VIRTUAL WORKSHOP

Analysis and Integration of Single-Cell Neuronal Data in Python

Morphology, Electrophysiology, and Transcriptomics

A free two-day workshop introducing computational workflows for the analysis and integration of electrophysiological, morphological, and transcriptomic data of neurons using Python. We will cover the packages Pynapple, NeMoS, Navis, and CAJAL, providing a hands-on experience with these tools using public Patch-clamp and Patch-seq datasets.

SEPTEMBER 23-24, 2024

SEP 23

10:50 AM - 11:00 AM EDT	**Welcome and Introduction to Day 1**
11:00 AM - 1:00 PM EDT	**Analysis of Electrophysiology Data using Pynapple and NeMos** *Instructors:* Edoardo Balzani (Flatiron), Adrien Peyrache (McGill), Guillaume Viejo (Flatiron), Alex Williams (NYU)
1:00 PM - 1:30 PM EDT	**Break**
1:30 PM - 3:30 PM EDT	**Analysis and Visualization of Neuronal Morphologies using Navis** *Instructor:* Philipp Schlegel (Cambridge U.)

SEP 24

10:50 AM - 11:00 AM EDT	**Welcome and Introduction to Day 2**
11:00 AM - 1:00 PM EDT	**Analysis and Integration of Single-Cell Morphology, Electrophysiology, and Transcriptomic Data using CAJAL** *Instructors:* Pablo Camara (UPenn), Patrick Nicodemus (UPenn)
1:00 PM - 1:30 PM EDT	**Break**
1:30 PM - 2:30 PM EDT	**Open Discussion**

REGISTRATION: https://forms.gle/twx3ne3HHoV48eMS8

Basic familiarity with Python is required

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