Deep Learning Assessment of Tumor Proliferation in Histopathological Images for Categorical and Molecular Breast Cancer Severity Diagnosis

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The emergence of high-throughput histopathological images over the past decade provides new opportunities for computational techniques to study cancerous tumors. Current analysis of tumor proliferation, the most salient prognostic biomarker for invasive breast cancer, is limited to subjective mitosis counting by pathologists in localized regions of tissue images and fails to address additional features critical to holistic analysis. Objective reports require expensive molecular RNA expression tests which are cost-prohibitive in developing countries. This study presents the ?rst data-driven integrative approach to characterize the severity of tumor growth and spread on a categorical and molecular level, utilizing multiple biologically salient deep learning classi?ers to develop a comprehensive prognostic model. Our approach achieves pathologist level performance on three-class categorical tumor severity prediction in under two seconds. It additionally pioneers prediction of molecular expression data from a tissue image at a fraction of current cost, obtaining a Spearman's rank correlation coef?cient of 0.60 ($p < 0.001$) with ex vivo RNA molecular expression data. Furthermore, our novel framework identi?es over 200 unprecedented biomarkers critical to the accurate assessment of tumor proliferation, validating our proposed integrative pipeline as the ?rst to holistically and objectively analyze histopathological images. Our generalizable cost-effective model can be applied to diagnosis, prognosis, and identi?cation of biomarkers associated with a wide range of cancerous diseases and phenotypes.

Awards Won:

Second Award of $2,000

Association for the Advancement of Artificial Intelligence: Honorable Mention