

MRI Radiomics for Survival Stratification in Glioblastoma: Benchmarking Against Clinical Variables in a Retrospective Observational Study of the UPENN-GBM Cohort

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Research Article

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MRI Radiomics for Survival Stratification in Glioblastoma: Benchmarking Against Clinical Variables in a Retrospective

Observational Study of the UPENN-GBM Cohort

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Article type

Original Article

Study design

Retrospective observational secondary analysis of a publicly available, fully de-identified glioblastoma cohort.

MRI Radiomics for Survival Stratification in Glioblastoma: Benchmarking Against Variables in a Retrospective Observational Study of the UPENN-GBM Cohort

Abstract

Background

Glioblastoma (GBM) is the most aggressive primary brain tumor in adults and exhibits substantial biological heterogeneity not fully captured by conventional clinical and molecular prognostic factors. MRI radiomics has emerged as a promising approach for deriving quantitative imaging biomarkers associated with patient outcomes. This study aimed to compare conventional clinical survival modeling with MRI radiomics-based machine learning for survival stratification in a public glioblastoma cohort.

Methods

This retrospective study included 230 patients with glioblastoma from the UPENN-GBM dataset. Clinical variables included age, sex, Karnofsky Performance Status, MGMT promoter status, and IDH1 mutation status. A total of 144 MRI radiomic features were extracted and reduced to 61 after preprocessing and feature selection. A multivariable Cox proportional hazards model was developed using clinical variables, while a Random Survival Forest (RSF) model was trained using radiomic features. Model performance was assessed using the concordance index (C-index), and survival stratification was evaluated using Kaplan–Meier analysis.

Results

The clinical Cox model demonstrated moderate prognostic performance (C-index 0.635). Increasing age was associated with worse survival, while IDH1 mutation and MGMT promoter positivity showed favorable survival trends. The radiomics RSF model achieved comparable prognostic discrimination (C-index 0.653) and stratified patients into high-risk and low-risk groups. Kaplan–Meier analysis demonstrated significant survival separation between risk groups (log-rank $p < 0.001$).

Conclusions

MRI radiomics-based machine learning enabled meaningful survival stratification in glioblastoma and provided complementary prognostic information alongside conventional clinical variables. Further external validation is required before clinical implementation.

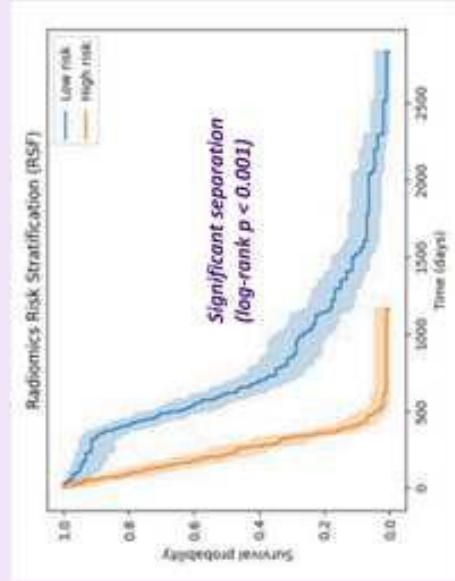
Trial registration

Not applicable.

Keywords

Glioblastoma; Magnetic Resonance Imaging; Radiomics; Survival Analysis; Machine Learning

MRI Radiomics for Survival Stratification in Glioblastoma: Benchmarking Against Clinical Variables Using the UPENN-GBM Cohort



MRI radiomics-based Random Survival Forest modeling achieved prognostic performance comparable to conventional clinical Cox modeling (C-index 0.653 vs. 0.635) and produced significant survival stratification between high- and low-risk glioblastoma patients (log-rank $p < 0.001$).

- Conventional clinical and molecular variables incompletely capture the biological heterogeneity of glioblastoma, limiting accurate individualized survival risk stratification in routine clinical practice.

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- MRI radiomics-based Random Survival Forest modeling enabled significant survival stratification between high-risk and low-risk glioblastoma patients, confirmed by Kaplan–Meier analysis (log-rank $p < 0.001$).
- This study critically evaluates MRI radiomics as a complementary prognostic tool alongside conventional clinical variables in glioblastoma, demonstrating reproducible survival stratification using a fully public dataset, supporting transparent and accessible radiology AI benchmarking and future clinical translation.

