From Images to Knowledge with ImageJ & Friends

virtual conference

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Stephan Preibisch, Stephan Saalfeld, Anna Kreshuk, Pavel Tomancak and Virginie Uhlmann

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webKnossos: Share, Annotate and Proof-Read your Large-Scale 3D Image Datasets Online

Tutors: Norman Rzepka (norman.rzepka@scalableminds.com)

Session 1: 2020-11-30 15:00 UTC – 2020-11-30 19:00 UTC
Session 2: 2020-12-02 08:00 UTC – 2020-12-02 12:00 UTC

Proposal for webKnossos Tutorial

Information about the tutor

Norman Rzepka is the co-founder of scalable minds, a startup that develops software tools and provides services for biomedical image analysis. He leads the development efforts of webKnossos, an open-source data sharing and annotation platform for large 3D image data, and Voxelytics, a Machine Learning toolbox for automated image registration and segmentation. Norman holds a M.Sc. in IT-Systems Engineering from the Hasso Plattner Institute in Potsdam, Germany. He previously presented at the 2018 ImageJ and Friends conference at EMBL Heidelberg.

Title and abstract of the tutorial

Title

webKnossos: Share, Annotate and Proof-Read your Large-Scale 3D Image Datasets Online

Abstract

webKnossos [1] is an open-source data sharing and annotation platform for large-scale 2D and 3D image datasets. Increasingly large image datasets are required for discovery in life sciences. The core features of webKnossos are fast 3D data streaming, uniquely fast skeleton annotation, and efficient volume annotation. webKnossos facilitates image analysis workflows on multi-terabyte datasets, including visualization of raw microscopy data, distributed training data generation, proof-reading of automatic segmentation, and mesh rendering of reconstructed objects. As a scientific resource, webknossos.org serves as a database for published image datasets including their annotations.

In this tutorial session, you will learn how to accomplish typical image analysis workflows with webKnossos. Together, we will work through some workflows while introducing the key functionalities of the software. The workflows include data exploration and sharing with collaborators, neurite skeletonization as well as automated segmentation and proof-reading. Additionally, you will learn how to integrate webKnossos in your existing setup by interoperating with other tools. During the tutorial, you will be able to use your own data and work with exported results. Alternatively, we will provide access to public datasets from the community. Documentation for the software tools and steps of the tutorial session will be provided.

[1] Boergens Berning Bocklisch Bräunlein Drawitsch Frohnhofen Herold Otto Rzepka Werkmeister Werner Wiese Wissler & Helmstaedter, webKnossos: efficient online 3D data annotation for connectomics. Nat. Meth. (2017) 14, 691–694.

Tutorial Outline

The tutorial will be organized as a hands-on session around typical workflows (e.g. neurite tracing, nuclei segmentation, data exploration). The selection of workflows will be prioritized based on the interests and backgrounds of the participants. As part of the workflows, the tutorial will focus on interoperability with other tools. Participants will be able to bring their own data for work with webKnossos. For that, we will also introduce tools from the webKnossos ecosystem, including conversion and offline analysis tools. Documentation for the software as well as the steps of the tutorial session will be provided.

Schedule

- Introduction of topic and tutor (20min)
- Introduction of participants and their use cases (30-50min)
- Overview of webKnossos features (10min)
- Intro to supported data formats (10min)
- Practical work (150min)
  - Setup
  - Data formats for webKnossos
    - Conversion tools
    - Import and export workflows
  - Workflow A: Exploration of data
    - Importing dataset
    - Viewing datasets
    - Configuring image settings
    - Sharing data with outside collaborators
  - Workflow B: Skeletonization and point annotations
    - Annotating cell bodies
    - Tracing neurites with flight mode
    - Exporting annotations and analysis with Python
  - Workflow C: Segmentation
    - Generating training data
    - Running ML models (outside of webKnossos)
    - Importing predictions and segmentations
    - Proof-reading of automated segmentation
    - Generating and exporting meshes from segmented objects
- Summary and discussion (60min)
  - Custom workflows of participants
  - Advanced topics (e.g. annotation task distribution, advanced deployment)
  - Other questions

Technical requirements

Minimal requirements: A recent web browser and a locally installed Python 3 environment

For work with own datasets:

