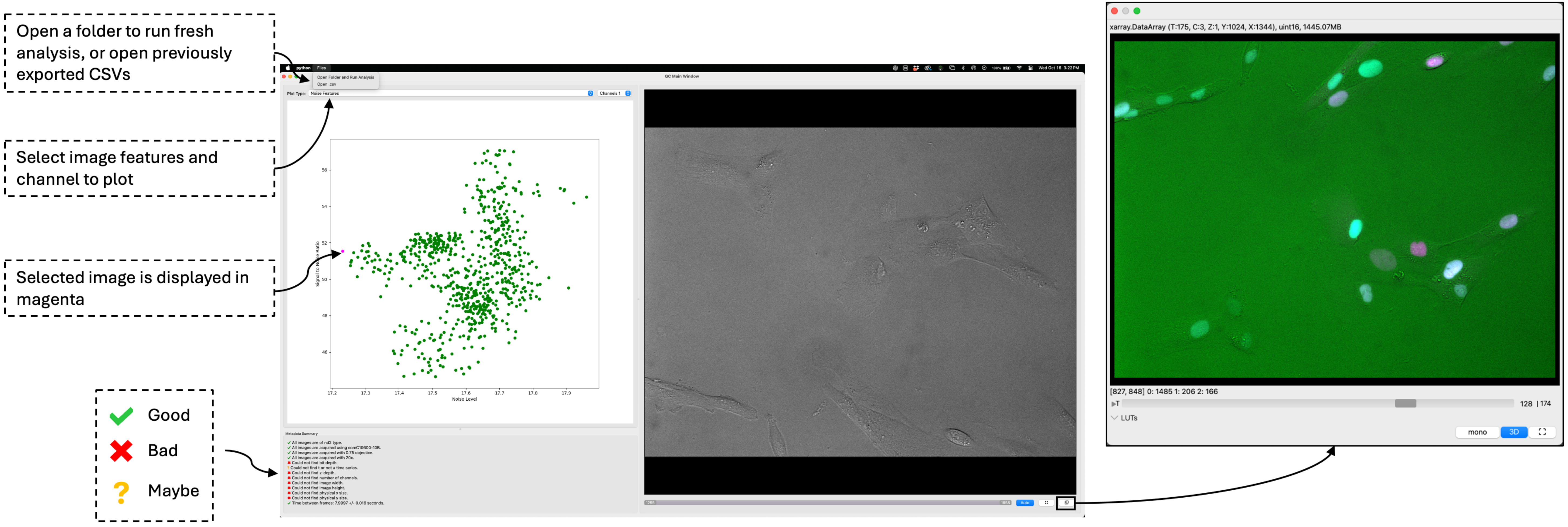


## Abstract

Image exploration and quality control (QC) are essential first steps in any bioimage analysis task. Traditionally, researchers manually inspect randomly sampled images, examine metadata, and extract image features to investigate the data. This process ensures a deeper understanding of the image data and allows for informed algorithm development. However, it often requires multiple open-source tools and/or custom code.

Here we propose a novel Python application designed to streamline image exploration and quality control in bioimage analysis. Our application supports multiple image formats, extracts metadata to ensure consistency, and performs comprehensive feature extraction. By incorporating anomaly detection, it identifies issues such as focussing, illumination artifacts, chromatic aberration, over/under exposure, and dynamic range utilization. Additionally, our tool integrates a lightweight n-dimensional image viewer for efficient visualization of images.

By automating the initial QC steps, our application reduces the need for extensive manual inspection, facilitating more structured and comprehensive image analysis which ultimately enhances the accuracy and reproducibility of experimental results in bioimage analysis.



## What problem does this project address?

This project addresses the problem of manually inspecting bioimages for quality control, which is time-consuming and often fragmented into multiple tools for data viewing, meta-data exploration, and image quality check.

## How do we aim to solve the problem?

We developed an easy-to-use tool that automates the early stages of image analysis by simplifying metadata and feature extraction. It helps detect issues like focus problems, illumination artifacts, noise, and exposure errors. To use the tool, users only need to specify the folder containing the images. The tool then automatically extracts metadata and image features, storing them output locally as CSV files. It also visualizes these features in a plot, summarizes the metadata, checks for consistency. Users can further inspect individual image slices or the entire image stack using the integrated viewer.

