Personalized Neurooncology Radiogenomic Classification and Recommendation Model With AI and MRI

Koska, Cagan (School: Izmir Atakent Anadolu Lisesi)

Glioblastoma is the most frequent and the most lethal primary malignant brain tumor. Treatment with temozolomide for the MGMT methylated subgroup may increase median survival time two folds. 1p19q codeletion, IDH and EGFR mutation also affect management decision and prognosis of glial tumors. Current state of the art diagnosis of genetic status of glial tumors is tissue diagnosis which requires invasive methods. Besides, MGMT methylation is an epigenetic property, therefore, may exhibit temporal and spatial variations. Recurrent biopsies may lead to high cost, time loss and professional workload utilization and high morbidity for the patient. Deep learning, particularly convolutional neural networks (CNN) proved their value in various image classification tasks. MRI is the main imaging evaluation tool which can provide important diagnostic clues for various brain pathologies. This research proposes a novel AI tool which classifies glial tumors into various genetic subtypes including MGMT methylation, IDH mutation, EGFR mutation and 1p19q codeletion status using 3DCNN, radiomics, novel imaging biomarkers and public data obtained from Kaggle-RSNA and TCIA. Furthermore, segmentation of various habitats of the tumor and extraction of novel imaging biomarkers using these segmentations such as necrosis/tumor ratio, tumor/edema ratio, enhancement fraction, T2/FLAIR signal ratio of viable tumor were developed. Radiomics maps of these habitats and total tumor were additionally provided. The extracted information was both presented as an automatic report indicating the genomic status of the tumor, area and volumes of the habitats and the numeric values of imaging biomarkers and deployed as a Streamlit application.

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