

Abstract

High-performance computers (HPC) are essential for bioimage analysis, however the barrier to entry can be high. This project aims to simplify access to bioimage analysis tools and deep learning models on local HPC clusters, enabling frictionless access to software and large computation.

Inspired by the Bioimage ANalysis Desktop (BAND) and ZeroCostDL4Mic, we developed lightweight bash scripts to deploy image analysis tools such as Fiji, QuPath, Ilastik, Cellpose, CellProfiler, and Napari in user-specified directories. Unlike containers, this solution allows users to save software changes, such as installed plugins, across sessions. We also created custom module files for deep learning packages like StarDist, SAM, and micro-SAM for easy environment loading. Finally, we developed Jupyter Notebooks for data preparation, model training, and benchmarking. These have been deployed on Harvard Medical School's (HMS) HPC cluster, Orchestra 2 (O2), which uses Open OnDemand (OOD) for an interactive interface.

While specific to HMS, this approach can be easily adapted to most HPC clusters. We aim to share our findings with the broader bioimage analysis community and discuss alternative or parallel approaches.

Link: <https://hms-iac.github.io/Bioimage-Analysis-on-O2/>

What problem does this project address?

The project aims to simplify access to bioimage analysis tools and deep learning models at Harvard Medical School's institutional cluster Orchestra 2 (O2) by reducing the complexities of installation.

What do we propose?

- Interactive tools and GUI:** Executable bash scripts in shared folders allow users to install bioimage analysis tools, with a .desktop file created for easy, persistent access, enabling software to be launched like a local installation.
- Deep learning environments:** Pre-configured environments with necessary dependencies are stored in shared directories, with Linux modules allowing users to load and integrate deep learning models seamlessly.
- Jupyter notebooks:** Custom Jupyter Notebooks manage data loading, preprocessing, training, and testing, generating detailed reports on model performance for sharing or publication.