Keywords

Glioblastoma; Magnetic Resonance Imaging; Radiomics; Survival Analysis; Machine Learning

List of Abbreviations

C-index – Concordance Index

GBM – Glioblastoma

GLCM – Gray-Level Co-occurrence Matrix

GLSZM – Gray-Level Size Zone Matrix

IDH1 – Isocitrate Dehydrogenase 1

KPS – Karnofsky Performance Status

MGMT – O6-Methylguanine-DNA Methyltransferase

MRI – Magnetic Resonance Imaging

NGTDM – Neighboring Gray Tone Difference Matrix

RSF – Random Survival Forest

TCIA – The Cancer Imaging Archive

UPENN-GBM – University of Pennsylvania Glioblastoma Dataset

Background

Glioblastoma (GBM) is a highly aggressive brain tumor with poor prognosis despite multimodal treatment [1]. Regardless of advances in neurosurgical resection, radiotherapy, and systemic therapy, prognosis remains poor, with median survival generally limited to approximately 12–15 months. Considerable heterogeneity exists in patient outcomes; in order to improve personalized treatment, it is essential to identify specific tumor characteristics that capture this variability and aid in predicting survival [2].

Current survival estimation relies largely on clinical and molecular variables including age, Karnofsky Performance Status (KPS), extent of resection, MGMT promoter methylation status, and IDH mutation status. Although clinically valuable, these factors do not fully reflect the biological heterogeneity of GBM. Accurate prediction of glioblastoma (GBM) progression is essential for improving therapeutic interventions and outcomes [3].

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Radiomics is an emerging imaging science that converts routine radiological scans into high-dimensional quantitative descriptors related to tumor shape, texture, signal intensity, and spatial heterogeneity. It involves extracting many quantitative data obtained from medical images and analysing them. In neuroradiology it may be used to discover magnetic resonance imaging (MRI) features of glioblastomas that are impossible to identify by human vision alone [4]. Studies have shown that magnetic resonance imaging (MRI)-based deep learning radiomics (DLR) has the potential to assess glioma grade [5].

In glioblastoma, MRI radiomics has shown promise for molecular classification, treatment response assessment, and survival prediction. Several prior studies have reported MRI radiomics-based prognostic models in GBM, including integrated clinical-radiomic survival stratification frameworks. Previous studies show intratumor heterogeneity is partly responsible for the poor prognosis of glioblastoma (GBM) patients [6].

However, many analyses rely on institutional cohorts, proprietary pipelines, or limited reproducibility. Despite the rapid growth of studies, no algorithms in the field have reached

clinical implementation, mainly due to the lack of standardized methods, hampering study comparisons and reproducibility across different datasets [7].

Addressing challenges, such as model reproducibility, model generalizability, model interpretability, and multi-omics data integration, is crucial for the clinical translation of radiomics in glioma [8]. Independent benchmarking using public datasets remains valuable for transparent validation and educational accessibility.

Accordingly, this study aims to compare conventional clinical survival modeling with MRI radiomics-based machine learning in a fully public glioblastoma cohort. We hypothesized that radiomic features would enable meaningful survival stratification alongside standard clinical variables.

Methods

Study Design and Data Source

This retrospective observational study used publicly available, fully de-identified glioblastoma imaging and clinical data obtained from The Cancer Imaging Archive and linked open repositories. No direct patient contact or intervention occurred.

Generative artificial intelligence tools were used to assist with language refinement and manuscript organization during preparation of this manuscript. All scientific analyses, data interpretation, methodological decisions, conclusions, and final manuscript content were reviewed and approved by the authors, who remain fully responsible for the accuracy and integrity of the work.

Study Population

Patients with histologically confirmed glioblastoma and available preoperative MRI plus survival data were included. Cases with missing essential imaging or outcome variables were excluded.

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Final cohort size: 230 patients

Clinical Variables

The following baseline variables were analyzed:

- Age at scan (years)
 - Sex
 - Karnofsky Performance Status (KPS)
 - MGMT promoter status
 - IDH1 mutation status
 - Survival time
 - Event status

MRI Processing and Radiomics Extraction

Radiomic features obtained from the publicly available dataset were analysed. Tumor regions were segmented according to available dataset masks/workflows. Quantitative radiomic features were extracted from multiple MRI sequences.

