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PAPER

Toward Improved Glioma Mortality Prediction: A Multimodal Framework Combining Radiomic and Clinical Features

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ABSTRACT

Gliomas, especially diffuse gliomas, remain a major challenge in neuro-oncology due to their highly heterogeneous nature and poor prognosis. Accurately predicting patient mortality is essential for improving treatment strategies and outcomes, yet current models often fail to fully utilize the wealth of available multimodal data. To address this, we developed a novel multimodal predictive model that integrates diverse magnetic resonance imaging (MRI) sequences—T1, T2, FLAIR, DWI, SWI, and advanced diffusion metrics such as high angular resolution diffusion imaging (HARDI)—with detailed clinical data, including age, sex, tumor genetic markers, and WHO CNS tumor grade. Using the UCSF Preoperative Diffuse Glioma MRI (UCSF-PDGM) dataset, our study introduces an innovative framework that integrates deep learning (e.g., VGG16 for extracting embeddings from a diverse array of MRI modalities, including standard sequences and advanced diffusion metrics) with machine learning algorithms (e.g., XGBoost) to combine imaging and clinical data. This approach captures complementary insights that surpass the capabilities of both single-modal models and previous multimodal methods, which often rely on predefined radiomic features or limited integration of data types. Our results demonstrate significant improvements in predictive accuracy for glioma mortality, showcasing the value of integrating raw imaging embeddings with detailed clinical variables. By providing a more comprehensive understanding of tumor behavior and patient outcomes, our study advances glioma prognosis and supports the development of more personalized and effective treatment strategies.

KEYWORDS

Glioma prognosis, artificial intelligence, multimodal integration, magnetic resonance imaging (MRI)-derived embeddings, machine learning, clinical data

1 INTRODUCTION

Gliomas, a diverse group of brain tumors, represent one of the most challenging malignancies in neuro-oncology due to their aggressive nature and high mortality

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rates [1] [2]. These tumors account for the majority of primary brain cancers, with prognosis and survival outcomes varying significantly based on the tumor grade, molecular characteristics, and patient-specific factors [2]. Despite advances in medical imaging and treatment strategies, the ability to accurately predict patient outcomes remains limited, particularly for diffuse gliomas, which often exhibit complex and heterogeneous behavior [3]. Magnetic resonance imaging (MRI) has become a cornerstone in the diagnosis, treatment planning, and monitoring of gliomas. Different MRI modalities, such as T1-weighted, T2-weighted, and FLAIR, provide crucial insights into tumor characteristics, including size, location, and infiltration into surrounding brain tissue [4] [5]. However, traditional MRI analysis techniques are often insufficient to capture the full extent of tumor heterogeneity and its impact on patient prognosis. The integration of advanced MRI modalities and diffusion metrics, which offer detailed quantitative data on tissue microstructure, has shown promise in enhancing the precision of prognostic models [6]. Recent advances in using machine learning to analyze multimodal data in neuro-oncology underscore the importance of combining imaging data with clinical and genetic markers to achieve improved predictive accuracy [27]. Despite the significant advancements in MRI technology and its widespread application in neuro-oncology, current methods for predicting glioma prognosis remain constrained by several limitations. Traditional predictive models that rely on a single MRI modality or limited clinical variables may fail to capture the complex, multifaceted nature of gliomas [7]. Furthermore, existing models may suffer from overfitting, particularly when trained on small datasets or when applied to independent patient cohorts, leading to limited generalizability and reduced accuracy in clinical settings. Another critical gap in current research is the insufficient integration of advanced diffusion MRI metrics, which offer deeper insights into tissue integrity and tumor infiltration [8] [9], but are rarely incorporated into predictive models. For instance, while T1- and T2-weighted MRI scans can provide valuable information about tumor morphology and edema, they do not adequately reflect the underlying microstructural changes in brain tissue [10]. Most existing approaches also lack the ability to fully leverage the rich, multidimensional data available from various MRI sequences and clinical records. This fragmented use of data often results in predictive models that are either too simplistic or too specialized, limiting their effectiveness across diverse patient populations. Addressing these gaps is crucial for improving the precision and reliability of glioma prognosis. Enhanced predictive accuracy can lead to better-informed clinical decisions, more personalized treatment strategies, and ultimately, improved patient outcomes. Studies such as those by Khazaaleh et al. emphasize the potential of unsupervised machine learning models to handle complex, multidimensional datasets, offering an avenue to overcome these challenges [28]. As gliomas are highly heterogeneous and often aggressive, the ability to predict survival and tailor treatment accordingly can make a significant difference in patient quality of life and survival rates. Therefore, developing robust, multimodal models that integrate various MRI modalities and clinical data is critical in addressing the ongoing challenge of accurately predicting survival outcomes in glioma patients. Current approaches, including those that combine clinical and MRI features, have demonstrated improvements in predictive models for glioma outcomes. However, these studies often rely on predefined MRI features or limited imaging modalities, which may not fully capture the intricate microstructural and biological heterogeneity of gliomas. To address these limitations, our study introduces a novel multimodal framework that integrates MRI embeddings extracted from a wide range of MRI modalities—including standard sequences (T1, T2, FLAIR) and advanced diffusion metrics (e.g., Eddy_FA, Eddy_MD) derived

from high angular resolution diffusion imaging (HARDI)—with detailed clinical data. By leveraging deep learning models such as VGG16 for feature extraction, our approach directly processes raw imaging data to generate modality-specific embeddings, capturing unique and complementary features across different MRI types. These embeddings are combined with clinical variables such as age, sex, and tumor genetic markers to form a comprehensive dataset for survival prediction, trained using an XGBoost model. Unlike previous studies, which focus on predefined radiomic features or limited integration of data types, our method harmonizes a broader and richer set of features into a unified pipeline, advancing the accuracy and applicability of survival predictions. This innovative approach provides a more nuanced understanding of glioma outcomes and supports the development of personalized treatment strategies.

