Mining open access data for teaching electrophysiology

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Slides & materials

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By the end of this talk you'll be able to:

- Identify multiple ways in which open access data can be used to teach basic principles of electrophysiology
- Access **Allen Institute** cell types data using Google Colab
- Expand your teaching (and research?) with **Neurodata Without Borders** datasets

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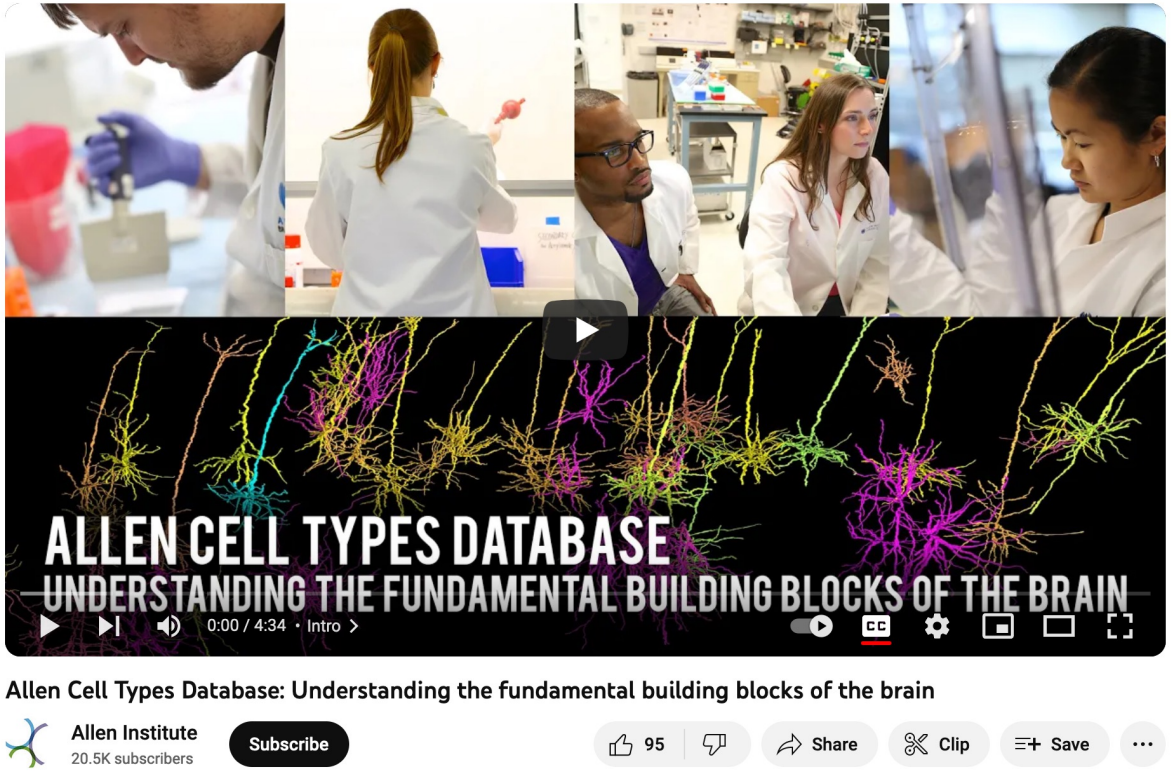
Why use open access data?

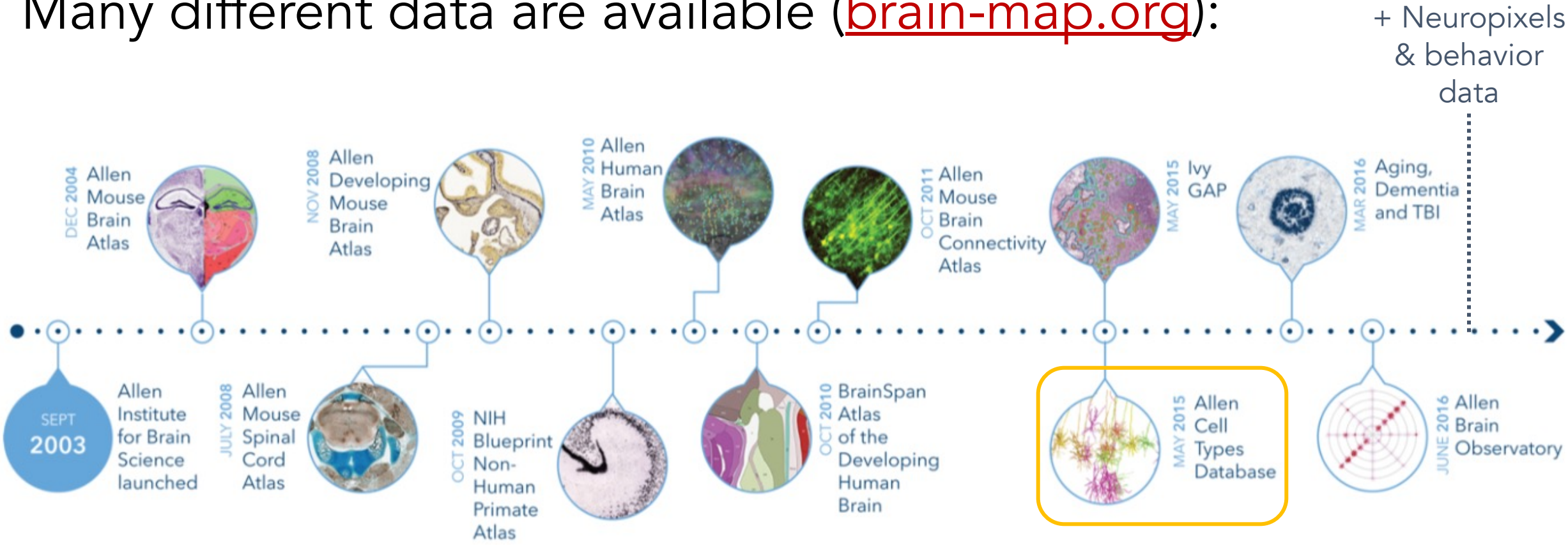
- Limited time and resources in undergraduate teaching laboratories
  - With open data we can conduct experiments on data we did not collect!
- Developing skills to work with open access data are broadly useful in both research and the workforce
  (Juavinett, 2022; Shah & Juavinett, 2022, Grisham et al., 2016, and *many others*)