Initial extraction yielded approximately 144 radiomic features, including:

- First-order intensity statistics
 - Texture features (GLCM, GLSZM, NGTDM and related matrices)
 - Shape and morphological descriptors
 - Statistical heterogeneity measures

Feature Preprocessing and Selection

To reduce redundancy and improve model robustness, the following preprocessing steps were performed:

- Variance threshold filtering
 - Removal of highly correlated variables
 - Collinearity reduction

Final retained radiomic feature set: 61 features

Survival Modeling

Clinical Model

A multivariable Cox proportional hazards regression model was fitted using:

- Age
 - Sex
 - KPS
 - MGMT status
 - IDH1 status

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Radiomics Model

A Random Survival Forest (RSF) model was trained using the 61 selected radiomic variables to estimate nonlinear survival risk.

Risk Stratification

Patients were dichotomized according to RSF-derived risk scores into:

- High-risk group (n = 115)
- Low-risk group (n = 115)

Statistical Analysis

Model performance was evaluated using the concordance index (C-index), with cross-validation used to assess both the Cox proportional hazards and Random Survival Forest models. No formal power calculation was performed because this was a secondary analysis of a fixed, publicly available cohort. The overall study workflow is illustrated in Figure 1.

[Insert Figure 1.]

Figure 1. Study workflow.

Generative AI use

ChatGPT (OpenAI) was used solely for language editing and formatting assistance. It was not used to generate, analyze, or interpret study data. All scientific content and final decisions were made by the authors.

Results

Cohort Characteristics

A total of 230 patients were included in the final integrated dataset.

Clinical Cox Model

The clinical survival model demonstrated moderate predictive performance:

- C-index 0.635

Key findings:

- Increasing age was significantly associated with worse survival
- IDH1 mutation demonstrated a protective directional trend
- MGMT status showed expected favorable trend
- KPS demonstrated weaker association in multivariable analysis

- KPS demonstrated weaker association in multivariable analysis

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Radiomics Random Survival Forest Model

The RSF model successfully incorporated the 61-feature radiomic dataset and demonstrated comparable survival prediction performance relative to conventional clinical modeling, with a small numerical difference in C-index.

The clinical Cox model had a cross-validated C-index of 0.635, while the radiomics Random Survival Forest model had a cross-validated C-index of 0.653. This modest numerical difference should be interpreted with caution pending formal confidence interval analysis.

Survival Risk Stratification

Kaplan–Meier analysis demonstrated clear separation between:

- High-risk patients (n = 115)
- Low-risk patients (n = 115)

We observed significant survival separation between high-risk and low-risk groups (log-rank $p < 0.001$), as shown in Figure 2..

[Insert Figure 2. here]

Figure 2. Kaplan–Meier survival curves for RSF-derived high-risk and low-risk groups.

High-risk patients demonstrated significantly reduced overall survival compared to low-risk patients (log-rank $p < 0.001$). Shaded areas represent 95% confidence interval.

Dataset Summary

- Total patients: 230
 - Clinical variables: 5 principal covariates (+ time/event outcomes)
 - Initial radiomic features: ~144
 - Final selected radiomic features: 61

Discussion

This study demonstrates the feasibility of performing clinically relevant survival modeling in glioblastoma using fully public imaging datasets. Conventional clinical variables provided moderate prognostic discrimination, with age emerging as the strongest predictor. MRI radiomic features enabled meaningful survival stratification and may reflect tumor characteristics not fully represented by routine clinical variables.

The Random Survival Forest framework was particularly suitable for high-dimensional radiomic data because it accommodates nonlinear relationships and complex interactions. Clear Kaplan–Meier separation between predicted risk groups supports the practical value of imaging-derived prognostic signals.

Unlike many prior studies based on proprietary institutional cohorts, the present analysis emphasizes transparency, accessibility, and reproducibility through open-data methodology. Public-cohort benchmarking studies are especially relevant for early-stage investigators and for independent validation of radiology AI concepts.

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Future challenges in this field are increasing data availability, improving the general understanding of how AI handles data and establishing solid correlations between image features and tumor's biology [9].

