

From Images to Knowledge with ImageJ & Friends

virtual conference

Nov 30 - Dec 2, 2020

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

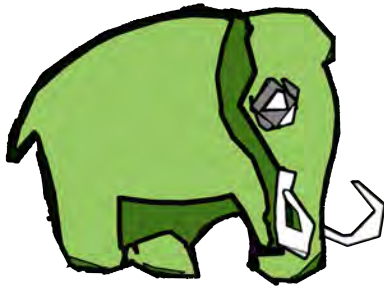


Introducing Mastodon to BioImage Analysts: Interactive and automatic tracking of millions of cells in large images

Tutors: Jean-Yves Tinevez (jean-yves.tinevez@pasteur.fr)

Session 1: 2020-12-01 08:00 UTC – 2020-12-01 12:00 UTC

Session 2: 2020-12-02 17:00 UTC – 2020-12-02 21:00 UTC

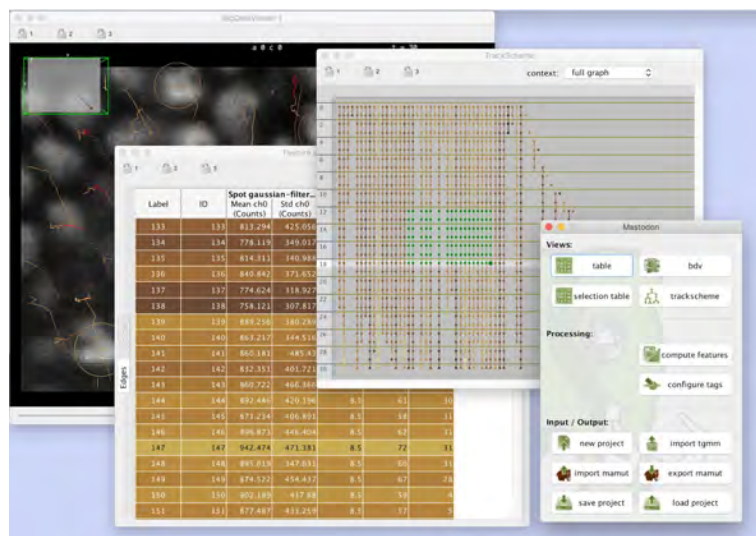
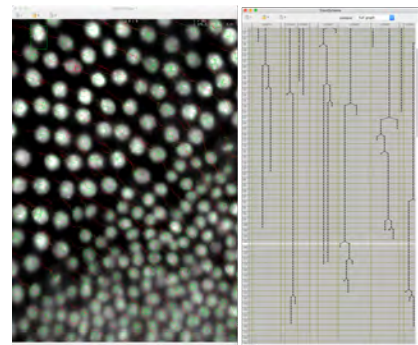


Introducing Mastodon to BiolImage Analysts: Interactive and automatic tracking of millions of cells in large images.

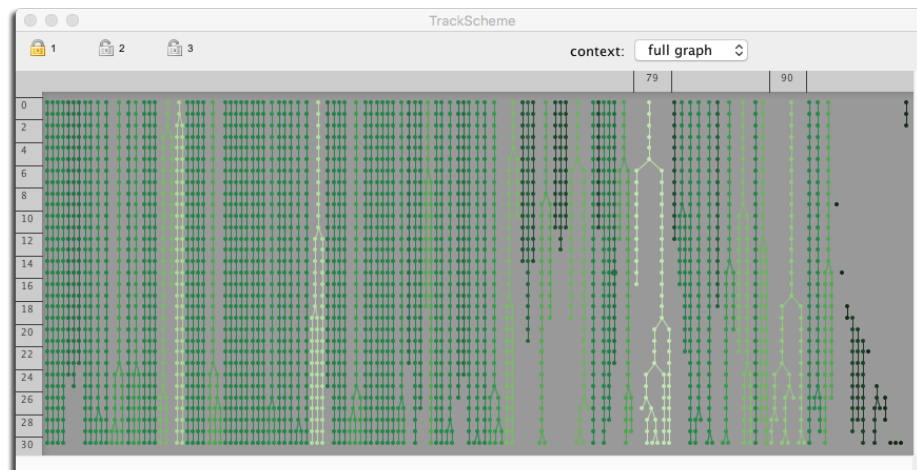


A tutorial for the “From Images to Knowledge with ImageJ & Friends (I2K)” conference. Nov 30-Dec 2, 2020.

