaging Subgroup

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Data Joint

Collaborative data pipelines

Community

MICrONS

Mesoscale Activity Project

International Brain Lab

Princeton U19

UCSD U19

Tolias Lab, Baylor College of Medicine Reimer Lab, Baylor College of Medicine Sinz Lab, Wilhelm Schickard Institute for Computer Science Berens Lab, Werner Reichardt Centre for Integrative Neuroscience Euler Lab, Werner Reichardt Centre for Integrative Neuroscience **Bethge Lab**, Werner Reichardt Centre for Integrative Neuroscience Shcheglovitov Lab, University of Utah Moser Group, Kavli Institute for Systems Neuroscience **Mouse Motor Lab**, Rowland Institute at Harvard University Harvey Lab, Harvard Medical School Smirnakis Lab, Harvard Medical School Angelaki Lab, New York University McGinley Lab, Baylor College of Medicine Seung Lab, Princeton University Siapas Lab, California Institute of Technology Svoboda Lab, Janelia Research Campus Busse Lab, Ludwig-Maximilians-Universität München Katzner Lab, Ludwig-Maximilians-Universität München Engel Lab, Cold Spring Harbor Laboratory Tuthill Lab, University of Washington Applied Physics Lab, Johns Hopkins University





Coordinating multiple experimental modalities

Headplate

Right

LED 1

Piston

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Complex, structured behaviors



Multiple neural imaging / perturbation methods

Mouse.

restrained

Imaging objective

Left

LED

body

cylinders

Cellular resolution

Mesoscale (dorsal cortex)

Anatomical registration



Retinotopy mapping

Brain clearing + lightsheet microscopy ↓ Registration to common brain atlas



Rat, voluntary head-fixation

Sue Ann Koay

Steps for processing calcium imaging data



Data Storage/Organization

- Local
- Cloud (e.g., Drive/Dropbox)
- Database (e.g., Datajoint)

Motion correction

- Cross-correlation, Moco, etc
- Ratiometric imaging w red/green fluorophores

Alignment to standard brain/ventral nerve cord for correspondence w/ confocal/EM data

- Computational Morphometry Toolkit (CMTK)
- nBlast (for matching neural morphologies)

Data Segmentation

- None (sparse driver lines)
- Clustering pixel correlations
- PCA/ICA, NNMF, etc

Signal deconvolution

- Spikefinder, Genie, NND, etc
- None (in most neurons, firing rates are too high and fluctuate too rapidly to extract spikes from GCamp data)

Analysis

• Custom code in Python or Matlab

John Tuthill

Data Storage/Organization

- Cost
- Unwieldiness

Motion correction

 Lack of effective methods for correcting anisotropic tissue deformation

Alignment to standard brain/ventral nerve cord for correspondence w/ confocal/EM data

• Technically challenging for many labs

Data Segmentation

• Lack of flexible algorithms/toolboxes

Segmentation tools are optimized for extracting signals from cell bodies in mammalian cortex. In most cases, we want to image from axons/dendrites (this is not fly specific).

Analysis

 Each experiment/dataset is slightly different and requires bespoke analysis

John Tuthill



A typical 2-photon imaging experiment in behaving Drosophila (FlyLoops U19)



Chris Dallmann, Tuthill Lab, University of Washington

vGlut-Gal4; UAS-GCaMP7f

Complexity

- 20,000 cells per session × multiple days
 = 100,000 unique cells = 1 million
 neuron-hours from one animal.
- Multi-modality: Behavior + Visual stimulation + Anatomical
- Quality control: eye closing, brain state, optical quality, movement
- Sandbox testing vs. real life





Flexibility

Maximize rate of discovery

Deal with complexity through flexibility without loss of integrity, coordination, and quality control

Variety of methods. Spikefinder challenge (Berens et al 2018): competition for best calcium deconvolution. Apply new methods in existing pipeline as they emerge.





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Canonical Pipelines

Data pipelines quickly become overly complex with lab-specific detail

New projects need fully-functional minimal starting points

Project: minimal but fully-functional data pipelines

Thank you