Why Allen Institute data?

- Well curated with very detailed metadata
- High quality media for students
- *Dedicated team* to educational efforts & responsive to technical questions (https://community.brain-map.org)



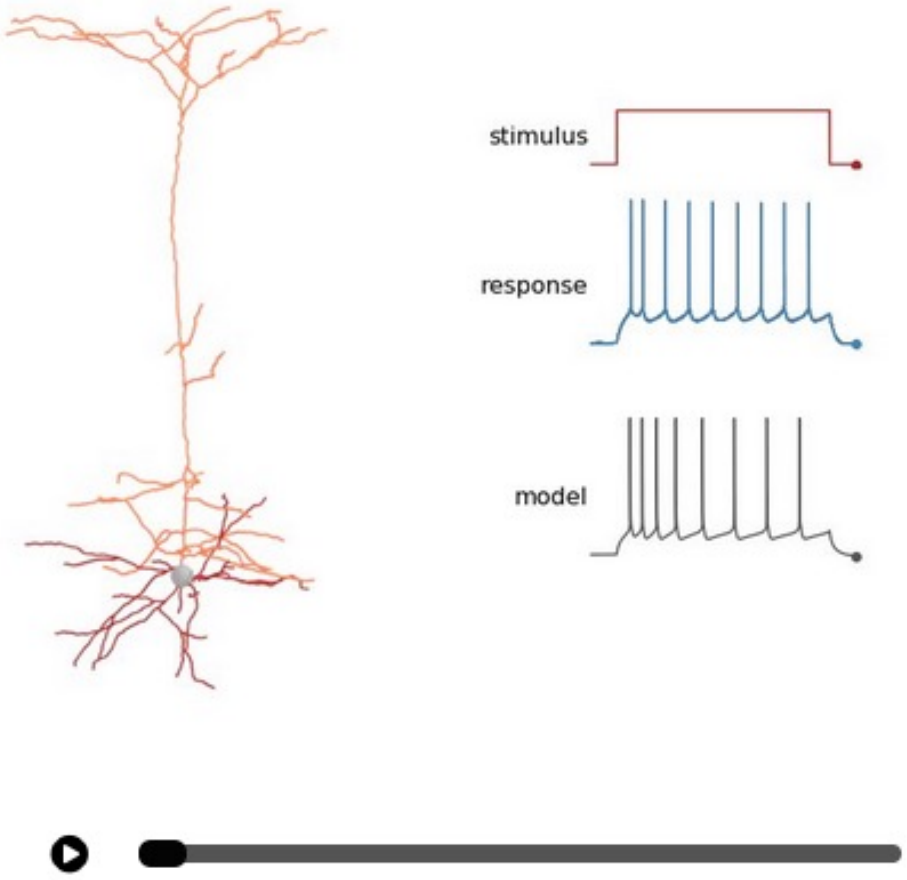
Many different data are available (brain-map.org):



