From Images to Knowledge with ImageJ & Friends
virtual conference

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Conferences

Quantitative Neuroanatomy with Simple Neurite Tracer

Tutors: Tiago Ferreira (ferreirat@janelia.hhmi.org)
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Session 1: 2020-11-30 14:00 UTC – 2020-11-30 18:00 UTC
Session 2: 2020-12-01 22:00 UTC – 2020-12-02 02:00 UTC

Title

Quantitative Neuroanamty with SNT

Abstract

Quantification of neuronal morphology is essential for understanding neuronal connectivity and many software tools have been developed for neuronal reconstruction and morphometry. However, such tool remain domain-specific, tethered to specific imaging modalities, and were not designed to accommodate the rich metadata generated by recent whole-brain cellular connectomics. To address these limitations, we created SNT: ImageJ's unifying framework for neuronal reconstruction and morphometry, and analysis of single-cell connectomics, that replaces and extends the popular *Simple Neurite Tracer* software.

In this tutorial, participants will learn how SNT can be used to tackle diverse analyses in cellular neuroscience, namely:

- Use SNT's graphical user interface for interactive and script-aided tracing of 5D imagery
- Use SNT as a SciJava multi-language scripting library
- Incorporate center-line reconstructions into image processing routines
- Use SNT to quantify multi-species, whole-brain cellular connectomics data
- Use SNT to explore morphometry traits of groups of cells
- Use SNT's novel visualization tools, and analysis algorithms to perform sophisticated visualizations of whole-brain connectomics (mouse, fly, and zebrafish) data

In addition, participants will be able to propose specific challenges related to their own research.

Proposed Syllabus

Introduction

Overview of neuronal morphometry
Overview of existing toolboxes for neuronatomy
Why use ImageJ for neuroanatomy?
Overview of SNT

Sessions

Scripted tracing
Scripted analysis of single-cell morphometry
Scripting SNT using Python and pyimagej (Jupyter notebooks)
Graph-based analysis of single cells/cell groups
Attendees proposed challenges

Requirements

Fiji install
Anaconda (or pyimagej) install

Prerequisites

- Keen interest in quantitative neuroanatomy/quantitative analysis of neuronal tissue
- Ability to use Fiji to perform basic operations (open/save files, run scripts, etc.)
- Basic exposure to SNT, which can be fulfilled by watching the introductory video tutorials at https://imagej.net/SNT:_Screencasts
- Ability to run Jupyter notebooks
- Familiarity with one of SciJava scripting languages is beneficial but not required
- Familiarity with basic image processing terminology (image segmentation, ROI, intensity profile, etc.) will be assumed

If you are considering signing up for the tutorial, and aren't sure whether you meet these requirements, please get in touch with one of the tutors.

Proposed times
Flexible.

Information about the tutors

Tiago A. Ferreira: Tiago leads the imaging effort at Janelia's MouseLight project. Fiji developer since 2014, he has developed some of the most used and cited Fiji plugins (Ferreira et al. Nat Methods 2014; Ferreira & Ou, Development 2014; https://doi.org/10.5281/zenodo.495245). More recently, Tiago spearheaded the development of SNT: The complete ImageJ-based framework for generation, visualization, quantification, and modeling of neuroanatomical data (bioRxiv 2020.07.13.179325; doi: https://doi.org/10.1101/2020.07.13.179325).

Cameron Arshadi. Cameron is a senior annotator at Janelia's MouseLight project, having reconstructed many hundreds of neuronal arbors at the whole-mouse-brain scale. Cameron has a strong Python background, and recently embraced Java as his second coding language. He developed most of SNT's regression tests, and graph-based algorithms.