EDA Presentation - Cellular State Image Analysis

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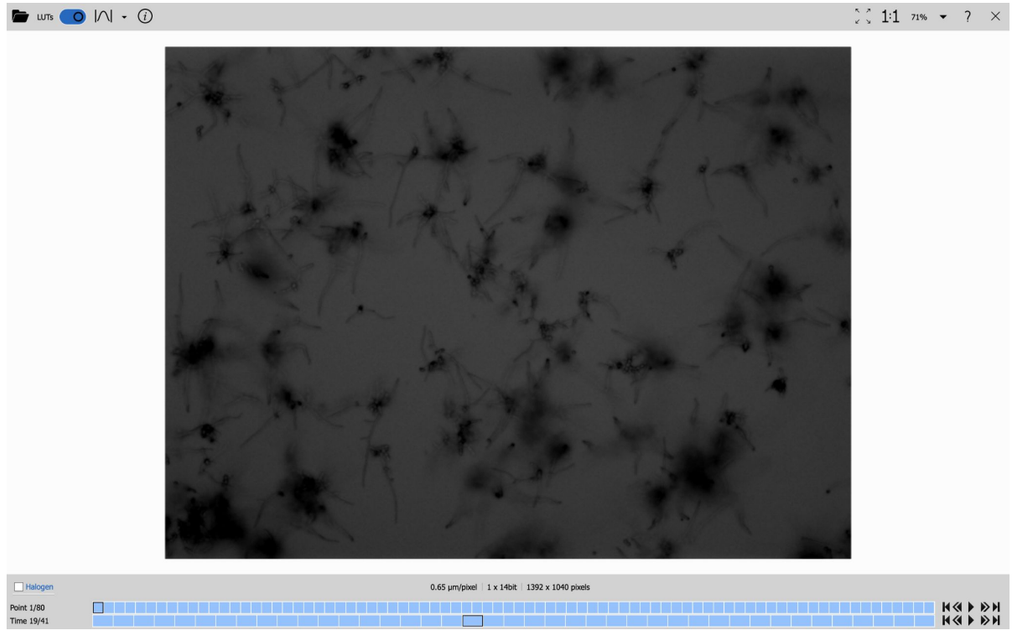
Data

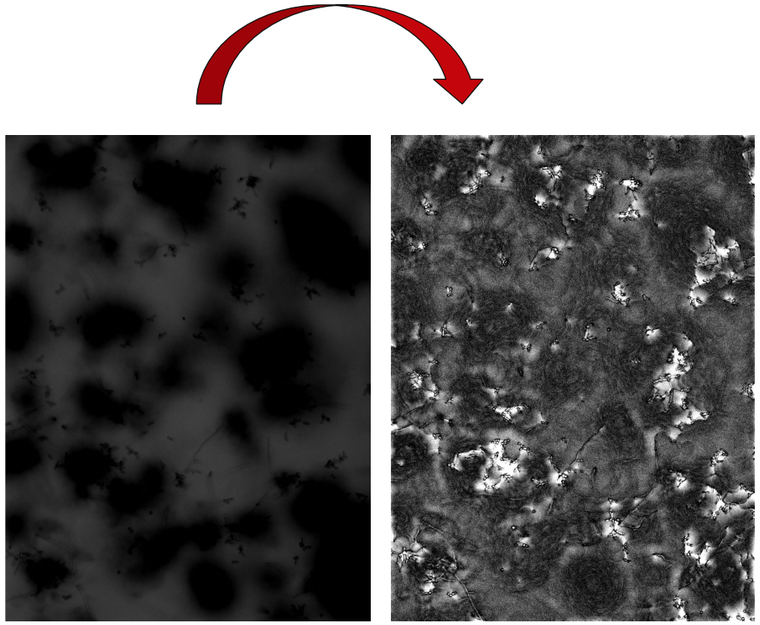
- Nd2 files with 20 hours of image data taken from a Nikon microscope
- Data was also provided through .tif and .xml files