Focus for today

About the cell types database

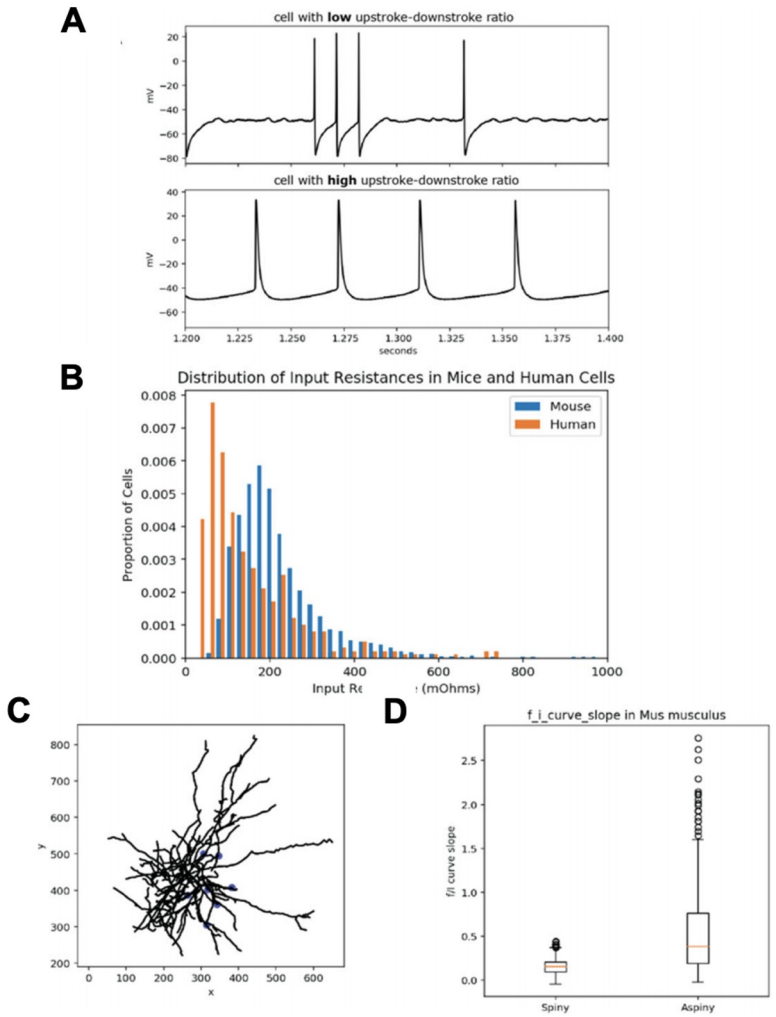
- Whole-cell patch clamp data from mouse and humans
- Many **pre-computed features**, such as tau, input resistance, adaptation ratio, average ISI, etc.
- Also includes **metadata** about cells: human/mice, transgenic line, cell size, layer of cortex



Example #1

Cell Types Lesson Objectives:

- Relate the diverse intrinsic electrophysiological features of neurons to their structure and function
- Compare electrophysiological characteristics of neurons in humans and mice
- Practice using coding notebooks to run and edit Python code
- Develop a sense of belonging and self-efficacy in coding and neuroscience research



Juavinett, "Learning to code while analyzing an open access dataset," *JUNE*, 2020