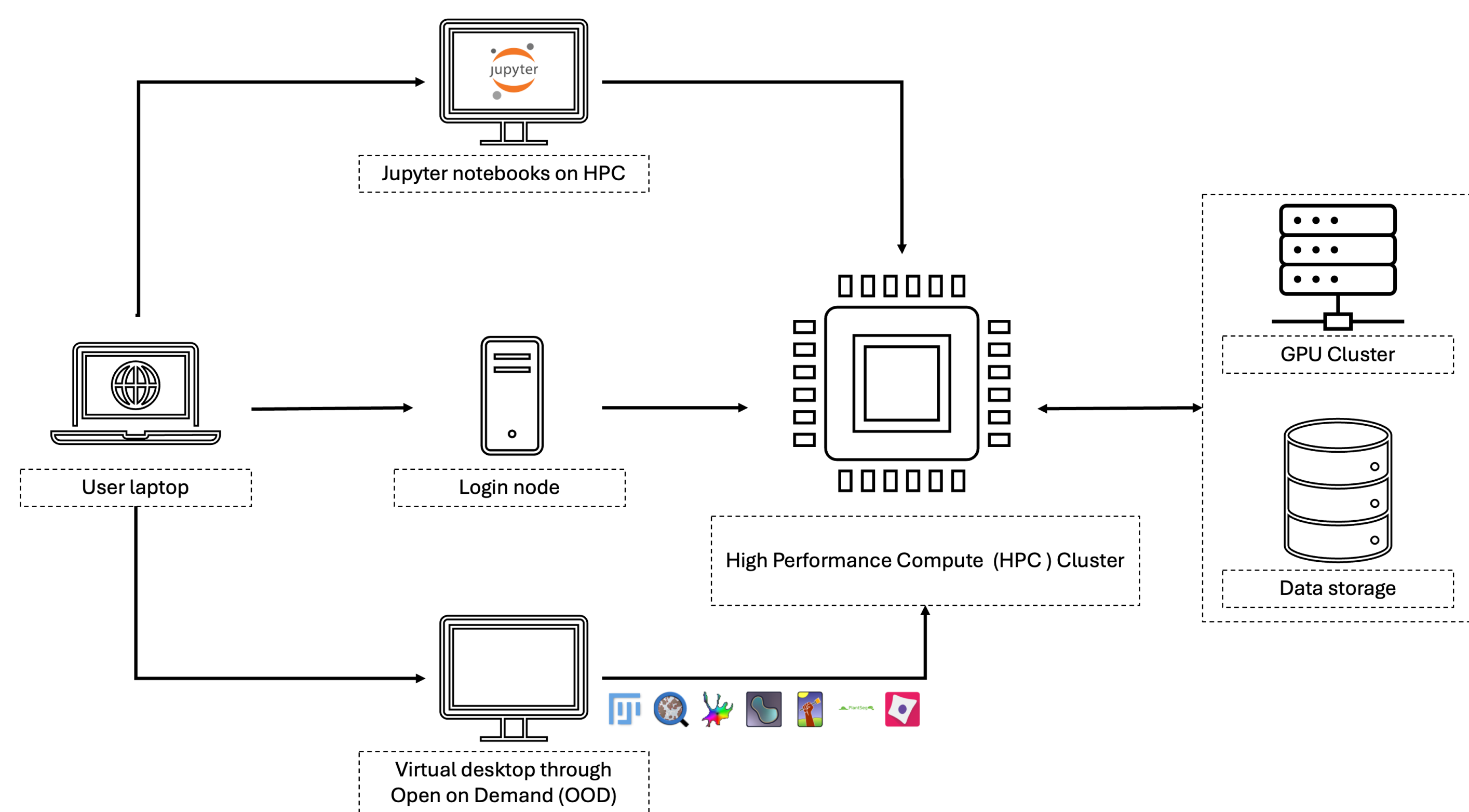


Figure 1. Diagram illustrating user access to bioimage analysis tools on HPC resources.

The proposed solution was made available on Harvard Medical School's (HMS) Orchestra 2 (O2) cluster which is equipped with Open OnDemand (OOD) that enables access to computing resources through a desktop interface or coding environments like Jupyter Notebook and Visual Studio Code.

Advantages

- Direct access to data:** Users can easily access large datasets stored on the HPC cluster without the need for data transfers.
- Easy installation of software:** With pre-configured bash scripts, users can easily install essential bioimage analysis tools and deep learning software in their personal HPC accounts, eliminating the complexities often associated with manual installation and testing.
- Standardized model training and testing environments:** Custom-built environments ensure that all users have access to the same software packages and dependencies, ensuring reproducible workflow.
- Quick access to state-of-the-art deep learning models:** Ready-to-use deep learning modules, including popular models like StarDist and Segment Anything (SAM), allowing users to load and apply state-of-the-art models without needing to handle complex setup processes.
- Session persistence with installed plugins:** Unlike containerized solutions, this setup retains all user-installed plugins and configurations across different sessions, providing a consistent and uninterrupted working environment.

Support and Funding

Currently Available Tools



Figure 2. Overview of currently available bioimage analysis (BIA) tools. From left to right: Cellpose3[12] for cell segmentation, CellProfiler[11](4.3.7) for high-content screening, Fiji[8] for general image analysis, ilastik [3] (1.4.0.post1) for image segmentation and annotation, napari[5] (0.4.19) for interactive multi-dimensional image analysis, plantseg[14] for plant tissue segmentation, and QuPath [2] (v0.5.1) for whole slide image analysis.