Cellular progression

- Planktonic cells
- Clump dispersed
- Pseudohyphae
- Hyphae
- Biofilm

Exploratory Data Analysis

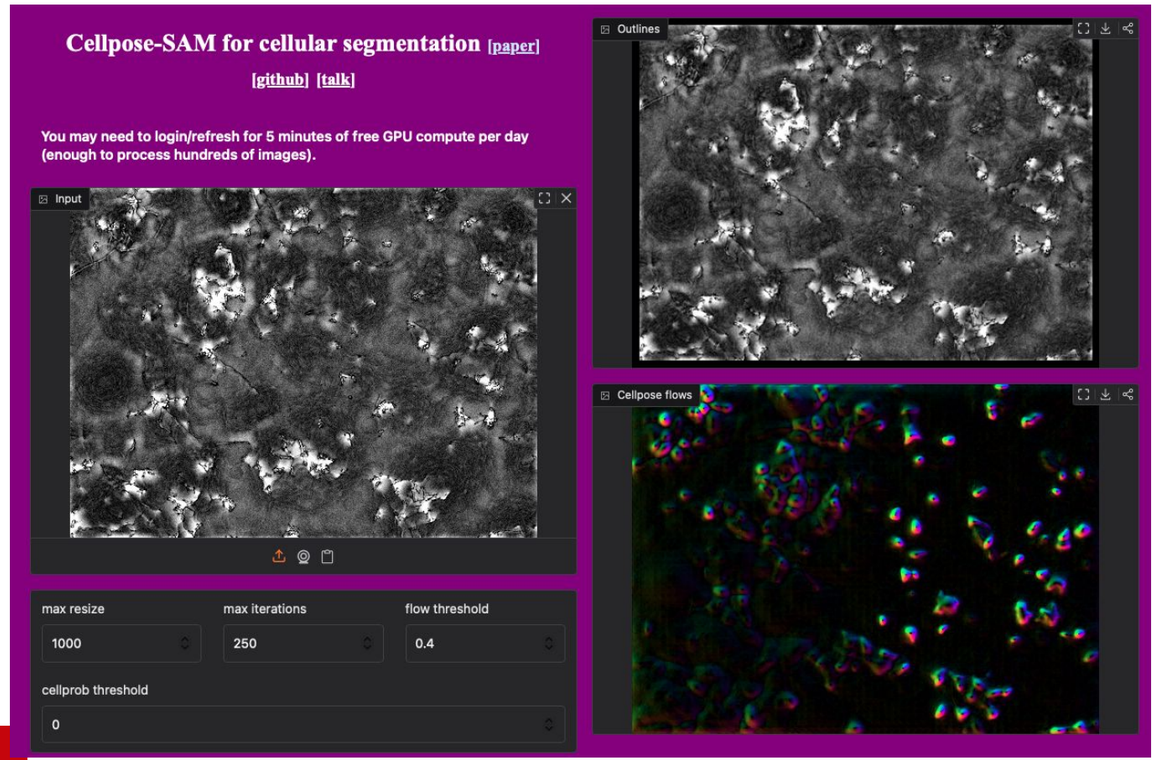


Cleaning & Pre-Processing

1. Loaded Nd2 files into a viewer and converted to tiff files
2. Pre-processing: noise reduction, gaussian smoothing, rescaling, and other Scikit packages