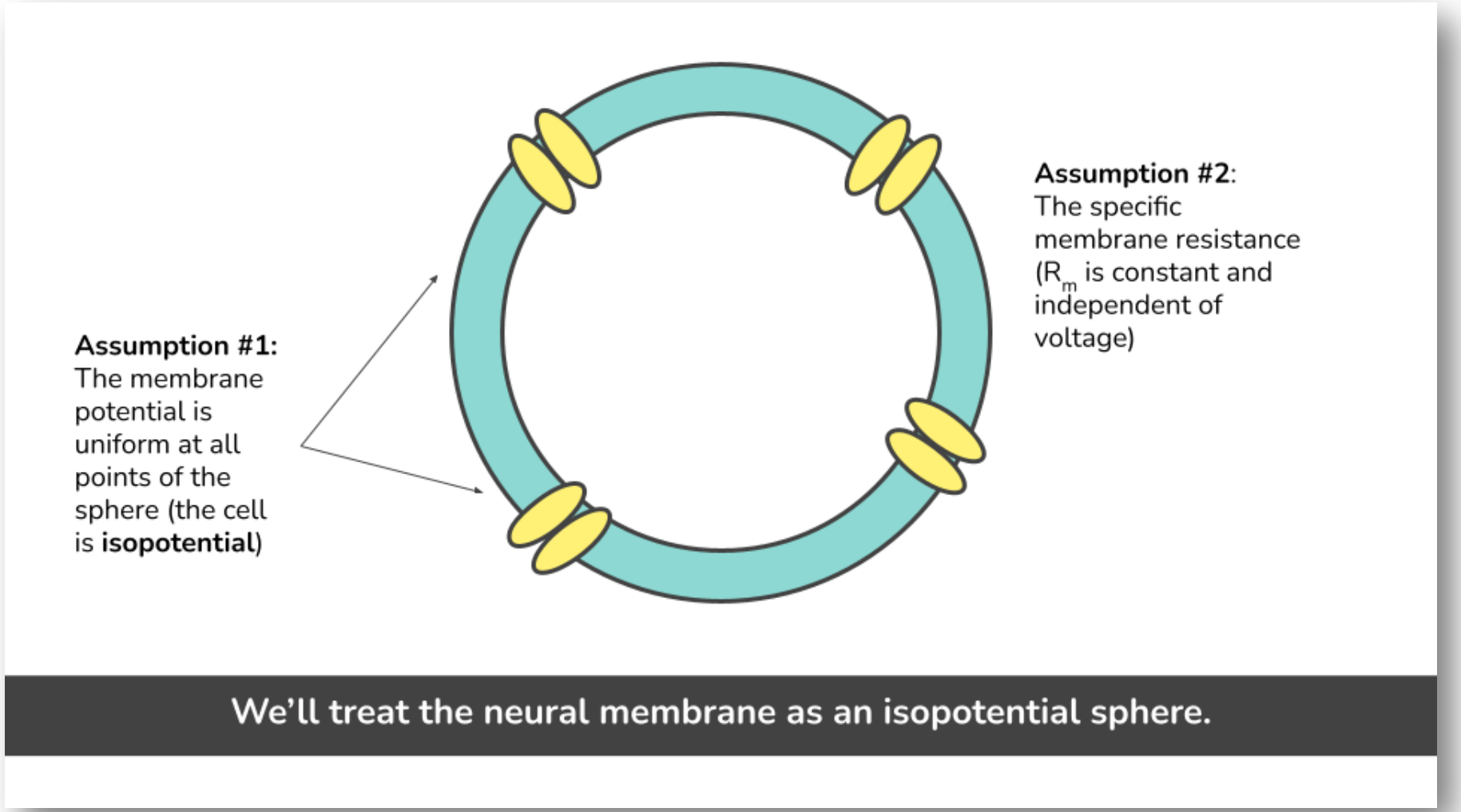
Example #2

How do cell features correlate, and why?

Before this lesson, students should be able to:

- Describe how patch clamp recordings enable us to obtain high fidelity signals from neurons
- Define time constant, input resistance, and rheobase
- Identify ways that cell types differ, structurally and physiologically

Either before or after the lesson, you can explain the biophysics behind how these properties relate



Example #2

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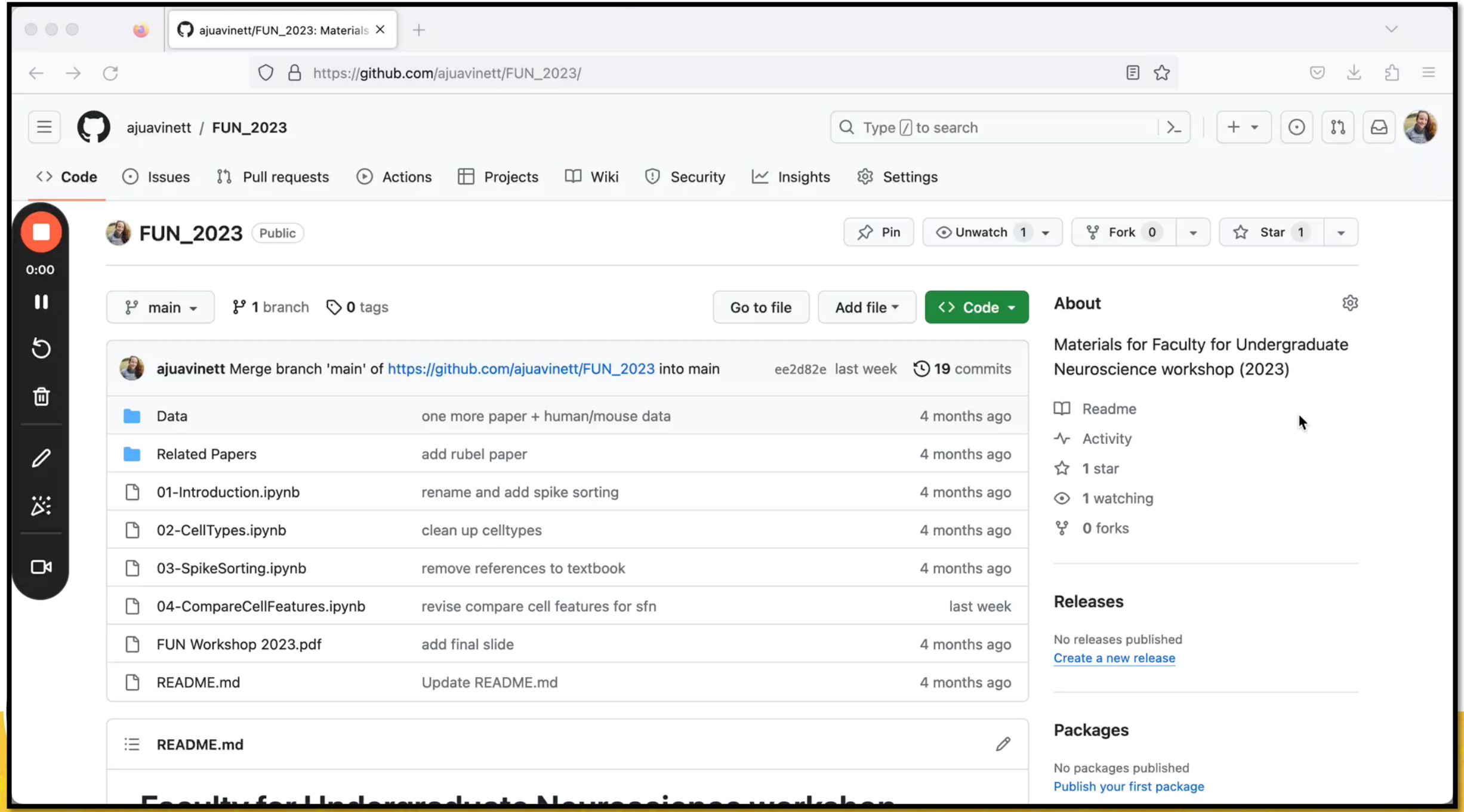
- Define time constant, input resistance, and rheobase
- Identify ways that cell types differ, structurally and physiologically

After this lesson, students will be able to:

- Investigate relationships between surface area, rheobase, input resistance, and time constant
- Generate a scatterplot in Python
- Explain how and why cell features are correlated
- Appreciate the variability in real data and the importance of statistics


ajuavinett/FUN_2023: Materials
https://github.com/ajuavinett/FUN_2023/
ajuavinett / FUN_2023
Type / to search
Code
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main
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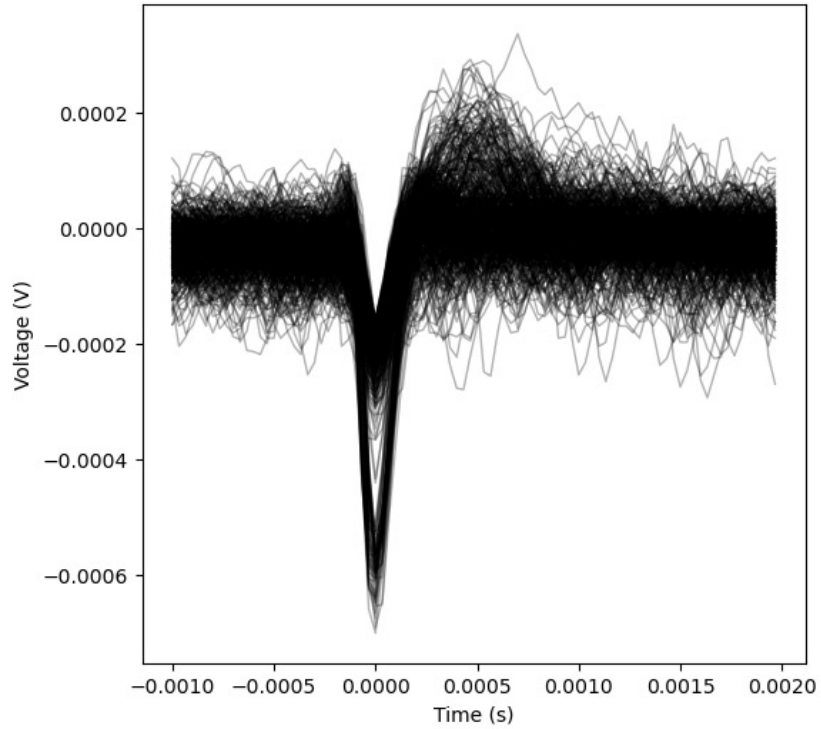
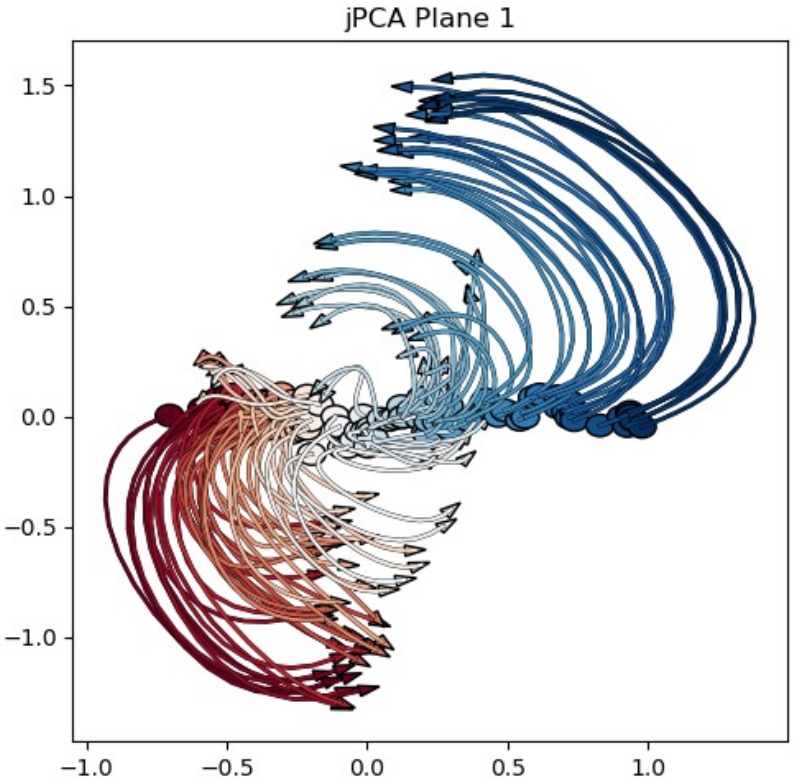
Go to file
Add file
Code
ajuavinett Merge branch 'main' of https://github.com/ajuavinett/FUN_2023 into main
ee2d82e last week
19 commits
Data one more paper + human/mouse data 4 months ago
Related Papers add rubel paper 4 months ago
01-Introduction.ipynb rename and add spike sorting 4 months ago
02-CellTypes.ipynb clean up celltypes 4 months ago
03-SpikeSorting.ipynb remove references to textbook 4 months ago
04-CompareCellFeatures.ipynb revise compare cell features for sfn last week
FUN Workshop 2023.pdf add final slide 4 months ago
README.md Update README.md 4 months ago
README.md
About
Materials for Faculty for Undergraduate Neuroscience workshop (2023)
Readme
Activity
1 star
1 watching
0 forks
Releases
No releases published
Create a new release
Packages
No packages published
Publish your first package

