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

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Conferences
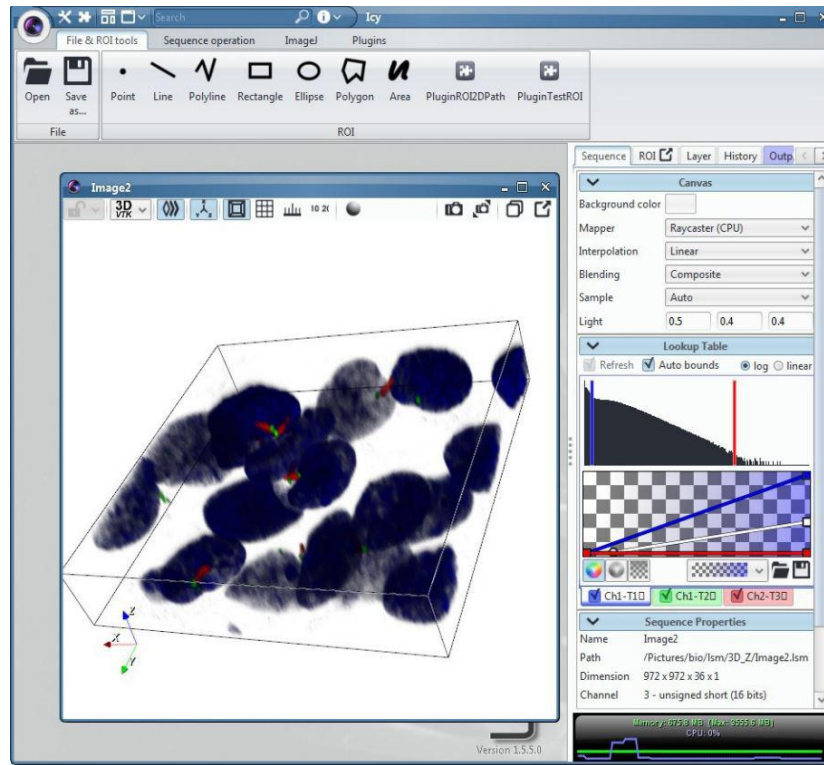
Developing your own Icy plugins

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Session 1: 2020-12-01 12:00 UTC – 2020-12-01 16:00 UTC
Session 2: 2020-12-02 08:00 UTC – 2020-12-02 12:00 UTC

Developing your own Icy plugins

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

Icy[1] is a free open-source bio-image analysis software. Its development started in 2010 and it has been continuously improved along its lifetime and had continuously brought new features to users and developers. Icy is appreciated for its intuitive GUI, its powerful ray-traced 3D visualization and its cutting-edge analysis methods[2][3].

[1] **Icy: an open bioimage informatics platform for extended reproducible research** (2012)
de Chaumont F, Dallongeville S, Chenouard N, Hervé N, Pop S, Provoost T, Meas-Yedid V, Pankajakshan P, Lecomte T, Le Montagner Y, Lagache T, Dufour A, Olivo-Marin JC.
Nat Methods. 9(7):690-6. doi: 10.1038/nmeth.2075

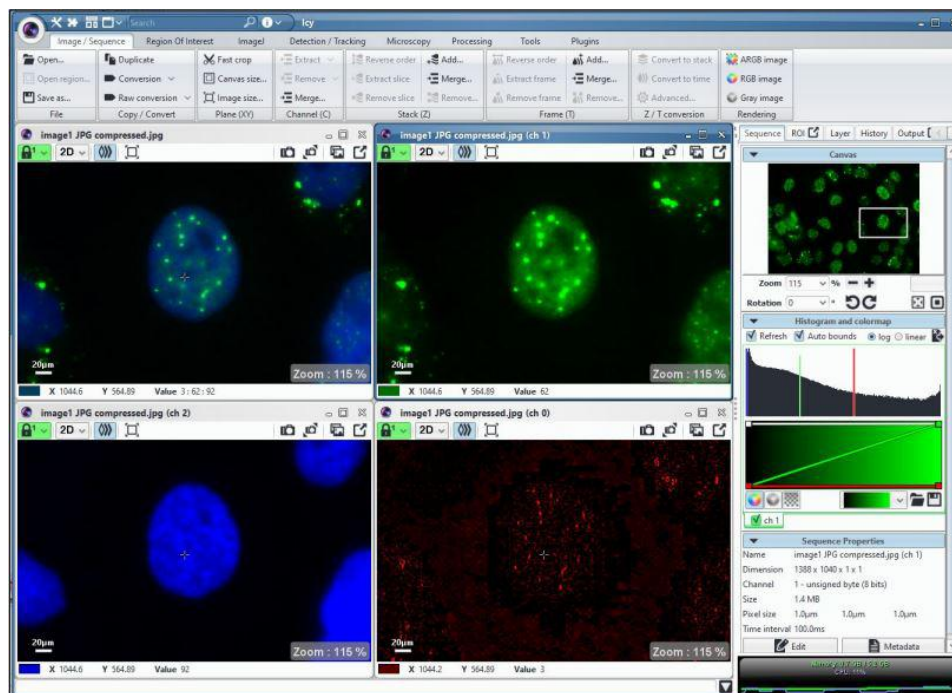[2] **Live Mouse Tracker: real-time behavioral analysis of groups of mice** (2018)
Fabrice de Chaumont, Elodie Ey, Nicolas Torquet, Thibault Lagache, Stephane Dallongeville, Albane Imbert, Thierry Legou, Anne-Marie Le Sourd, Philippe Faure, Thomas Bourgeron, Jean-Christophe Olivo-Marin
bioRxiv 345132; doi: https://doi.org/10.1101/345132

