A quantitative study of a model eukaryotic life cycle through computer vision

Shreya Ramakanth[1*], Taylor Kennedy[1], Berk Yalcinkaya[2], Nika Tadic[1], Sandhya Neupane[1], Bryn Merritt[1], Nicolas E Buchler[2], Orlando Arguello-Miranda[1]

[1]Department of Plant and Microbial Biology, North Carolina State University
[2]Department of Molecular Biomedical Sciences, North Carolina State University
*Presenter

The quantitative study of the life cycle of microorganisms is crucial to the discovery of new drugs, pesticides, and vaccines that target specific developmental states of parasites and pathogens. However, very few experimental systems detect and track cells throughout the entire life cycle of sexually-reproducing eukaryotic microorganisms. Although several computational tools have been developed to detect (Cellpose, Cell-ACDC, YeaZ) and track (TrackMate) microbial cells, no computational model addresses the tracking of single cells throughout the abrupt morphological changes of life cycle transitions.

In this project, we deployed a computer vision approach to detect and track single cells during their life cycle. To detect single cells regardless of morphological diversity, we trained convolutional neural networks-based algorithms to generate pixel flow-driven cell segmentation models. As proof of concept, we detected specific life cycle stages, such as proliferation, quiescence, meiosis, sporulation, germination, and mating in the model eukaryotic unicellular yeast *Saccharomyces Cerevisiae*. To track single cells despite abrupt movements, we generated a frame interpolation-enhanced tracking algorithm (FIET) based on optical flow estimation and set theory principles. Our pipeline leverages the accuracy of the detection and tracking models to produce quantitative measurements of single cells during all life cycle and morphological transitions, with minimal parameter tuning and fast computational time.

FIET enabled us to measure the evolution of morphological features during different life cycle stages. We found that cell size regulation is crucial at decision-making points between developmental programs, such as quiescence and meiosis, and during the completion of sporulation/gametogenesis. Remarkably, we showed that cell size and shape are reset during the sporulation-germination transition, indicating that several morphological features are not passed down to future generations.

In conclusion, FIET can lead to automated approaches to quantitatively characterize sexually-reproducing microorganisms throughout their entire life cycle, which can be used to screen for new drugs, pesticides, and vaccines. To enable open access to our computer vision pipeline, we created an off-the-shelf graphical user interface (GUI) with our pre-trained segmentation models and single-cell tracking algorithms.