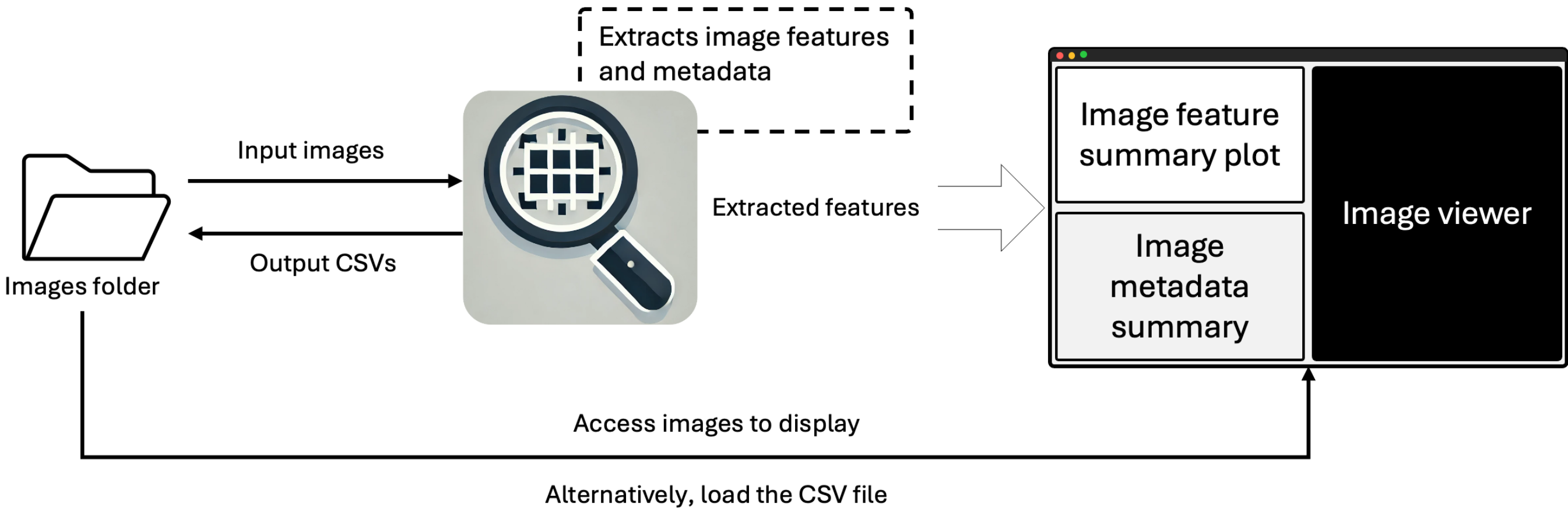


Figure 1. Caption

## Scan for digital poster and full list of references

logos/qrcode\_poster.png

logos/qrcode\_poster.png

## Currently Installable Software

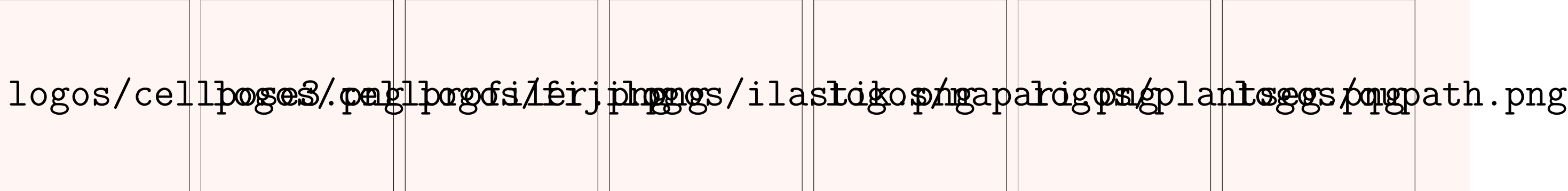


Figure 2. Overview of currently available bioimage analysis (BIA) tools. From left to right: Cellpose[11] for cell segmentation, CellProfiler[10](4.3.7) for high-content screening, Fiji[7] for general image analysis, ilastik (1.4.0.post1)[3] for image segmentation and annotation, napari[5] (0.4.19) for interactive multi-dimensional image analysis, plantseg[12] for plant tissue segmentation, and QuPath (v0.5.1)[2] for whole slide image analysis.

### Available deep learning packages:

1. StarDist [8]
2. Segment Anything [4]
3. Micro-SAM [1]
4. CellPose [11]
5. Ilastik [3]

### Available notebooks:

1. U-Net [6]
2. VGG16 [9]
3. Segmentation evaluation

## Current limitation

The current version only supports .nd2 files, however, we plan on extending it to all bio-formats.