Available deep learning packages:

- StarDist [9]
- Segment Anything [4]
- Micro-SAM [1]
- CellPose [12]
- Ilastik [3]

Available notebooks:

- U-Net [7]
- VGG16 [10]
- Segmentation evaluation

Example

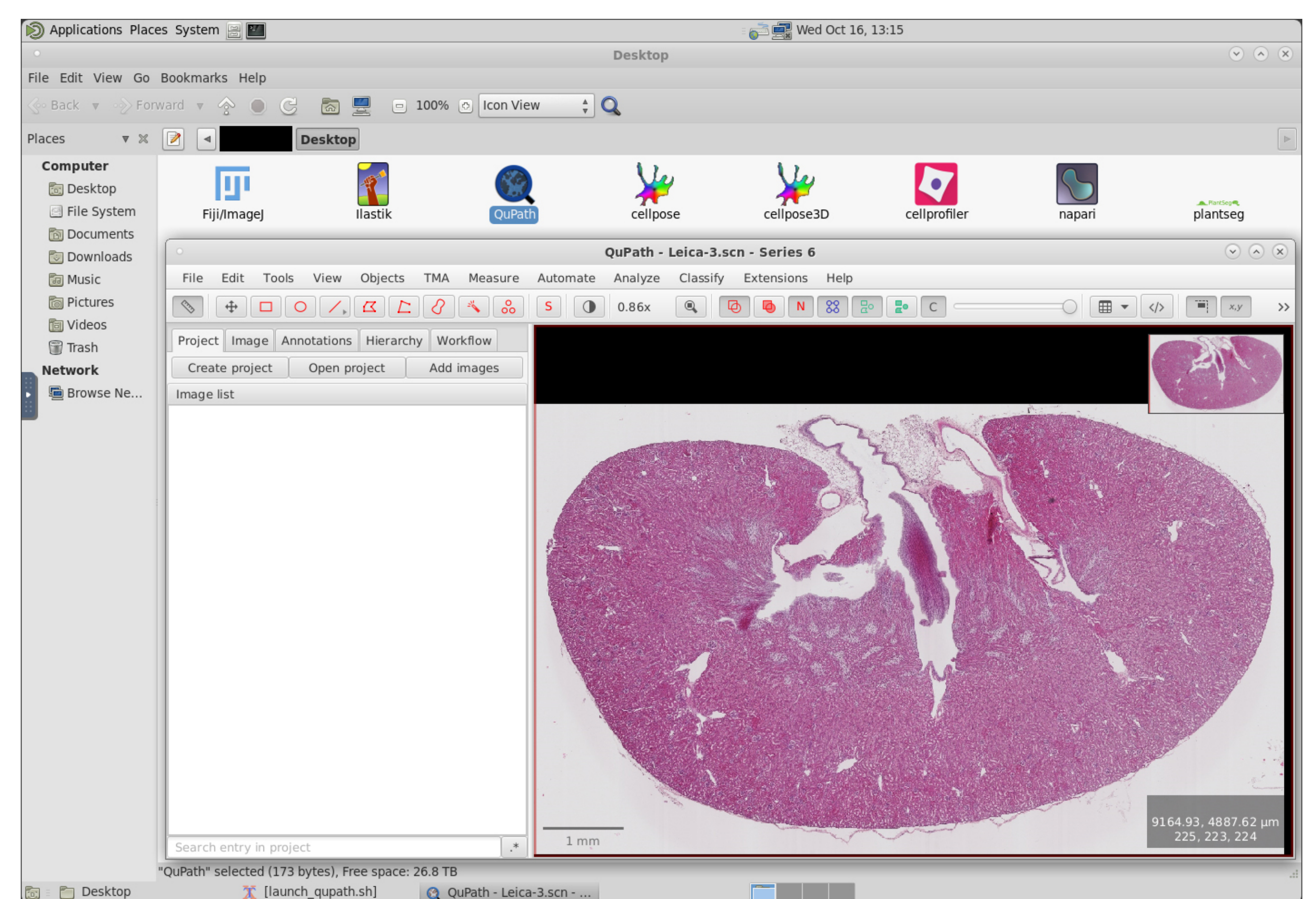
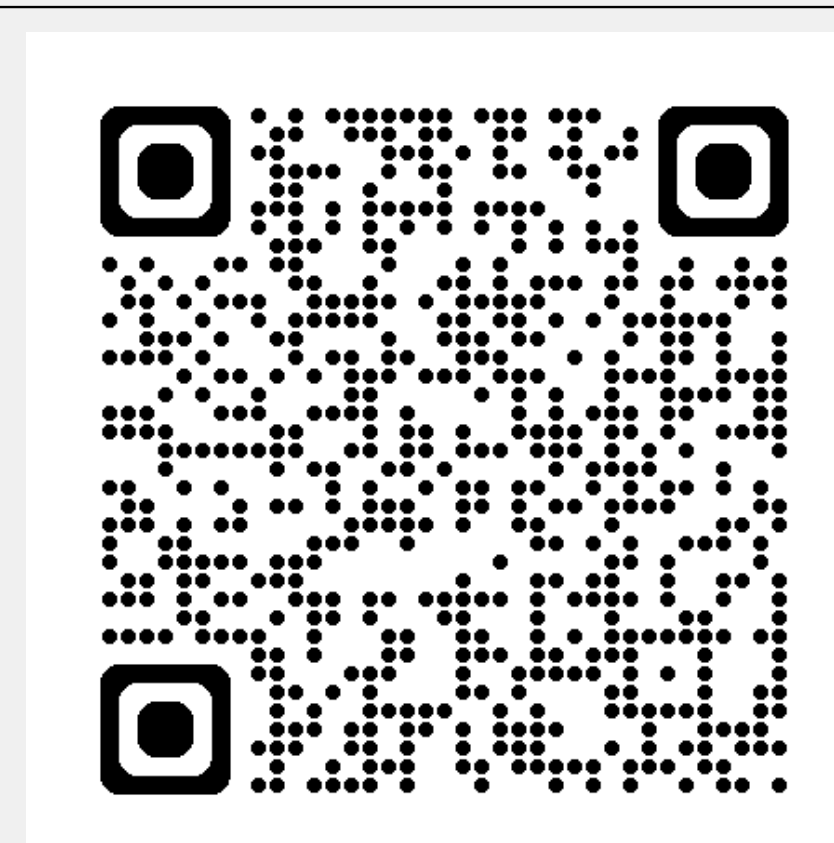