Ongoing work

Using Neurodata Without Borders datasets to teach more advanced topics, from spike sorting to dimensionality reduction





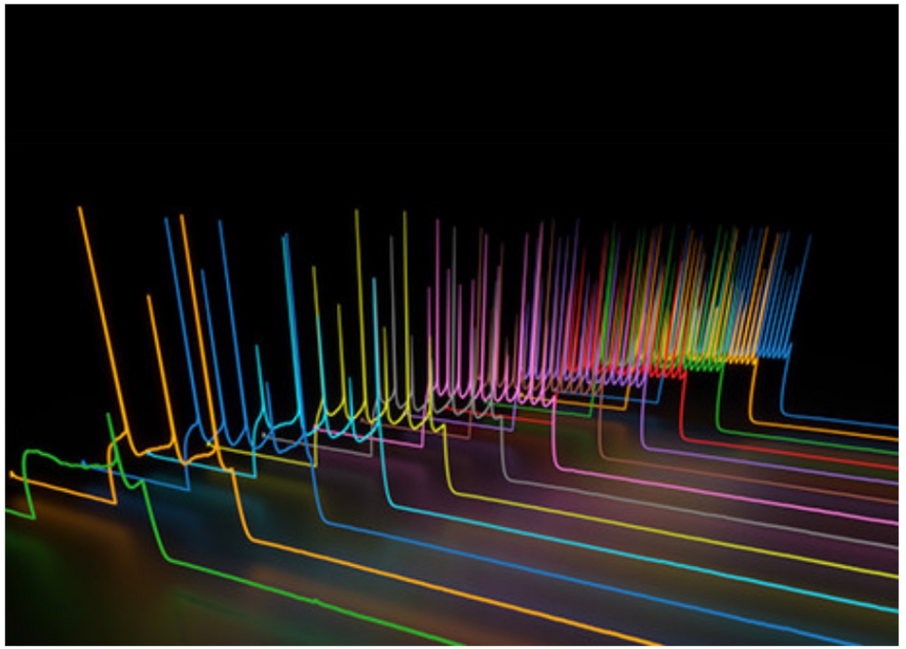
NEURODATA WITHOUT BORDERS

ABOUT COMMUNITY

Neurodata Without Borders

Neurodata Without Borders (NWB) is a data standard for neurophysiology, providing neuroscientists with a common standard to share, archive, use, and build analysis tools for neurophysiology data. NWB is designed to store a variety of neurophysiology data, including data from intracellular and extracellular electrophysiology experiments, data from optical physiology experiments, and tracking and stimulus data.

The **NWB team** consists of neuroscientists and software developers who recognize that adoption of a unified data format is an important step toward breaking down the barriers to data sharing in neuroscience.



(Courtesy of the Allen Institute for Brain Science)

