Using Cell Profiler to Measure Protein Intensity

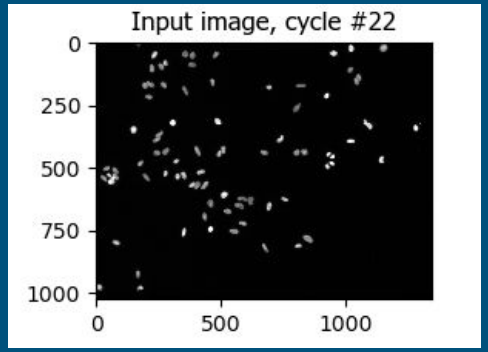
By Holly Akati

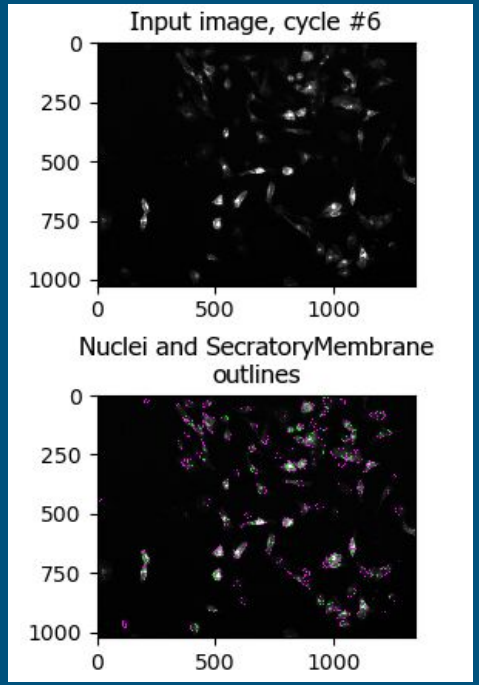
Where the dataset is from and how did we use it?

- The dataset is derived from a genome-wide primary screen and a subsequent validation screen using siRNA libraries targeting different genes.
- The experiments were performed using HeLa Kyoto cells, a widely used cell line for studying cellular processes.
- In this research paper, the authors provided a dataset containing different types of microscopy images, each labeled with specific markers. Let me walk you through what these labels represented.
- First, there were images labeled 'DAPI'. These images highlighted the cell nuclei, and the nuclei were considered the primary objects of interest in our analysis. These are labeled 'Nuclei' in the pipeline.
- Next, there were images labeled 'CFP'. These showcased a secretory membrane protein called tsO45G. This was the key marker that I wanted to quantify and study its localization patterns across different samples. These were referred to as the 'tsO45G' images.
- Then there was a third set of images labeled '647'. These contained a marker called phalloidin, which stained the plasma membranes. This was used to identify the entire cell as a secondary object in the analysis.

Pipeline: What was segmented and measured?

