Style Transfer Augmentation: A Novel Deep Learning Approach to the Classification of Cancer Subtypes Using Genetic Status in Histopathology Images

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The leading upstream cause of cancer deaths is the inability to accurately classify cancer types and subtypes. The existing method of MRI scanning for cancer diagnosis cannot effectively differentiate between malignant and benign tumors, leading to misdiagnosis, and cannot accurately identify all types of cancers. Thus, my project presents a novel, robust method to predict primary cancer types and subtypes, specifically MSI and MSS in colorectal cancer, by leveraging histopathology images translated from clinically approved genetic biomarkers. First, I transform the biomarkers into varying stain shades overlain on ~67K histopathology images by mapping their protein interactions onto interactomes. I then develop and perform the Style TRansfer Augmentation for histoPathology (STRAP) technique to apply on these images for the neural network to learn increasingly generalizable image representations. The results are compared against stain augmentation and stain normalization, two widely used augmentation techniques. Next, I train a 54-layer MobileNetV2 convolutional neural network on the three image-augmented datasets. The models are validated on ~100K images, and the STRAP model successfully achieved the highest AUROC at 0.876 for classification. The model’s automated analysis of clinically approved genetic biomarkers and histopathology images can be generalized to other cancer types and diseases to offer vital insights into future clinical events. Unlike previous “black-box” models, this platform is a pragmatic tool with industrial viability that offers clinicians the ability to leverage its personalized predictions as a crucial component in amplifying diagnostic accuracy, determining robust treatments, and preventing these deaths from occurring in the first place.

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