www.nwb.org

See also Rübel et al. (2022): https://elifesciences.org/articles/78362

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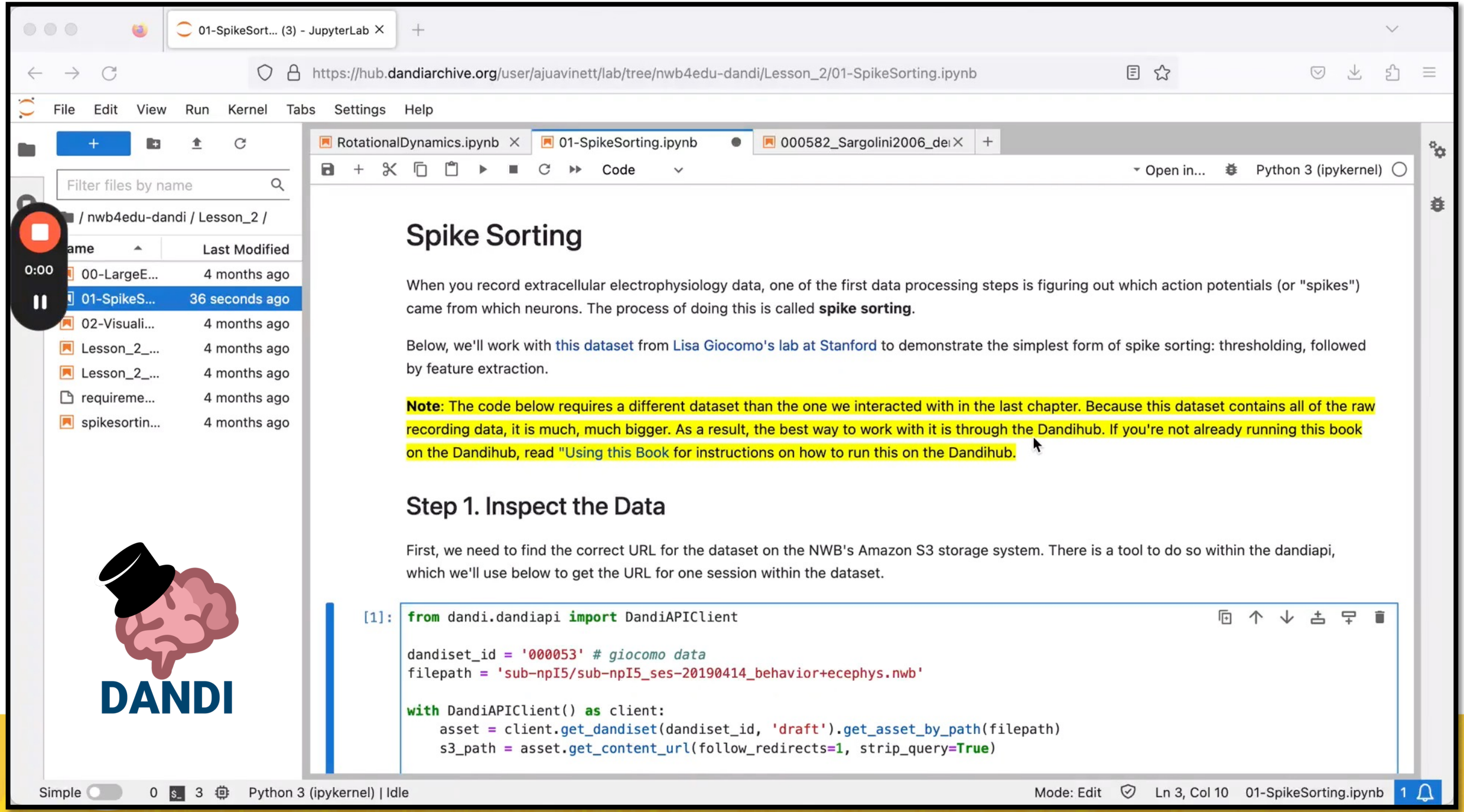
01-SpikeSort... (3) - JupyterLab
https://hub.dandiarchive.org/user/ajuavinett/lab/tree/nwb4edu-dandi/Lesson_2/01-SpikeSorting.ipynb
File Edit View Run Kernel Tabs Settings Help
RotationalDynamics.ipynb
01-SpikeSorting.ipynb
000582_Sargolini2006_de
Code
Open in...
Python 3 (ipykernel)
Filter files by name
/ nwb4edu-dandi / Lesson_2 /
Last Modified
00-LargeE... 4 months ago
01-SpikeS... 36 seconds ago
02-Visuali... 4 months ago
Lesson_2_... 4 months ago
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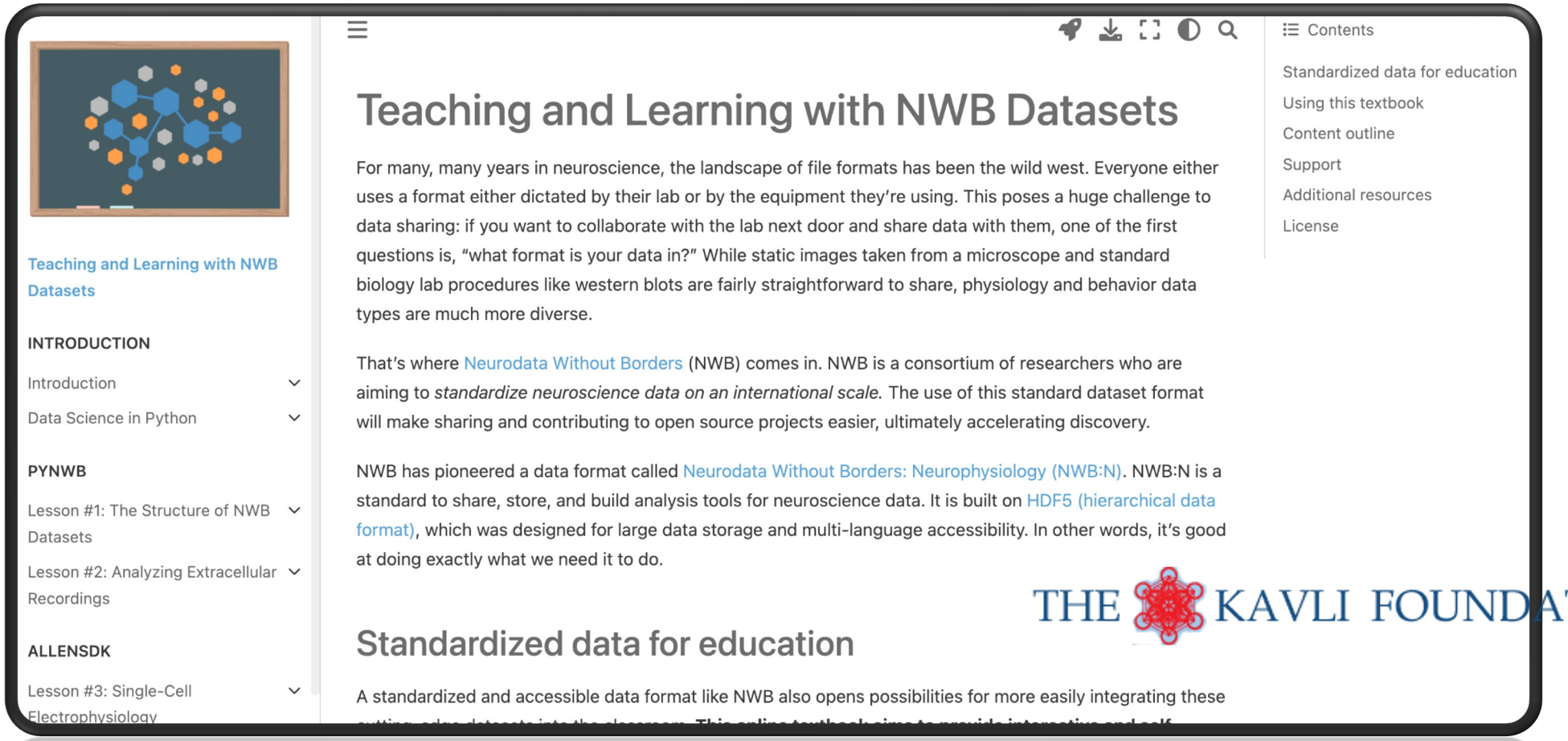
0:00
Spike Sorting
When you record extracellular electrophysiology data, one of the first data processing steps is figuring out which action potentials (or "spikes") came from which neurons. The process of doing this is called spike sorting.
Below, we'll work with this dataset from Lisa Giocomo's lab at Stanford to demonstrate the simplest form of spike sorting: thresholding, followed by feature extraction.
Note: The code below requires a different dataset than the one we interacted with in the last chapter. Because this dataset contains all of the raw recording data, it is much, much bigger. As a result, the best way to work with it is through the Dandihub. If you're not already running this book on the Dandihub, read "Using this Book for instructions on how to run this on the Dandihub.
Step 1. Inspect the Data
First, we need to find the correct URL for the dataset on the NWB's Amazon S3 storage system. There is a tool to do so within the dandiapi, which we'll use below to get the URL for one session within the dataset.
[1]:
from dandi.dandiapi import DandiAPIClient
dandiset_id = '000053' # giocomo data
filepath = 'sub-npI5/sub-npI5_ses-20190414_behavior+ecephys.nwb'
with DandiAPIClient() as client:
asset = client.get_dandiset(dandiset_id, 'draft').get_asset_by_path(filepath)
s3_path = asset.get_content_url(follow_redirects=1, strip_query=True)
DANDI
Simple 0 3 Python 3 (ipykernel) | Idle
Mode: Edit Ln 3, Col 10 01-SpikeSorting.ipynb 1

