Comparing supervised- and unsupervised image segmentation methods on cell microscopy images

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2025

1 Problem Statement

Microscopy imaging provides a cost-effective alternative to complex lab-based methods for analyzing cell behavior. We would like to investigates deep-learning driven analysis of microscopy images to quantify NK cell behavior and it's impact on cancer cells. By comparing supervised and unsupervised approaches, we aim to research the potential of an automated, cost-effective method, instead of traditional lab-based methods.

2 Motivation

Image segmentation has showed promising results in many medical related problems. By automating the extraction of features such as cell shape and size and clustering patterns, segmentation methods can reduce the cost and time associated with analyzing the microscopy images compared to traditional methods. Segmentation of cell images can enhance our understanding of cellular behavior, and enable researchers to gain insights into cell deaths, and interactions in biological systems. This is particularly important for studies on natural killer (NK) cell behavior in cancer therapy, where microscopy based analysis offers a cost effective alternative to other methods.

3 Project Goals

We will start by implementing and fine-tuning U-Net as our supervised learning model, and W-Net as our unsupervised learning method for NK-cell segmentation. If this proves successful, we might consider expanding our project to develop our own supervised model from scratch. Lastly, we will explore different metrics to evaluate and compare the two models we have implemented.

4 Methodology

The aim of this project is to compare supervised and unsupervised learning methods for analyzing microscopy images. Given the limited labeled data, we will use U-Net for supervised learning and W-Net for unsupervised learning.
For data preparation, we will apply data augmentation to our dataset, in order to get more labeled data for our supervised learning method. We will also normalize the data and split them into training, validation, and test sets. U-Net will be trained using labeled data to predict segmentaion masks, while W-Net, will learn from unlabeled data. To assess how well these models perform, we will use metrics like intersection over union, dice score and accuracy. For further evaluation, we would also consider the ability of each model to handle limited labeled data and computational efficiency. Lastly, by comparing the results, we hope to understand which approach, supervised or unsupervised, is better for analyzing NK and cancer cells in microscopy images.