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Radiogenomics and machine learning predict oncogenic signaling pathways in glioblastoma

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Abstract

Background Glioblastoma (GBM) is a highly aggressive brain tumor associated with a poor patient prognosis. The survival rate remains low despite standard therapies, highlighting the urgent need for novel treatment strategies. Advanced imaging techniques, particularly magnetic resonance imaging (MRI), are crucial in assessing GBM. Disruptions in various oncogenic signaling pathways, such as Receptor Tyrosine Kinase (RTK)-Ras-Extracellular signal-regulated kinase (ERK) signaling, Phosphoinositide 3- Kinases (PI3Ks), tumor protein p53 (TP53), and Neurogenic locus notch homolog protein (NOTCH), contribute to the development of different tumor types, each exhibiting distinct morphological and phenotypic features that can be observed at a microscopic level. However, identifying genetic abnormalities for targeted therapy often requires invasive procedures, prompting exploration into non-invasive approaches like radiogenomics. This study explores the utility of radiogenomics and machine learning (ML) in predicting these oncogenic signaling pathways in GBM patients.

Methods We collected post-operative MRI scans (T1w, T1c, FLAIR, T2w) from the BRATS-19 dataset, including scans from patients with both GBM and LGG, linked to genetic and clinical data via TCGA and CPTAC. Signaling pathway data was manually extracted from cBioPortal. Radiomic features were extracted from four MRI modalities using PyRadiomics. Dimensionality reduction and feature selection were applied and Data imbalance was addressed with SMOTE. Five ML models were trained to predict signaling pathways, with Grid Search optimizing hyperparameters and 5-fold cross-validation ensuring unbiased performance. Each model's performance was evaluated using various metrics on test data.

Results Our results showed a positive association between most signaling pathways and the radiomic features derived from MRI scans. The best models achieved high AUC scores, namely 0.7 for RTK-RAS, 0.8 for PI3K, 0.75 for TP53, and 0.4 for NOTCH, and therefore, demonstrated the potential of ML models in accurately predicting oncogenic signaling pathways from radiomic features, thereby informing personalized therapeutic approaches and improving patient outcomes.

Conclusion We present a novel approach for the non-invasive prediction of deregulation in oncogenic signaling pathways in glioblastoma (GBM) by integrating radiogenomic data with machine learning models. This research

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