[3] **Mapping molecular assemblies with fluorescence microscopy and object-based spatial statistics** (2018)
Lagache T., Grassart A., Dallongeville S., Faklaris O., Sauvonnet N., Dufour A., Danglot L.,Olivo-Marin J. C.
Nature communications 9(1):698. doi:10.1038/s41467-018-03053-x

A large part of nowdays Research based on imaging requires the development of custom analysis pipelines. As its core, Icy was made to facilitate and accelerate these developments for everyone. Users can adapt and create new algorithms with scripts and with the graphical programming interface called protocols. They offer a rapid and convenient way to assemble several components in a full analysis workflow. All plugins, scripts and protocols can be uploaded on the Icy website: http://icy.bioimageanalysis.org along with documentation to be shared with everybody. Uploaded resources are also directly searchable and downloadable from within the software.

For the development of components, or highly performant and customized workflows, Java plugins are better suited. Plugins are a small piece of Java code, reusing Icy facilities, that plug into the Icy user interface, and can be used as any other Icy components. They offer the power of the Java language to your scientific application while benefiting from the facilities of the Icy API.

Tutorial content

System Requirements: Before the tutorial, please install Java developer version (JDK1.8 minimum, see info on this page: http://icy.bioimageanalysis.org/download/) and an IDE (Eclipse / IntelliJ IDEA / Netbeans). Note that in the tutorial we will mainly use Eclipse.

This tutorial is focused on the development on Icy plugin following good practices. We will first show how to configure the Java development environment using Maven. This is independent of the IDE and participants will be free to use the IDE of their choice. Note that in the tutorial we will mainly use Eclipse.

We will then explain the image data structure in Icy and create a small plugin to access the pixels in the image using our latest feature in Icy, "cursors". More precisely, you will learn how to read an image, process it and create a new image as a result of an analysis. To handle large image data, we will also introduce virtual sequences. Next, we will show how to manipulate Regions Of Interest (both using existing ROIs and creating new ROIs as the result of an analysis). We will also present the concept of Overlay to offer rich information and smooth user interaction. To conclude, we will introduce easy and homogenous graphical interface building using EzPlug and the creation of
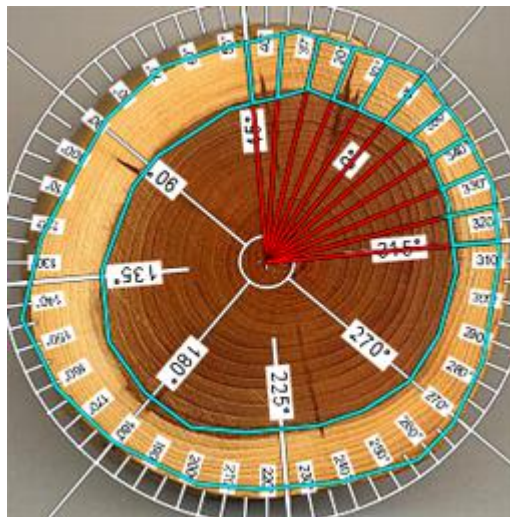
protocols blocks to provide friendly and efficient ways for end-users (non developers) to use your plugins.

At the end of this tutorial, you should be able to create Icy plugins that can perform basic image processing operations on the whole image or part of it and produce different types of results. You'll have several examples of small plugins performing operations, such as maximum intensity projection, mean intensity on a ROI, creation of ROIs from the segmentation using a simple threshold and creation of overlay on the image.

You will be able to enhance your developments through good practices such as using Maven to manage projects, correctly documenting functions and generating documentation for end-users. We will briefly show how to upload your plugin on the Icy website along with end-user documentation.

Target audience

Bioimage analysts with an experience in Java development, for instance development of an ImageJ plugin.

Duration

3-4h

Tutors

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