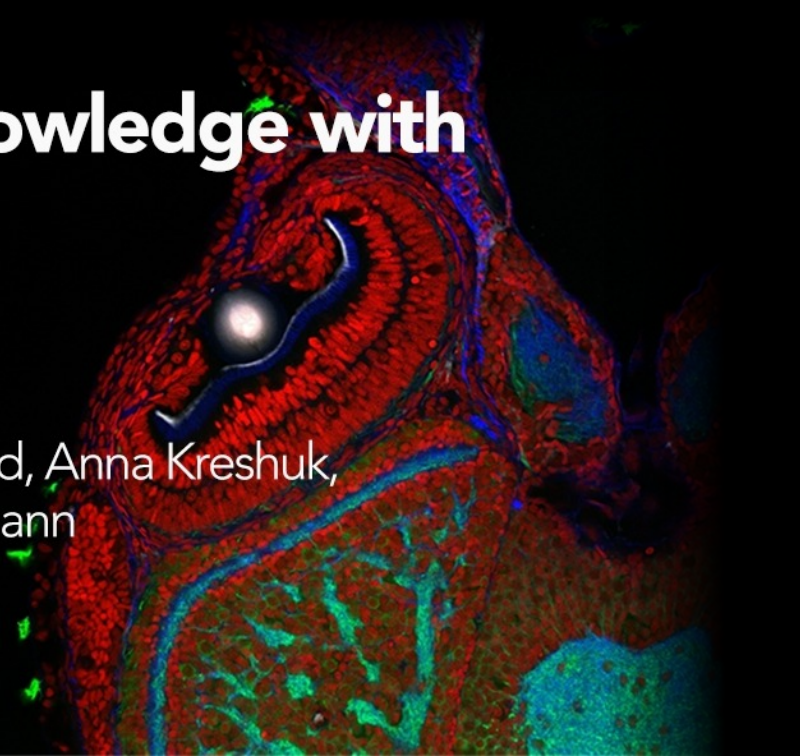# From Images to Knowledge with ImageJ & Friends
virtual conference

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Conferences

Collaborative neuron tracing, analysis and data sharing with CATMAID

Tutors: Tom Kazimiers (tom@kazmos.de)
Michael Winding (mjw226@cam.ac.uk)

Session 1: 2020-12-01 13:00 UTC – 2020-12-01 17:00 UTC
Session 2: 2020-12-02 07:00 UTC – 2020-12-02 11:00 UTC

Title: Collaborative neuron tracing, analysis and data sharing with CATMAID.

Abstract:
CATMAID has been around for some time and so far its focus has been on skeleton data to represent neurons, created manually or with the help of segmentation data. Annotated synapses then link individual skeletons to form a network. This tutorial will give users an introduction to general CATMAID workflows, both for manual tracing and working with skeletonized segmentation data. Users will reconstruct and assemble parts of representative neurons and will use the data they created to explore various tools in CATMAID. Users will learn how to create their own personal tracing spaces, how to share data and prepare it for publication. We will see how already published data can be accessed and used. Another topic will be the naming of neurons and how the textual representation of neurons can be changed throughout CATMAID and exploited for grouping operations in many places. We will also talk about different ways to communicate with the CATMAID server and write small programs that will use data on the server. A separate topic will be the work with light microscopy data and how it can be organized and annotated with CATMAID.

Information about the tutors:
In close collaboration with various neuroscience labs, Tom Kazimiers has worked since 2013 at Janelia Research Campus on the collaborative open source neuron reconstruction and analysis suite CATMAID. Since 2020 he continues this work as the founder of the open source software consultancy kazmos GmbH.

Michael Winding has worked with Marta Zlatic and Albert Cardona at Janelia Research Campus and the University of Cambridge since 2016. Using CATMAID, he has led the reconstruction and analysis of the whole brain connectome of Drosophila larva.

Technical requirements:
Regular computer / laptop and regular internet connection (the faster the better), recent Chrome, Chromium or Firefox browser installed.

Outline:
1. Introduction to CATMAID, its basic concepts, user account creation, project navigation. Outline of goals of the tutorial.

2. Relation to other tools and data sets in the connectomics community. Brief discussion on what it takes to host own CATMAID environment and how different CATMAID services can interact.

3. Image data handling. This includes looking at some EM data as well as some LM data and how their appearance can be manipulated. Using a public N5 data set, users will be able to add a dataset and create their own projects. Users will then be able find and open their projects on the front-page. We will talk about permissions and change project visibility.

4. Image data annotation. Based on the created example projects, users will learn how they can define a vocabulary (ontology) of terms and relations between them in order to annotate different image datasets in a consistent manner. These vocabulary based annotations can then be searched across different datasets and analyzed for clusters right from within CATMAID.

5. In a shared project we will look at EM data and manual neuron reconstructions. Some examples are shown that show typical neurons in 2D and 3D. There will be an introduction to tracing and common workflows. Everyone we will then trace a part of a neuron, starting from locations assigned to the users, with the goal that users will come across each other's work and join their work by merging data and connecting neurons with synapses.

6. We will use skeletonized neurons based on segmentation data to extend the previously tracing data more quickly. In order to do this, we will see how we can link in remote data like this segmentation skeletonization.

7. Looking for similar neurons. We will have a look at neuron similarity using NBLAST. The created neuron fragments are used to find neurons in published data that the fragments may be part of. We will look at how this method works and its parameterization. As a second part we will discuss how skeletons can be virtually transformed, e.g. from one hemisphere into the other hemisphere and how such transformations can be used with NBLAST as well.

8. With some similar published neurons found, users will learn how those can be used to find strongly connected partners quickly using a sampling method on the target neuron. We will also see how the CATMAID's CircuitMap extension can be used to find synapses and strongly connected partners automatically using segmentation data.

9. In a second shared project where many already published neurons are available, we will look at common analysis tools and visualizations in CATMAID.