Figure 3. Screen capture of QuPath running on O2

Motivation and Acknowledgement

- Bioimage Analysis Desktop (BAND)
- Biolmage Model Zoo [6]
- Zero Cost Deep Learning for Microscopy [13]

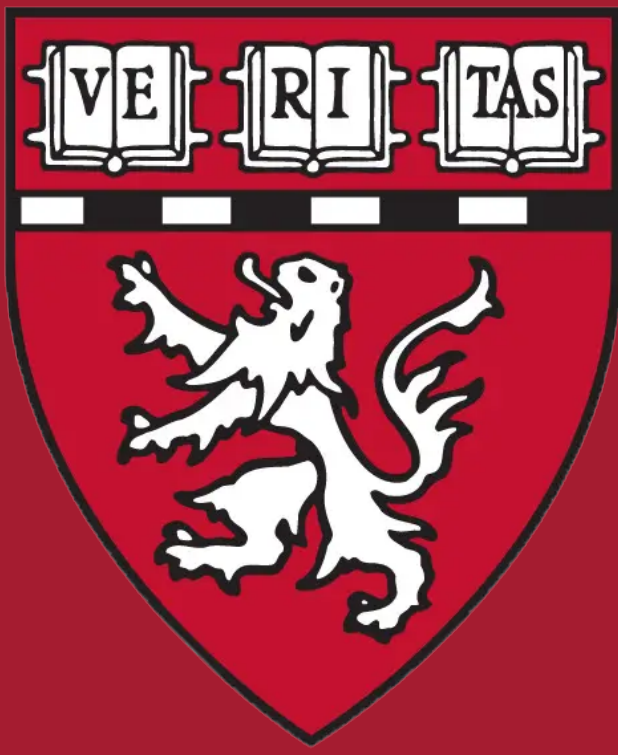
Scan for digital poster and full list of references





Enabling Access to Bioimage Analysis Tools on a University Cluster

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