CW12-Sage-Bioimage Analysis (including ML/DL)-

Title: Bioimage Analysis Software Packages: Our Old Friends in the Age of AI

Proposer/co-presenter: Daniel Sage

Position/Workplace: Research staff in a group (any level), Center for Imaging, Ecole Polytechnique Fédérale de Lausanne (EPFL)

Workshop Abstract.

Bioimage Analysis Software Packages: Our Old Friends in the Age of AI

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Over the last decades, quantitative bioimaging has evolved with a rich ecosystem of open-source, community-driven software packages. From the iconic ImageJ to platforms such as Fiji, CellProfiler, QuPath, Icy, Ilastik, and napari, these software packages have shaped the field, becoming familiar companions for biologists, microscopists, and developers, while supporting a wide range of imaging workflows, powerful scripts, analysis tools, and training practices.

However, as image analysis has rapidly shifted toward AI and deep learning, several tasks are now more effectively addressed by dedicated deep-learning models. In this context, some of our old friends appear to be left out of the AI game. This is particularly true for user-friendly, easy-to-install, Java-based platforms such as Fiji and Icy, whose access to powerful Python-centric deep-learning models remains very limited.

In this workshop, we present our recent work bridging Java-based platforms with modern deep-learning models through JDLL and Appose, an efficient connector between Java and Python. Through hands-on exercises, participants will (1) run pretrained segmentation models, including StarDist, Cellpose, and models from the BioImage Model Zoo, directly in Fiji or Icy using DeepImageJ/DeepIcy; (2) accelerate the annotation of biological objects using the promptable Segment Anything Model through SAMJ; and (3) invoke deep-learning predictions from a macro as part of an image-analysis workflow. We will also demonstrate how to fine-tune a YOLO detector on biological images.

The workshop will discuss the opportunities, challenges, limitations, ethical questions, and risks associated with AI-based approaches in bioimage analysis.

Material: https://go.epfl.ch/spaom2026

References:

E. Gómez-de-Mariscal et al., DeepImageJ: A User-Friendly Environment to Run Deep Learning Models in ImageJ, Nature Methods, 2021.

C. García-López-de-Haro et al., SAMJ: Fast Image Annotation on ImageJ/Fiji via Segment Anything Model, Nature Communications, 2026

C. Fuster-Barceló et al., Bridging the gap: Integrating cutting-edge techniques into biological imaging with deepImageJ, Biological Imaging, Cambridge University Press, 2024.

W. Ouyang et al., BioImage Model Zoo: A Community-Driven Resource for Accessible Deep Learning in BioImage Analysis, bioRxiv 2022.06.07.495102, 2022.

C. García-López-de-Haro et al., JDLL: A Library to Run Deep Learning Models on Java Bioimage Informatics Platforms, Nature Methods, January 2024.

D. Sage, A. Badoual, Image Processing and Image Analysis in Microscopy, Photonic Imaging for Biology, Edition Wiley, 2025.

Cunha, E. Latron, S. Bauer, D. Sage, J. Griffié, Machine Learning in Microscopy—Insights, Opportunities and Challenges, Journal of Cell Science, 2024.

How will the Workshop run?

The workshop will combine short conceptual introductions, live demonstrations, and hands-on exercises. The training methodology will be practical and progressive: each topic will start with a brief explanation on a AI-based tool, followed by a guided exercise in Fiji and/or Icy. Participants will be encouraged to reproduce the examples on their own laptops, inspect the intermediate results, and discuss the outcome.

We will provide the teaching material in advance, including the instructions to install software packages (FIJI and/or ICY, plugins, DL models)

- Introduction: transition from classical bioimage analysis to AI-workflows; role of Fiji and/or Icy; access to Python-centric models.

- Running deep-learning tools: prediction with StarDist, Cellpose, and YOLO in Fiji and/or Icy.

- BioImage Model Zoo: running pretrained models with DeepImageJ and/or DeepIcy; evaluation and discussion of prediction quality.

- Model fine-tuning: fine-tuning a YOLO model for a bioimage-analysis task; discussion of annotations, training data, validation, and overfitting.

- AI-assisted annotation: accelerating annotation of biological objects with SAM through SAMJ; comparison of prompts and annotation quality.

- Demonstration - Workflow integration: incorporating AI predictions into macros, scripts, and complete image-analysis workflows as standard commands.

- Conclusion: discussion of opportunities, challenges, limitations, ethical questions, and risks of AI usage in bioscience.

Workshop Output:

Shareables: participants will take away electronic material, Shareables: some/all will be open-access permanently (DOI, GitHub, etc...), Shareables: participants will take away the fruit of their work hands-on, Output to SPAOM (optional): Before the end of SPAOM2026, a workshop report/output will be made available to SPAOM2026 participants.

List of equipment you bring:

Electrical plugs (1 per participant) and wifi for laptops, large screen for the speakers

List of equipment needed on site:

Electrical plugs and wifi for laptops, large screen

Samples considerations:

No sample

Co-presenter (if mentioned)

Carlos García-López-de-Haro."This community workshop is part of the activities of AIM-Net (RED2024-153844-T, funded by MICIU/AEI/10.13039/501100011033).”