

Project Proposal

Computer Vision Analysis of Cell Micrographs

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Problem Statement:

Testing samples for infectious cells such as tuberculosis or cancer can be time consuming and can require experts to analyze microscope images. An automatic image analysis of micrographs, magnified images taken through a microscope lens used to identify something that cannot be seen by the naked eye, can bring disease detection and analysis to areas that do not have access to experts and also make analysis cheaper.

Our goal is to develop an algorithm that when given a micrograph containing biological cells, returns information about the cells including type, number, size, health etc. The input should include a cell micrograph. The outputs depend on the cell type and number.

Approach:

The first objective of this project will be to develop algorithms to segment micrographs containing stained mycobacterium tuberculosis cells. We will use color thresholding to narrow our focus or completely segment the desired cells, depending on the type. We will also use Deformable contours (snakes) in our segmentation approach, and Blob detectors and Connected Components algorithms to determine cell count and location. Once the cells are segmented, we will analyze them to provide quantitative and qualitative information about the cells such as shape, number and size and possibly higher-level information such as velocity to the user. In order to evaluate the success of our algorithms, our segmentation will be overlaid on the original image and “experts” will visually confirm the validity of the outputs.

Experiment and Results

Our initial datasets will include micrographs of tuberculosis cells from Roanoke hospital and online datasets. Later, video of cancer cells moving through microfluidic chips would be incorporated as an extended study. The scope of the project can be expanded to include other data sets and different types of cells. We will be programming in python and using libraries such as numpy, scipy, OpenCV, and Scikit. We will need to implement various functions of our own to solve the specific problems of our project. We will implement segmentation techniques and will need to set the many thresholds and parameters necessary for successful segmentation without false positives. In addition, we will need to develop algorithms to analyse the resulting blobs and return relevant information. Success will be defined by the successful segmentation of biological cells from the background, low numbers of false positives, successful identification of cell types and correctly describing the cell attributes such as size, number, health, velocity and others. The experiment will reveal the number and types of cells in an image as well as defining characteristics of each of those cells.

Extended approach:

We would train a classifier (eg. SVM, for each type of cell - TB, Cancer etc.) based on the features that we extract (from pre-defined input patches) and test it to get a score for each of the classifiers as well as class prediction. To evaluate this approach (detection and classification performance) methods like intersection over union and precision-recall curves would be deployed.