## Support and Funding



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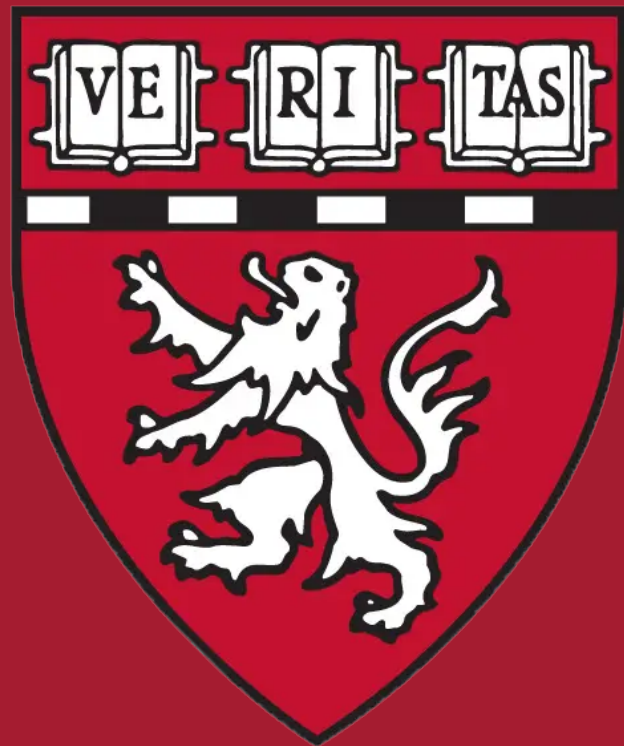




# Pre-Processing Quality Control and Image Exploration for Bioimage Analysis: A Novel Python Application

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## References

[1] Anwai Archit, Sushmita Nair, Nabeel Khalid, Paul Hilt, Vikas Rajashekar, Marei Freitag, Sagnik Gupta, Andreas Dengel, Sheraz Ahmed, and Constantin Pape. Segment anything for microscopy. *bioRxiv*, pages 2023–08, 2023.

[2] Peter Bankhead, Maurice B Loughrey, José A Fernández, Yvonne Dombrowski, Darragh G McArt, Philip D Dunne, Stephen McQuaid, Ronan T Gray, Liam J Murray, Helen G Coleman, et al. Qupath: Open source software for digital pathology image analysis. *Scientific reports*, 7(1):1–7, 2017.

[3] Stuart Berg, Dominik Kutra, Thorben Kroeger, Christoph N Straehle, Bernhard X Kausler, Carsten Haubold, Martin Schiegg, Janez Ales, Thorsten Beier, Markus Rudy, et al. Ilastik: interactive machine learning for (bio) image analysis. *Nature methods*, 16(12):1226–1232, 2019.

[4] Alexander Kirillov, Eric Mintun, Nikhila Ravi, Hanzi Mao, Chloe Rolland, Laura Gustafson, Tete Xiao, Spencer Whitehead, Alexander C Berg, Wan-Yen Lo, et al. Segment anything. In *Proceedings of the IEEE/CVF International Conference on Computer Vision*, pages 4015–4026, 2023.

[5] How Does napari Work. napari: A multidimensional image viewer for python a guide to some of the key concepts of napari.

[6] Olaf Ronneberger, Philipp Fischer, and Thomas Brox. U-net: Convolutional networks for biomedical image segmentation. In *Medical image computing and computer-assisted intervention–MICCAI 2015: 18th international conference, Munich, Germany, October 5-9, 2015, proceedings, part III 18*, pages 234–241. Springer, 2015.

[7] Johannes Schindelin, Ignacio Arganda-Carreras, Erwin Frise, Verena Kaynig, Mark Longair, Tobias Pietzsch, Stephan Preibisch, Curtis Rueden, Stephan Saalfeld, Benjamin Schmid, et al. Fiji: an open-source platform for biological-image analysis. *Nature methods*, 9(7):676–682, 2012.

[8] Uwe Schmidt, Martin Weigert, Coleman Broaddus, and Gene Myers. Cell detection with star-convex polygons. In *Medical Image Computing and Computer Assisted Intervention–MICCAI 2018: 21st International Conference, Granada, Spain, September 16-20, 2018, Proceedings, Part II 11*, pages 265–273. Springer, 2018.

[9] Karen Simonyan and Andrew Zisserman. Very deep convolutional networks for large-scale image recognition. *arXiv preprint arXiv:1409.1556*, 2014.

[10] David R Stirling, Madison J Swain-Bowden, Alice M Lucas, Anne E Carpenter, Beth A Cimini, and Allen Goodman. Cellprofiler 4: improvements in speed, utility and usability. *BMC bioinformatics*, 22:1–11, 2021.

[11] Carsen Stringer and Marius Pachitariu. Cellpose3: one-click image restoration for improved cellular segmentation. *bioRxiv*, pages 2024–02, 2024.

[12] Adrian Wolny, Lorenzo Cerrone, Athul Vijayan, Rachele Tofanelli, Amaya Vilches Barro, Marion Louveaux, Christian Wenzl, Sören Strauss, David Wilson-Sánchez, Rena Lymbouridou, et al. Accurate and versatile 3d segmentation of plant tissues at cellular resolution. *Elife*, 9:e57613, 2020.