Nucleus Detection using Deep Learning

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Introduction

According to the World Health Organization, cancer is the second-leading cause of mortality worldwide, being responsible for 1 in 6 deaths [1]. Considering this, the ability to automatically and accurately detect cell nuclei in images is highly desired, as doing so would allow researchers to study the effects of treatments and drugs at a cellular level without expending too much manpower or time manually searching for cells. This would allow scientists the ability to iterate more rapidly and focus more of their effort on developing treatments and cures. As much promise has been shown by a variety of CNN architectures [2][3] for semantic segmentation tasks, we investigate using deep learning for accurate nuclei detection.

Methods

Loss: binary cross-entropy loss Metric: Sørensen-Dice coefficient

 $2(Y_{true} \cap Y_{pred})$ $Y_{true} + Y_{pred}$

Summary: Implement simple CNN as baseline. Since we need to localize, try semantic seg CNN's such as U-Net and tune hyperparameters. Investigate transfer learning using available ResNet50 weights. Look into techniques such as data augmentation to allow our model to generalize better.

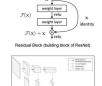
Baseline: Simple CNN





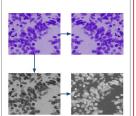
Transfer Learning w/ ResNet50

- Makes it possible to train deeper networks more easily
- Our model is a ResNet50-based FCN with connections fro the last 32×32, 16×16, and 8×8 layers of the ResNet50 [4]



Data Augmentation

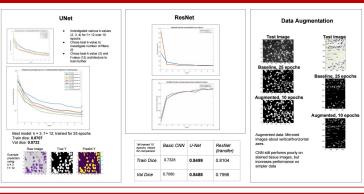
- Original training set yields poor performatimages with dark nuclei
- Convert entire training set to grayscale
- Invert images and add to original training set
- Translate/rotate images



Dataset

The dataset, provided via a Kaggle competition sponsored by Booz Allen Hamilton [5]], is comprised of divergent images of human cells, which likely have been stained for nuclei detection under fluorescence microscopy. Imaging conditions vary by modality, camera, and magnification (to motivate generalizability of the algorithm). There are **670 images**, along with their human-labeled nuclei masks. Given the relatively small training dataset, we chose to split our training dataset into 90%-train/10%-validation (i.e. 603/67)

Results



Discussion and Future Work

Our best model, a U-Net architecture, performs reasonably well on our training set, but generally fails to identify crowded nuclei in tissue section images with general RGB components, even with our initial data augmentation attempts. Future work could include generating GANs for producing new images for this purpose, as well as refining our data augmentation approach.

We also find that transfer learning applied with ResNet 50 gives us a performance in between a basic CNN and U-Net. We believe this is possibly due to the pre-trained ResNet weights not translating well to our segmentation task, as well as the ResNet architecture being potentially situationally suboptimal. We will continue to tune the U-Net model and train it for longer to see if performance improvements can be made. We will also implement SegNet, which uses max pooling indices instead of feature maps as in U-Net to compare performance and network training speed, as it is also an architecture that seeks to retain localization ability, which we have seen is clearly necessary with our images.

References