BrCaVision: Predicting Breast Cancer Prognosis by Detecting Mitosis, Identifying Histological Tumor Subtypes, and Scoring HER2 in Whole Slide Tissue Images Using Deep Learning

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Breast cancer is the leading cause of cancer deaths among women worldwide, but early detection and diagnosis can significantly improve a patient's prognosis. Conventionally, biopsy breast tissue is graded based on morphological and genetic features; lesion subtype, mitotic count, and HER2 (IHC) score are three of the most significant prognostic markers. However, the manual examination of breast tissue slides is time-consuming and subject to inter- and intra-pathologist variability. Also, many developing nations lack the skilled medical professionals necessary to provide thorough and timely diagnoses. Artificial intelligence innovations in healthcare can address these issues and the repercussions of late or incorrect diagnosis. In this research, I developed BrCaVision, a state-of-the-art automated system for determining malignancies, classifying histological subtypes, detecting mitosis, and scoring HER2 in a whole slide image (WSI). Using transfer learning methods, I constructed sophisticated convolutional neural network models that accomplished 85% accuracy for subtype determination and a sensitivity of 0.98 for mitosis detection in a fraction of the time required for gold-standard methodologies. Also, I developed a web application that allows medical professionals to input a WSI and obtain a HER2 score and heatmaps that mark tissue subtypes and mitotic cell locations. By deploying the application on a public web hosting service, professionals can acquire timely and accurate breast cancer diagnosis and prognosis prediction across the world. Being easily accessible and fully automated, BrCaVision serves as a step forward in the field of bioinformatics and can save lives with reliable, accurate, and efficient breast cancer detection.

Awards Won:
Third Award of $1,000