Helper packages

- Nd2File
- OpenCV
- Matplotlib
- Scikit-Learn



Insights & Challenges

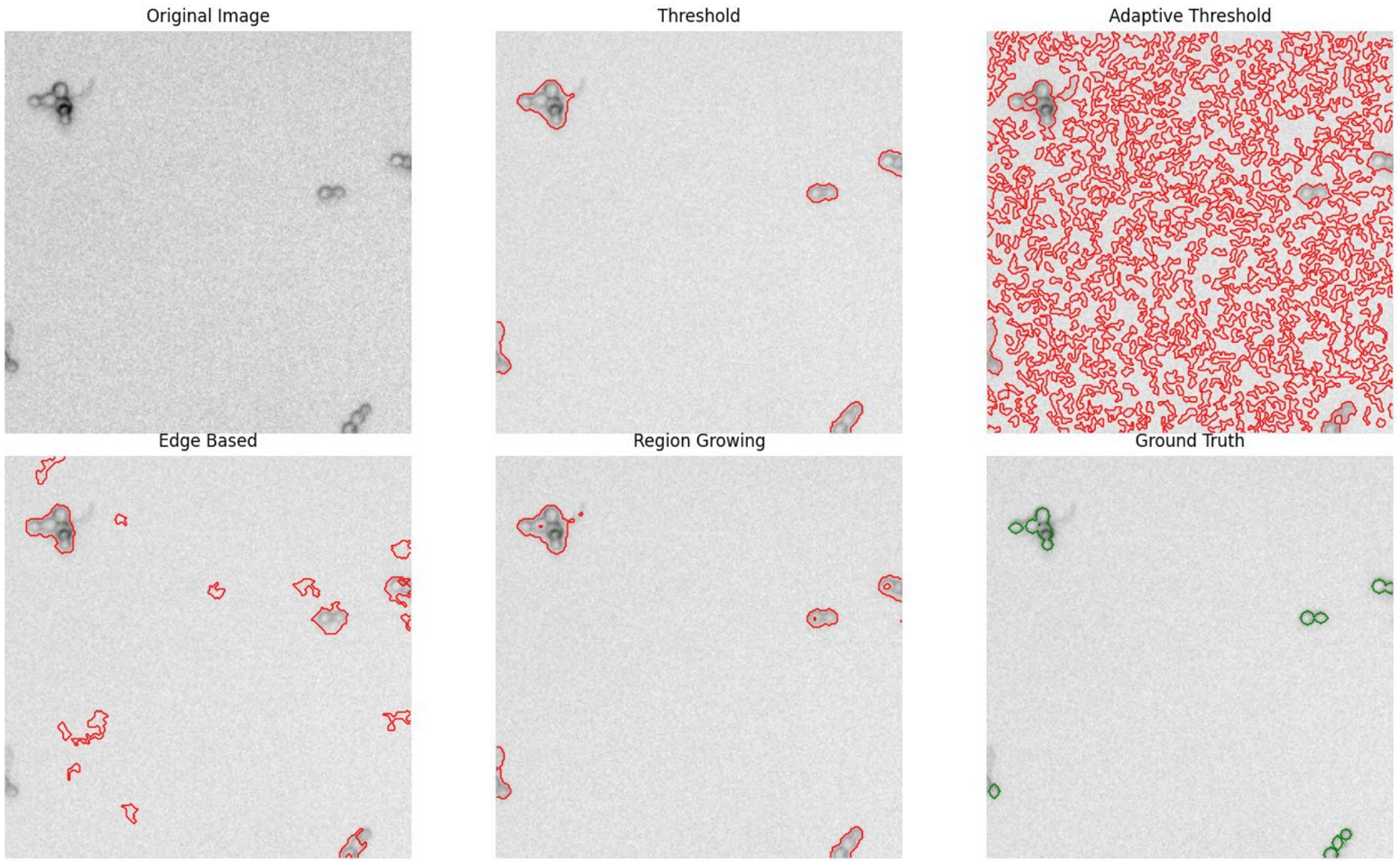
- After doing research and comparing current existing model performance, they tend to work with highly magnified cells.

- We faced challenges choosing the combination of image pre-processing techniques and segmentation models for different frames in the test .tif file.

- Choosing resolution/size of cropped frames to keep standardization

Baseline Model

- Edge based segmentation had the most consistent F1-score of around 0.4.
- There were issues with the granularity of the image which interfered with the segmentation
- Some of the other models we tested was able to find regions of planktonic clusters, however, it overestimated certain areas of darker pixels.



Next Steps

- We aim to improve our image pre-processing techniques:
  - Adaptive Background Subtraction
  - Multi-Scale Enhancement

- Test new image segmentation techniques:
  - Advanced Watershed
  - Contour Refinement