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Multimodal Deep Radiomic and Genomic Modeling for Post-Treatment Survival Prediction in Glioma

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Abstract

Accurate survival prediction following radiation therapy for glioma remains challenging due to heterogeneous tumor biology and treatment response. This study proposes a multimodal framework integrating deep radiomic features from longitudinal MRI, tumor growth dynamics, clinical variables, treatment dose metrics, and genomic alterations to predict overall survival in post-treatment glioma patients.

Introduction

Glioma exhibits substantial heterogeneity in imaging appearance, molecular profile, and treatment response. Conventional prognostic models often rely on limited clinical or molecular features and do not fully exploit longitudinal imaging data. Deep learning–based radiomics, particularly when combined with tumor growth dynamics and genomics, offers a promising avenue for improving individualized survival prediction. The data set containing 102 patients (training data is 68 and testing data is 34) is from the public data of TCIA (https://www.cancerimagingarchive.net/collection/mu-glioma-post/)

Methods and Materials

Patients with post-radiation MRI, segmentation masks, survival outcomes, and clinical/genomic data were retrospectively analyzed. For each imaging time point, tumor regions were automatically cropped and resampled to a fixed resolution and processed using a pretrained 3D ResNet-18 (MedicalNet) to extract high-dimensional deep radiomic features. Longitudinal tumor growth rate was computed from serial tumor volumes. Clinical variables included age, sex, race, tumor grade, and biologically effective dose (BED). Genomic markers included IDH1/IDH2 mutations, 1p/19q codeletion, ATRX mutation, MGMT methylation, EGFR amplification, PTEN mutation, CDKN2A/B deletion, TP53 alteration, TERT promoter mutation, BRAF V600E mutation, H3-3A mutation, and chromosome 7 gain/10 loss. Imaging, clinical, dose, and genomic features were concatenated into a unified feature vector per patient. Survival modeling was performed using ElasticNet regression, with risk defined as the negative predicted survival time. Model performance was evaluated using three-fold cross-validation on the training cohort and tested on an independent hold-out set using concordance index (C-index).

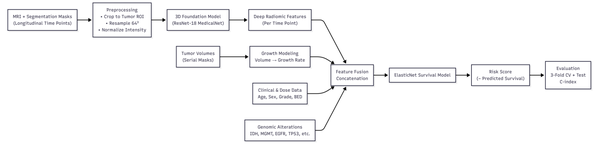
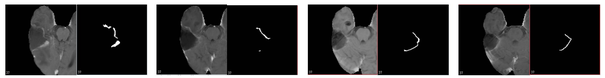


Figure 1. Pipeline overview (schematic description)



a b c d

Figure 2. The MRIs and masks for one patient. The masks contain two parts:
1. Non-enhancing Tumor Core (NETC). This label identifies non-enhancing components within the tumor, such as cystic, necrotic, or hemorrhagic portions.
2. Enhancing Tissue (ET). This label highlights the viable nodular-enhancing components of the tumor.

The post-treatment days are: a. 116, b. 158, c. 200, d. 391

Results

PERFORMANCE
- Mean 3-fold CV C-index: 0.66
- Test cohort C-index: 0.69
- Kaplan–Meier analysis showed clear separation between low- and high-risk groups.

TECHNICAL STRENGTHS
- Leverages foundation-model 3D CNN features pretrained on medical imaging.
- Incorporates longitudinal tumor dynamics, going beyond static imaging.
- Integrates genomics and radiation dose metrics within a single cohesive framework.

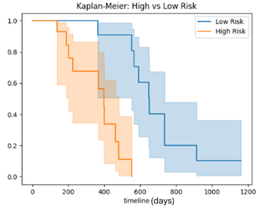


Figure 3. Kaplan–Meier analysis demonstrated clear separation between low- and high-risk groups.

Discussion

This approach enables comprehensive risk stratification after radiation therapy and provides a foundation for personalized follow-up scheduling and adaptive treatment planning. Kaplan–Meier analysis demonstrated clear separation between low- and high-risk groups, indicating effective risk stratification based on predicted survival risk. Future work will explore time-dependent survival models, attention-based feature fusion, and external multi-institutional validation.

Conclusions

This framework demonstrates the feasibility and potential benefit of combining deep radiomics, tumor growth modeling, and genomic biomarkers for post-radiation survival prediction in glioma. The approach is extensible to adaptive therapy and personalized risk-guided treatment strategies.

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