Creation of a Novel Machine Learning Model To Predict MGMT Promoter Methylation Status Using Multimodal MRI Images

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While treating Glioblastoma multiforme, a rapidly-progressive brain cancer with an average survival of less than a year, doctors traditionally conduct biopsies of the patient's tumor to assess its microenvironment, helping them provide personalized therapies. One genetic feature looked for is the acetylation or methylation of the O6-methylguanine-DNA-methyltransferase (MGMT) gene, which produces the protein O6-methylguanine-DNA-methyltransferase. Silencing of the MGMT gene decreases levels of MGMT protein and increases patient responsivity to therapies such as Temozolomide (TMZ). However, conducting biopsy extractions to determine the MGMT promoter methylation status can be life-threatening to patients already undergoing intense treatments. In this project, an end-to-end ML pipeline was developed to noninvasively analyze GBM MRI scans (with variations in patient orientation, 3D slice count, thickness and spacing), and predict the MGMT methylation status of the cancer presented with an accuracy of ~ 70%. The input files were retrieved from the Brain Tumor Segmentation Challenge dataset, which contains 1000+ high-resolution glioblastoma MRI scans. In the pre-processing stage, an affine transformation was applied to bring the images to the patient coordinate system; subsequently, black backgrounds were removed, and patches of 32x32x32 3D voxels were generated. Texture features such as T1c minimum and NGTDM values were extracted, and positional encoding of the voxels was applied to increase accuracy. A 3D-Unet model was used for tumor segmentation and a 3D Dense-Net was used for classification. The Dice Coefficient Loss function was used to account for the imbalance in the 3D voxels with tumors and healthy brain tissue.

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