Modern Life-Science microscopy technologies allow live sample 3D imaging in toto with high spatial and temporal resolution. The images they generate are 3D over time, possibly multi-channel and multi-view. The computational analysis of these images promises new insights in cellular, developmental and stem cell biology. However, a single image can amount to several terabytes, and in turn, the automated or semi-automated analysis of these images can generate a vast amount of cell and track annotations. The challenges of big data are then met twice: first by dealing with a very large image, and second with generating large annotations from this image. They will make interacting, analyzing and even inspecting the data especially difficult. Mastodon is our effort to provide a tool that can address these challenges.

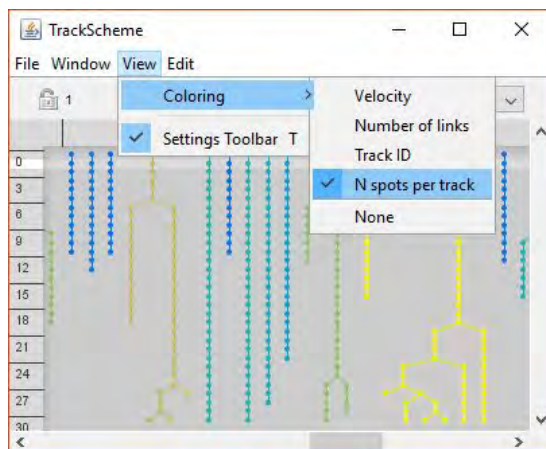


Mastodon is an end-user bioimage analysis tool and a software platform that allows for interactive and automatic cell tracking in large samples. Taking inspiration from TrackMate and MaMuT, it ships technologies that can harness large images and the large amount of cell annotations that can be generated, while offering the responsiveness of a fully interactive interface and the user-friendliness of an end-user tool. Also, because the challenges Mastodon addresses are general, it is also built as an open and extensible platform that developers can reuse to build new tools, or extend with custom plugins that perform analysis, cell detection or cell tracking.



Content.

In this tutorial we will introduce Mastodon usage for the first time. After a brief presentation of the tool we will show how you can use Mastodon for cell tracking, then how to script Mastodon in Jython and finally how to



extend Mastodon with your own Java plugins and analyzers.

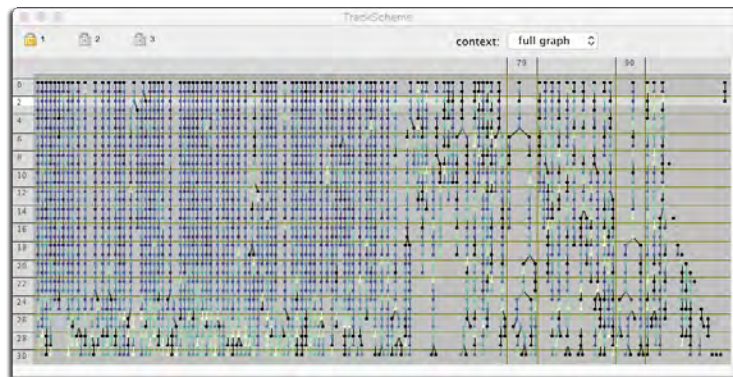
- Getting Mastodon and creating a new project.
- Inspecting multi-view images.
- Automated cell tracking with Mastodon.
- Inspection and manual of cell tracks.
- Basic analysis and result visualization.
- Interoperability. Import and export.
- Scripting Mastodon. Batch analysis.
- Writing and deploying your own track analyser for

Mastodon.

Target audience.

