

Title: Making Computer Vision Methods Accessible for Cell Classification

Humans have long used their visual systems to make decisions and discoveries. Microscopes have become more powerful, more widespread, and more commonly used for higher throughput experiments, but what has become equally as important as the optics is the computational technology to extract information from microscopy images. Computers can do what most people are bad at, i.e., compute a lot of calculations on a large set of data quickly and consistently. The field of computer vision tries to take advantage of this fact and use computational algorithms to analyze image data and gain higher level understanding. When we teach the computer how to make decisions based on previously seen data, we are using machine learning techniques.

However, there is a gap between what biologists want to discover from their images and their ability to implement appropriate algorithms. This thesis develops different computer vision methods and software implementations that are both user friendly and developer friendly and can be used to automate inefficient manual yet standard processes in biology. To ensure usefulness and real-world applicability, these are heavily application-driven, so each project is centered around a particular biological problem. We use image processing and engineering spectral features to classify cardiomyocytes. We then advance the machine learning capabilities of the open source software CellProfiler Analyst and apply it to imaging flow cytometry experiments. Next, we develop machine learning techniques for automating malaria counting and detection. Finally, we introduce a deep learning based object detection application and Keras package. This work demonstrates that applying advanced computer vision and machine learning methods from computer science leads to greater efficiency when analyzing cell experiments and introduces tools to allow access to these methods.