

C. elegans oogenesis segmentation project

Notes from a CellProfiler-based approach, July 2021

Overview:

The goal of this project is to create a workflow to accurately segment *C. elegans* oocytes.

The images are challenging to segment, as there is no nuclear stain and the cells are defined by bright staining at the borders. In addition, these are 3-dimensional images requiring 3D segmentation.

I attempted to create a solution using ilastik to generate a pixel classifier and then to segment using the ilastik probabilities in CellProfiler. Using this approach, I was unable to create a high quality segmentation. The cells are different size, and it was hard to accurately segment and declump the small and large cells.

Table of contents for each directory

CellProfiler-ilastikSegmentation

- **SaveAsTiff.cppipe**: pipeline used to import the original .nd2 images and export .tiff files for each channel
- **ilastik-segmentation.cppipe**: the pipeline used by Pearl for her best quality segmentation. They use the original images + ilastik predictions. You will need the declumpobjects.py plugin to run this pipeline.
- **oocyte-training.ilp**: ilastik project used to predict different regions of the image (background, out-of-focus light, cell interior, cell border)

cellprofiler-pipelines

- **SaveAsTiff.cppipe**: pipeline used to import the original .nd2 images and export .tiff files for each channel
- **Segmentation.cppipe**: Attempt to segment the original images directly (without using ilastik)

cellprofiler-plugins

The declumpobjects.py plugin used for this project.