- A sample 3D dataset, in TIFF or NIfTI format, up to 5GB in size

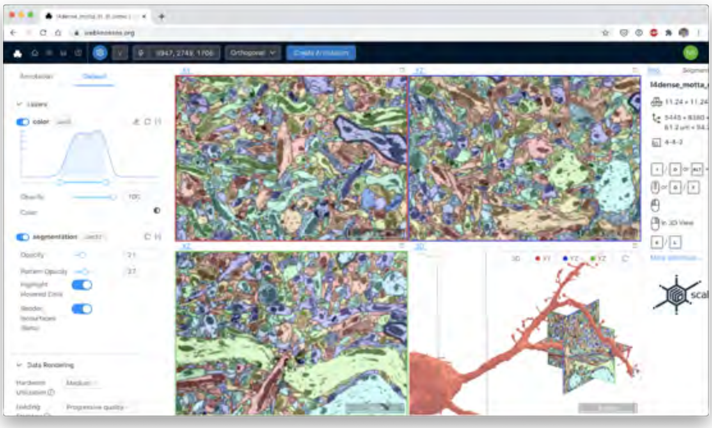
- 10GB harddisk space for conversion

Explanation:
For the purposes of the tutorial, we will work with a hosted version of webKnossos, which greatly reduces the setup time compared to a self-hosted instance.
Most functionality of webKnossos is usable through the web browser without any locally installed dependencies. However, in order to convert their own data and analyse exported data, participants need to have a Python 3 environment installed on their computers. Required modules and installation instructions will be provided prior to the tutorial session.

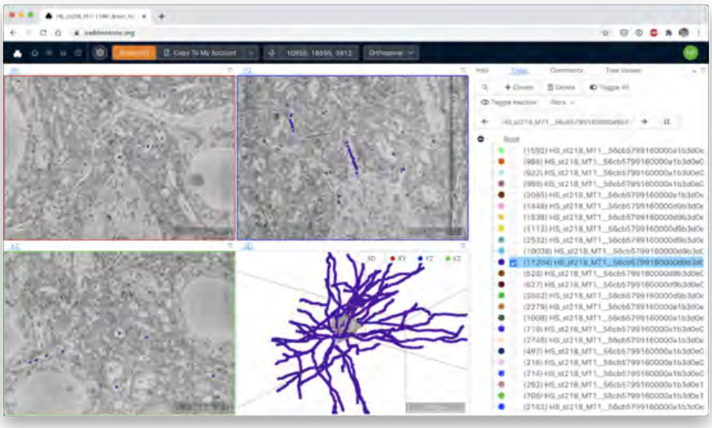
Time Availability

9:00-20:00 CET (UTC +1)

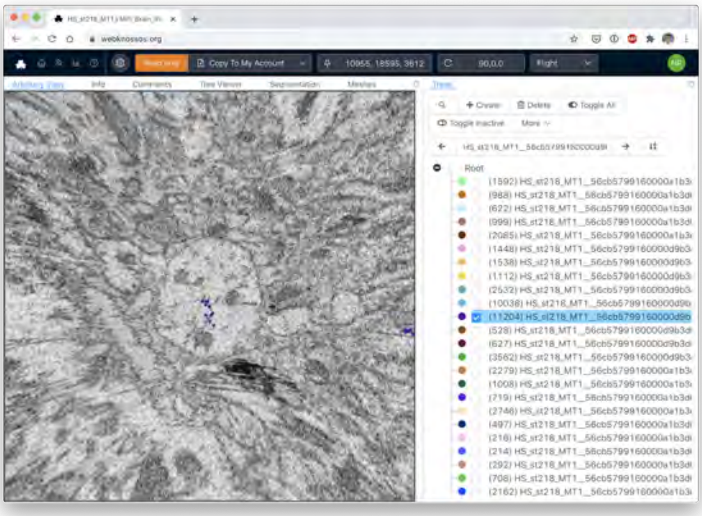
Screenshots



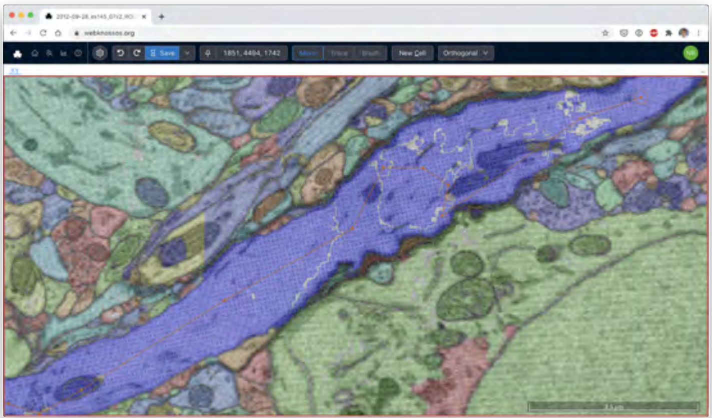
1: webKnososs interface with EM data of Mouse Cortex including a precomputed segmentation and on-demand generated meshes. (Raw EM data by Motta et al. 2019)



2: Neurite skeleton annotation in EM data of Rat Cortex. (Annotations and EM data by Schmidt et al. 2017)



3: Fast neurite skeleton annotation with “Flight Mode”.
(Annotations and EM data by Schmidt et al. 2017)



4: Proof-reading of over-segmented automated segmentation using “Merger Mode”.
(Raw EM data and segmentation by Motta et al. 2019)