Clinical Implications

If externally validated, MRI radiomics-based risk models may support:

- Prognostic counseling
 - Trial enrollment stratification
 - Follow-up intensity planning
 - Personalized neuro-oncology decision support

Limitations

This study has several limitations:

1. Retrospective design
2. Public cohort sample size smaller than multicenter consortia
3. Lack of independent external validation cohort
4. Potential heterogeneity in MRI acquisition parameters
5. Limited molecular covariates available in open datasets
6. Inclusion of only patients with complete survival events may limit generalizability and introduce selection bias compared with unselected clinical populations.

Reproducibility of features across varying MRI acquisition protocols remains a challenge in standardization of radiomics. Future multicenter harmonized studies should compare radiomics, radiogenomics, and hybrid clinical-imaging models prospectively.

Conclusion

MRI radiomics-based survival modeling enables meaningful prognostic stratification in glioblastoma using public imaging cohorts. Imaging-derived quantitative biomarkers may complement conventional clinical variables and improve personalized risk assessment.

Open-cohort benchmarking studies can advance reproducible, transparent, and accessible radiology AI research.

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<https://doi.org/10.7937/TCIA.709X-DN49>.

Declarations

Ethics approval and consent to participate

This study utilized publicly available, fully de-identified data obtained from The Cancer Imaging Archive. No direct patient recruitment, intervention, or access to identifiable personal health information occurred. Formal ethics approval and informed consent were not required as this constitutes secondary analysis of anonymized publicly available data in accordance with applicable repository usage policies.

Consent for publication

Not applicable. This manuscript contains no individual person's data, images, or case reports.

Availability of data and materials

The datasets analyzed during this study are publicly accessible through The Cancer Imaging Archive, subject to repository terms of use [10].

Competing interests

J.N. and N.P. declare that they have no competing interests.

Funding

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Authors' contributions

J.N. conceptualized the study, performed data analysis, interpreted results, and drafted the manuscript. N.P. critically reviewed the manuscript and approved the final version. All authors read and approved the final manuscript.

Acknowledgements

Not applicable.

Authors' information

J.N. is a medical student at the All India Institute of Medical Sciences (AIIMS), Mangalagiri, India, with a research interest in radiology, artificial intelligence and quantitative imaging.

Figure 1.

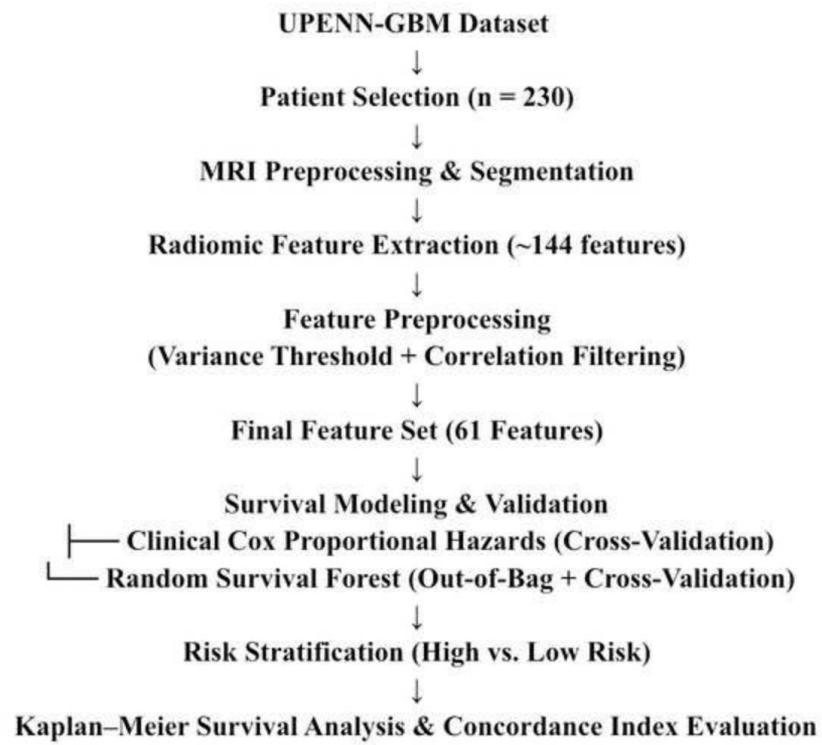


Figure 2.

