EECE 5698: Proposed Final Project

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An Image Signal Processing Pipeline to Streamline Cell Growth Measurements

In biological laboratory settings, cell counting and measurement is a tedious, time-consuming task. It often requires an individual to manually analyze each image through a microscope lens, which introduces room for error that can escalate due to user fatigue over time. This process has great potential to be streamlined and automated by implementing an image signal processing pipeline. Results would be produced more quickly and accurately, and this algorithm would free up the time of lab participants to complete other tasks. Inspired by the methodology in the paper "Blueprint for a Semi-automated Image Processing Tool to Characterize Stent Features: Application to a Pediatric Growth-Adaptive Stent", Giorgianni et al., the images would be processed to isolate, count, and measure features of interest.

We plan to utilize the open-source blood cell image dataset available at Blood Cell Segmentation Dataset on Kaggle.com for the development and testing of this algorithm. The dataset provides both raw microscope images and image masks, which can be used as ground truth to test our isolation algorithm. This image processing pipeline will draw concepts and suggestions from Giorgianni et al., while making significant adjustments for this new application. The algorithm will consist of several steps that ultimately result in the isolation and axial measurement of the whole cells present in the image. First, the raw images will be binarized to discard unneeded color channel information. Next, the images will be cleaned to remove background noise and any cells that are only partially in the image frame. Then the binarized images will be smoothed to get smoother cell shapes. Finally, the best fit ellipse will be applied to each object identified in the processed image, and the ellipse parameters, major and minor axes, will be exported to an excel sheet. This assumes the user will have access to the pixel to mm conversion factor for their imaging system, which is an intrinsic property of the system they chose to utilize.

Our end deliverable will be an end-to-end image signal processing pipeline in MATLAB code that accepts raw microscope images of cells and outputs cell count and cell measurements. Both Daniel and Ava will work together to pseudocode the algorithm, and Ava will begin with code implementation. Daniel will perform code debugging and testing. Both Ava and Daniel will run the code on a stack of images from the open-source data set to ensure results are satisfactory. Our timeline is as follows:

February 17 - 21 Pseudocoding
February 22 - March 14 Write MATLAB algorithm
March 15 - April 4 Debug and test code
April 5 - April 18 Analysis of results running code on different images
April 18 - End Share results and reflect on success of algorithm