Mitosis Detection and Tumor Grading Using Deep Convolutional Neural Networks

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Analyzing mitosis proliferation is crucial to physician grading of tumor severity and prognosis. Despite the time and effort poured into automated mitosis detection, no systems have been able to perform at the level of skilled pathologists, who manually examine slide images for mitotic cells. Deep learning is an emerging field of machine learning based on modeling high-level abstractions using large interconnected networks of neurons. We build a custom deep convolutional network architecture, based on the seminal GoogleNet model and principles of aggressive, multiscale data augmentation. Since mitoses are extremely rare compared to normal cells, we also develop a novel multi-stage “bootstrapping” algorithm to extract meaningful training examples from highly imbalanced data. Our deep convolutional neural network achieves an F1 score of 0.85 on the 717-image TUPAC dataset. This trained model also generalizes well, surpassing the best F1-scores obtained in previous mitosis competitions. We then develop a pipeline to grade whole slide images using an intuitive ROI selection algorithm and the trained mitosis detector. Our algorithms detect crucial regions within enormous whole slide images and use these regions to extrapolate levels of tumor-linked mitotic activity. The genes identified by our continuous mitosis scores outperform pathologist scores in their association to cancer and cell cycle functions/ pathways. Finally, we build a gene-level model to predict the mitosis scores from RNA- sequence data. From this model, we extract 10 gene predictions possibly linked to tumor mitotic activity. We hope our research is a step towards a future where physicians use precise, deep- learning- enabled analyses of mitotic activity to diagnose and treat patients.

Awards Won:

Second Award of $2,000