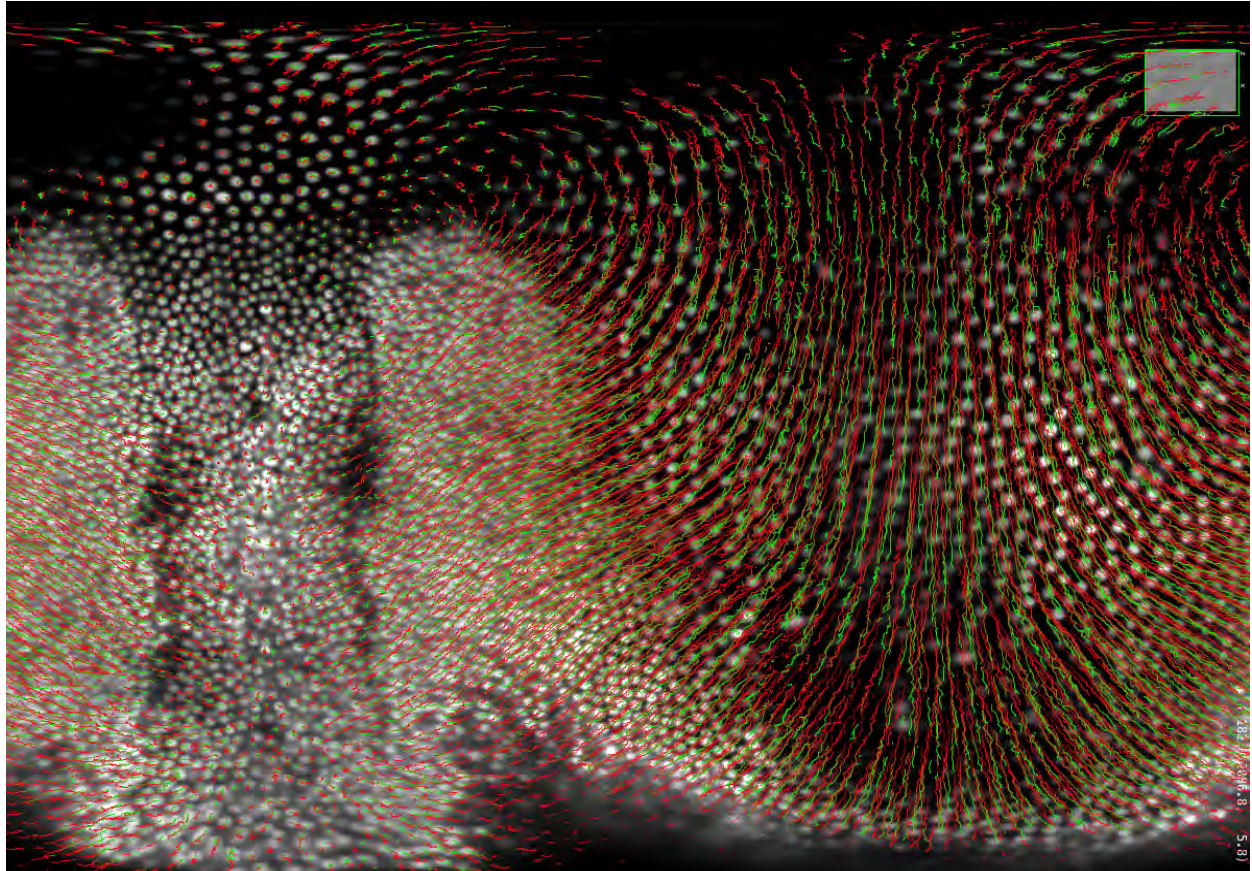
The focus of the I2K conference is on developers. However the largest part of this tutorial is made for end-users. For this we require only an up-to-date version of Fiji (<http://fiji.sc/>).

- The scripting part requires only very very basic knowledge of Python. We also use Fiji for scripting.
- The last part on writing Mastodon extensions in Java will take advantage of a maven template to simplify the demonstration. It requires an attendee to install:
 - The Java JDK 1.8 (<https://www.oracle.com/java/technologies/javase/javase-jdk8-downloads.html>)
 - an IDE (for instance Eclipse <https://www.eclipse.org/downloads/>)
 - Maven (<https://maven.apache.org/install.html>)
 - Git (<https://git-scm.com/book/en/v2/Getting-Started-Installing-Git>)



Warning.

Mastodon is still in beta and under active development. Things will crash. Given each tutorial session lasts 4 hours, the tutors might crash too.



Tutors.

- Jean-Yves Tinevez, IAH, C2RT, Institut Pasteur, Paris.
- Dmitry Ershov, IAH, C2RT, Institut Pasteur, Paris.
- Vladimir Ulman, IT4I, CBIA, Masaryk University, Czech Republic.