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

Ranit Karmakar, Federico M. Gasparoli, Simon Nørrelykke

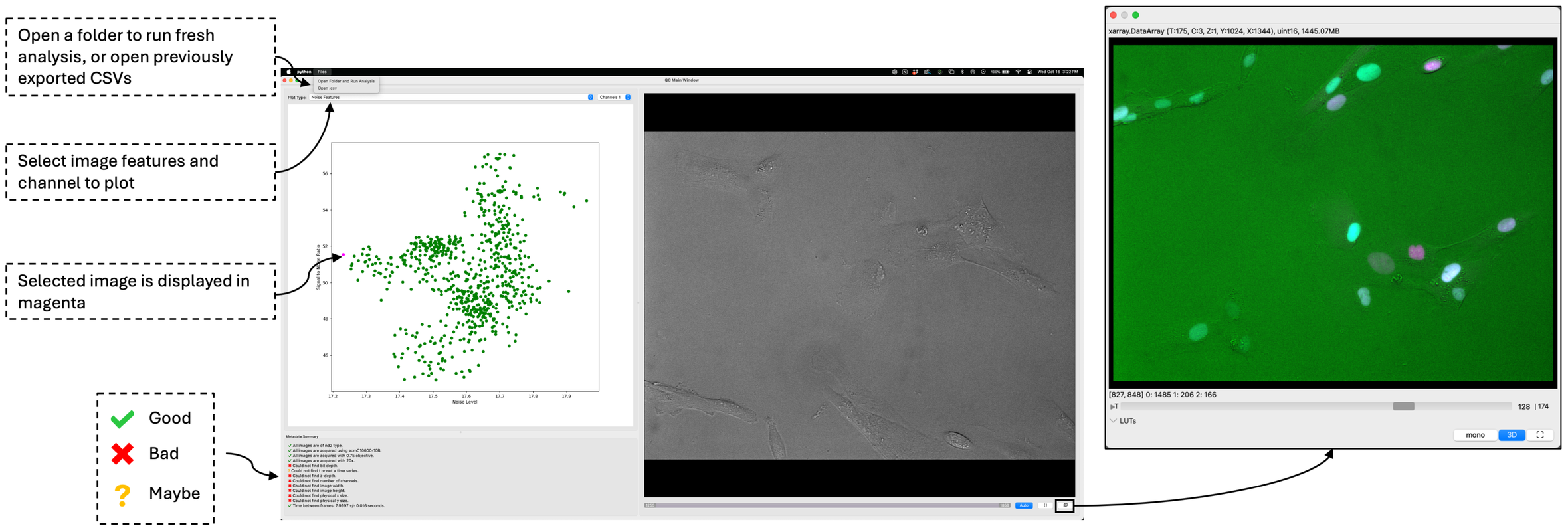
Image Analysis Collaboratory, Harvard Medical School

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, metadata 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.

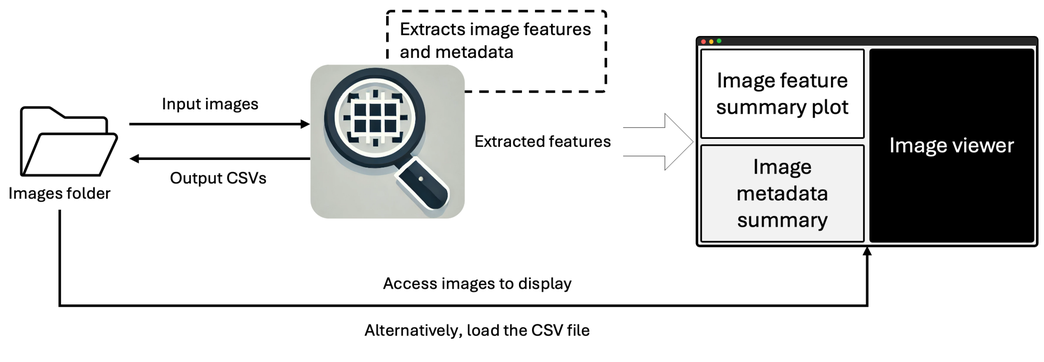


Figure 1. Workflow for image exploration and quality control using the proposed tool.

Method

Once the user specifies the folder containing the images, the tool extracts metadata using the bioio[1] package. The extracted metadata details are summarized in Table 1 below.

Table 1. Brief summary of extracted metadata.

Metadata			
Instrument	Image	Channel	Plane
Instrument name, lens objective, magnification etc.	Image dimension, dimension order, bit-depth etc.	Channel names, wavelength etc.	Pixel size, time delta, x-y-z- position etc.

In addition, image-level features are extracted from each image plane, as summarized in Table 2

Table 2. Brief summary of the extracted image features.

Image features			
Intensity	Noise	Sharpness	Texture
First order statistics, dynamic range, skewness, kurtosis etc.	Signal to noise ratio, noise estimation etc.	Variance of laplacian, Fourier spectrum etc.	GLCM LBP etc.

Metadata processing: After extracting the metadata, the tool checks for consistency between experiments. In the summary window, the metadata is displayed, and any inconsistencies or missing information are flagged for review.

Image feature processing: The extracted image features are displayed in a scatter plot, where each point represents a single grayscale slice of an image. Dimension reduction techniques are applied to plot the data in 2D.

Displaying images: Users can click on individual points in the scatter plot to view the corresponding image slices. To view the entire image stack, users can click the button in the bottom-right corner to launch the ndv[2] viewer.

Limitation and Future Scope

The current version only supports .nd2 files. However, plans for future improvements include expanding support to other bioio[1] formats and incorporating unsupervised methods to automatically identify and flag inconsistencies in image quality.

Scan me

Digital poster and full list of references.

Link to the GitHub repository.

Support and Funding

HARVARD MEDICAL SCHOOL

CENTER FOR COMPUTATIONAL BIOMEDICINE
HARVARD MEDICAL SCHOOL

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

Ranit Karmakar, Federico M. Gasparoli, Simon Nørrelykke

Image Analysis Collaboratory, Harvard Medical School

References

[1] Eva Maxfield Brown, Dan Toloudis, Jamie Sherman, Madison Swain-Bowden, Talley Lambert, Sean Meharry, Brian Whitney, and BioIO Contributors.
Bioio: Image reading, metadata conversion, and image writing for microscopy images in pure python, 2023.

[2] Talley Lambert.
ndv, 2024.