Input Images

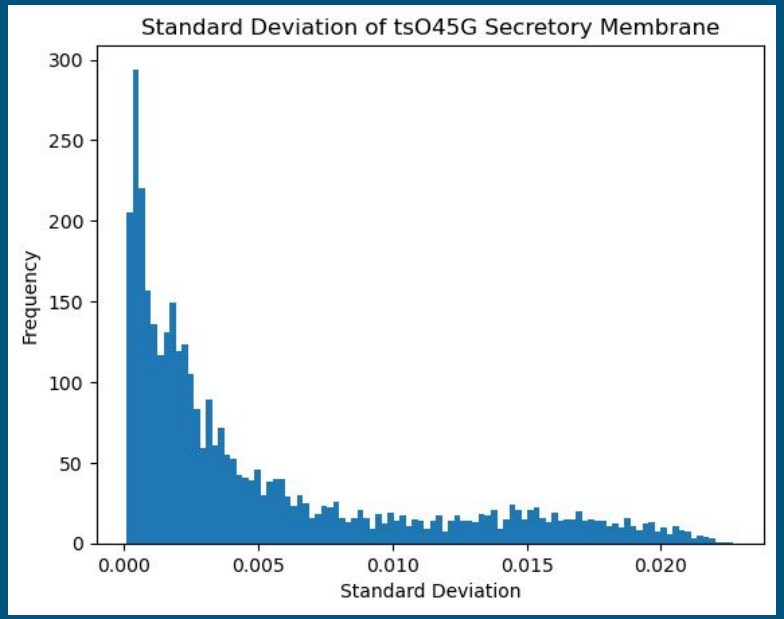


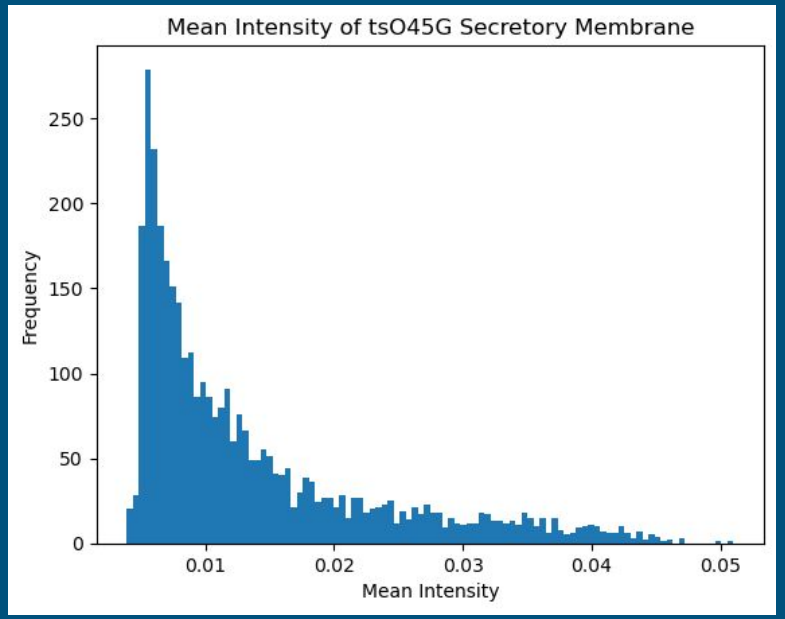


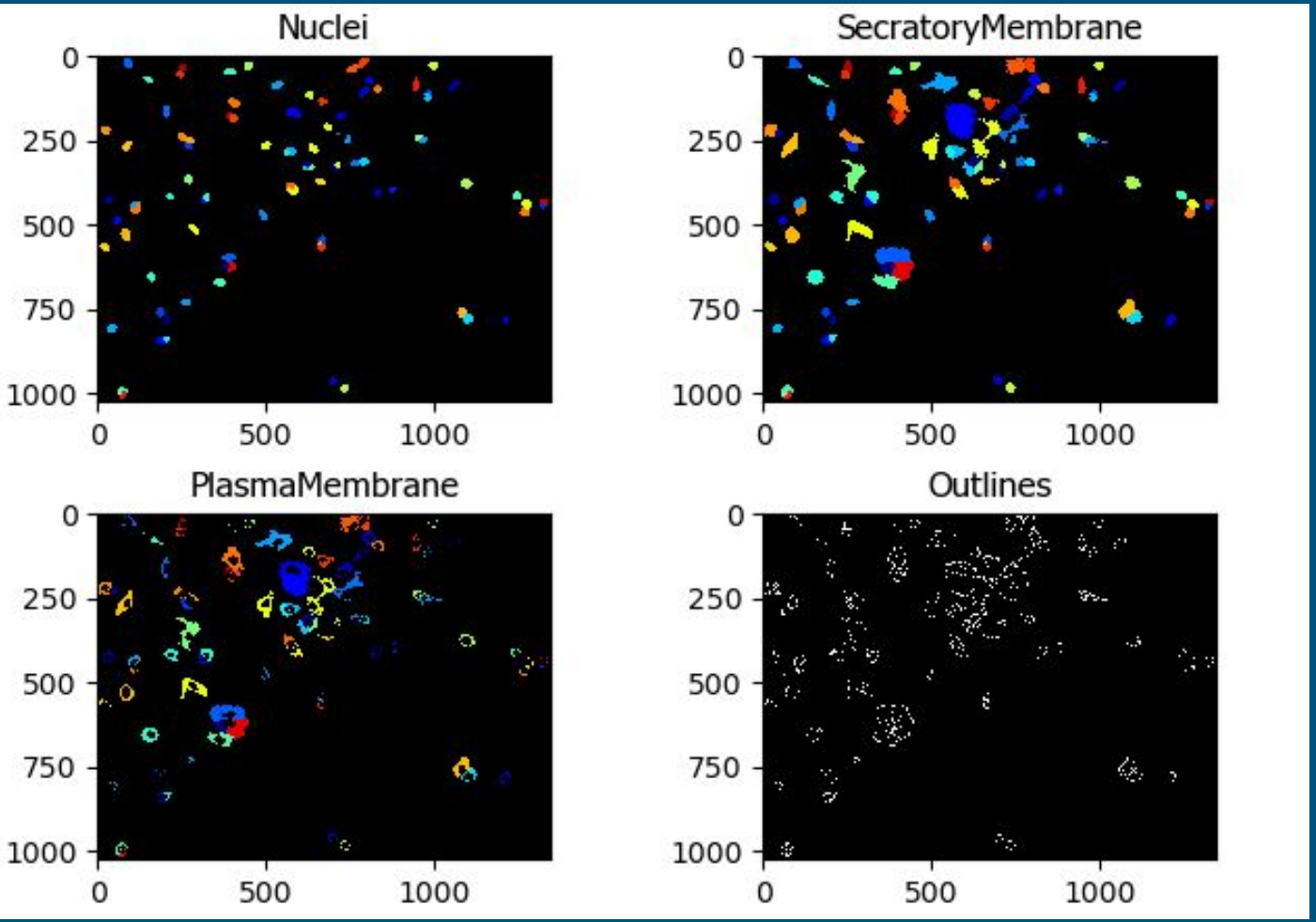
The dataset included 34 sets of images, each sets containing 1 DAPI image (nuclei), 1 CFP image (tsO45G/secretory membrane) and 1 647 image (phalloidin/plasma membrane). The goal was to identify the location of each object and measure the intensity of the secretory membrane in each set.