Online lessons using NWB datasets at nwb4edu.github.io



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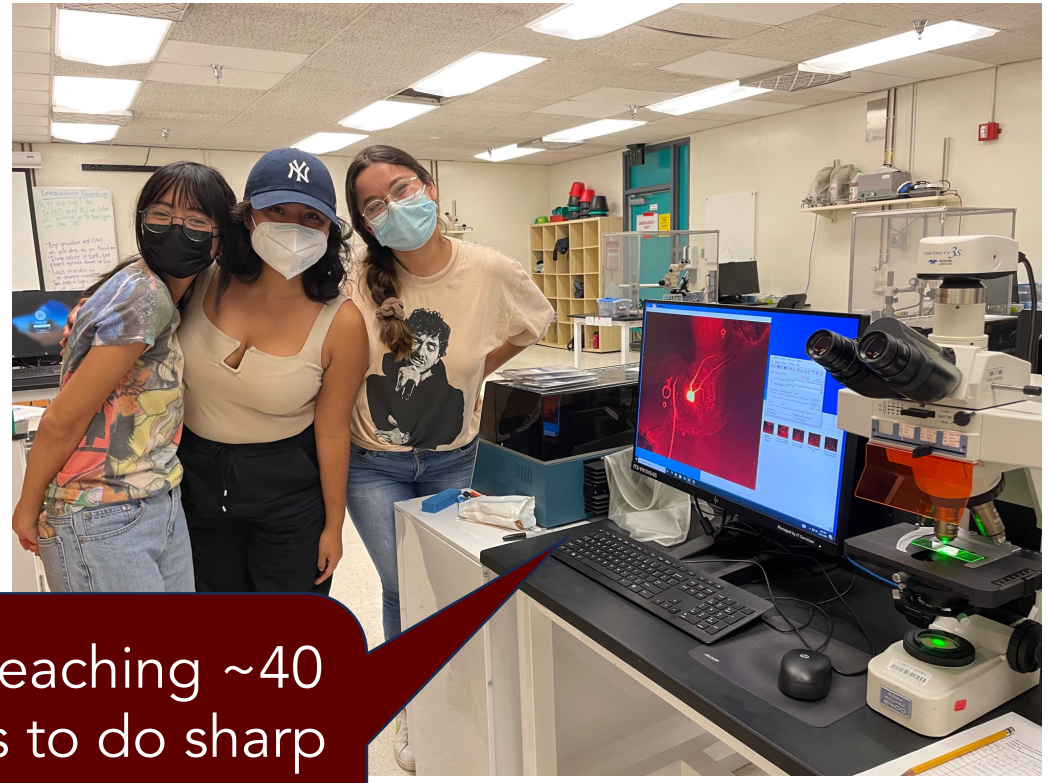
Thank you!

Everything you need to get started is here:
https://github.com/ajuavinett/FUN_2023/



Ask me about teaching ~40 undergraduates to do sharp intracellular recordings and dye fills in leech ganglia!