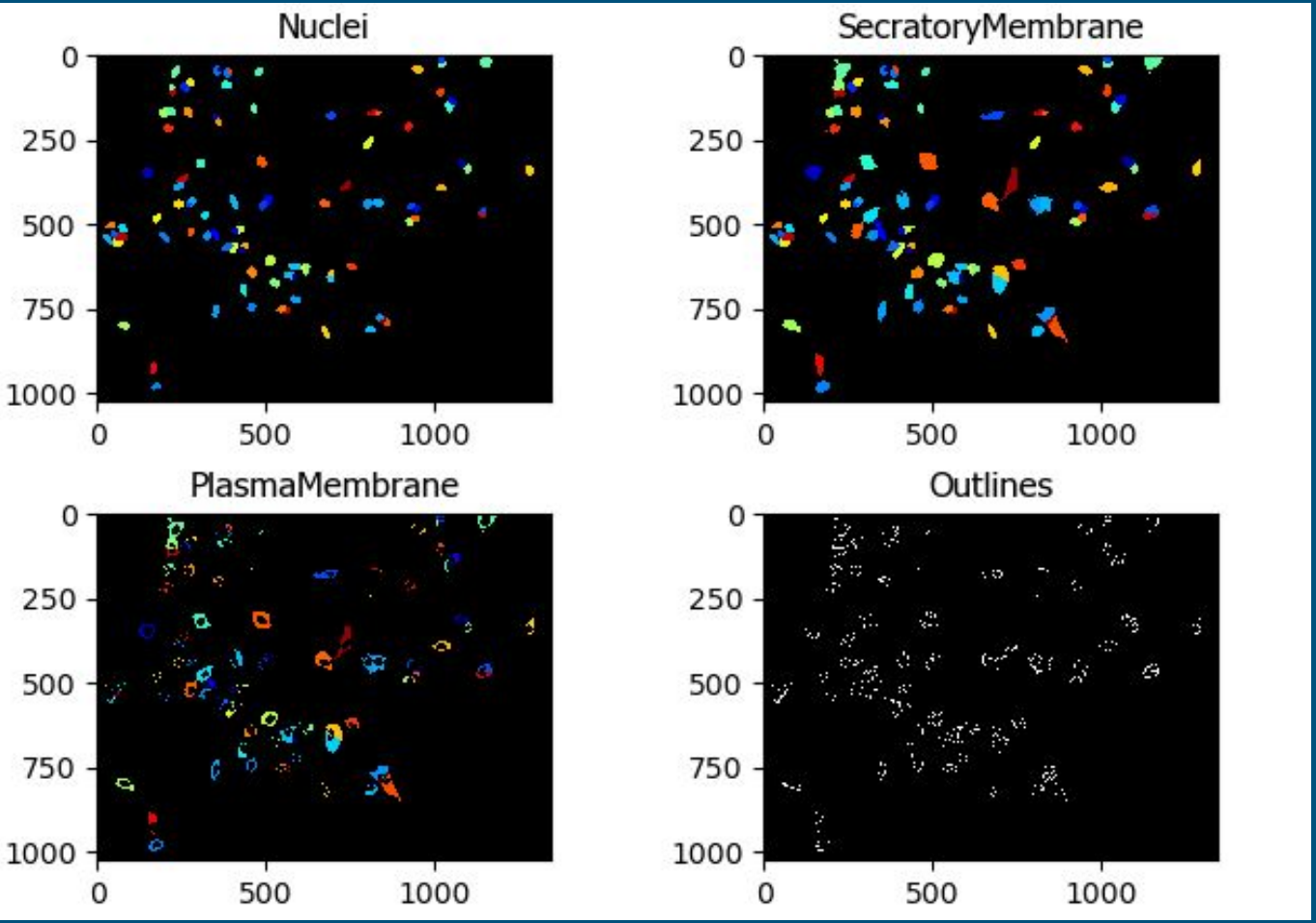
Results and Data Analysis

The results includes measurements related to the intensity of pixels along the edges of objects, such as integrated intensity edge, mean intensity edge and standard deviation of intensity edge






Nuclei
SecratoryMembrane
PlasmaMembrane
Outlines
0
250
500
750
1000
0
500
1000


Nuclei
SecratoryMembrane
PlasmaMembrane
Outlines
0
250
500
750
1000
0
500
1000

Possible Future Steps

- - Integrate additional data sources, such as protein-protein interaction networks or gene expression data, to further characterize the identified genes and their potential roles in secretory transport.

- Since the dataset is related to the study of the Golgi apparatus function in secretion using the tsO45G protein marker, the intensity measurements and their variations may provide insights into the activity or behavior of the Golgi apparatus under different conditions or across different objects/cells.