The work is structured as follows: Section 2 provides a comprehensive review of existing literature on glioma prognosis, highlighting the limitations of current predictive models and the need for a more holistic approach. Section 3.1 describes the dataset used in our study, including detailed information on the various MRI modalities and clinical variables incorporated into the model. Section 3.2 details the methodology employed, including the preprocessing steps for the MRI data, the feature extraction process using the VGG16 model, and the subsequent model training and evaluation techniques. Section 4 presents the results of our experiments, showcasing the performance of our model in predicting patient outcomes across different glioma subtypes. Section 5 discusses the implications of our findings, comparing them to existing studies and exploring their potential impact on clinical practice. Finally, Section 6 concludes the study by summarizing the key contributions, outlining the limitations, and suggesting directions for future research.

2 RELATED WORKS

Recent advancements in oncology have increasingly focused on the integration of multimodal data through machine learning to enhance clinical outcomes [11] [12]. The collective research underscores the significance of combining various data types—such as imaging, genomics, histology, and clinical records—to improve diagnostic accuracy, prognostic assessments, and treatment response predictions in cancer care [34] [35]. These studies highlight the transformative potential of multimodal approaches in identifying novel biomarkers, refining predictive models, and addressing the complexities of cancer by leveraging the strengths of diverse data sources [13] [14]. The integration of such multimodal techniques is poised to advance precision oncology, offering more personalized and effective treatment strategies for patients [16] [27].

The use of multimodal approaches in predicting patient outcomes [29] [30] has been specifically studied in recent studies, which further emphasizes the potential of integrating diverse data sources for enhancing prognostic accuracy [15]. Yuan et al. [17] demonstrated the effectiveness of multimodal data integration using deep learning to predict overall survival in glioma patients. The study utilized a comprehensive dataset that included imaging, molecular, and clinical data to train their deep learning models. By integrating these diverse data sources, the models achieved significant predictive accuracy, outperforming single-modality approaches. The research underscores the importance of combining different data modalities to capture the complex biological and clinical features associated with glioma survival. This approach not only enhances the precision of survival predictions but

also offers valuable insights into the underlying mechanisms driving patient outcomes, paving the way for more tailored treatment strategies in precision oncology. Further reinforcing the importance of multimodal data integration, a study focused on glioblastoma (GBM) patients [18] demonstrated the effectiveness of combining structural neuroimaging and resting-state functional MRI (RS-fMRI) with demographic data to predict survival outcomes. The research employed a deep neural network to classify patients into survival categories (<1 year, 1–2 years, >2 years) based on cortical thickness (CT) measures and functional network connectivity (FC), alongside age and sex. The model achieved a high accuracy of 90.6%, identifying key predictors such as the superior temporal sulcus, parahippocampal gyrus, and various brain networks. Notably, this study achieved these results without relying on treatment or tumor genomic data, highlighting the potential of pre-treatment neuroimaging in predicting GBM patient survival and further underscoring the role of multimodal approaches in enhancing prognostic accuracy. Building on this, another study [19] has expanded the scope of multimodal data integration by incorporating histopathology images and RNA-sequencing data to improve survival prediction in brain tumor patients. This study presents a significant advancement in the field of brain tumor prognosis by demonstrating the effectiveness of multi-modal data fusion, integrating histopathology images and RNA-sequencing data to enhance survival prediction in brain tumor patients. The researchers explored three fusion strategies—early, late, and joint fusion—and found that combining these distinct data types improved predictive accuracy compared to using a single modal alone. The study used deep learning models, specifically a ResNet-50 CNN and a multi-layer perceptron (MLP), to pull out important features from large datasets. This made risk stratification more accurate. The findings underscore the potential of multimodal approaches to provide more personalized and precise predictions in oncology, paving the way for improved patient-specific treatment strategies.

Diffusion-weighted MRI (DWI) has emerged as a valuable imaging modality in survival prediction for glioma patients. DWI provides insights into tumor cellularity and microstructural changes [20], which are crucial for assessing tumor aggressiveness. Studies have shown that incorporating DWI metrics into survival prediction models can significantly improve their performance [21]. For example, the study discusses the importance of diffusion MRI metrics, specifically the apparent diffusion coefficient (ADC), in predicting survival for patients with surgically resected brain metastases. It highlights that higher tumor ADC values are associated with improved survival and suggests that including these quantitative imaging biomarkers alongside traditional clinical scores such as the Graded Prognostic Assessment (GPA) and Recursive Partitioning Analysis (RPA) can enhance the accuracy of survival predictions. This combination can improve personalized treatment decisions without requiring additional invasive tests [22].

Despite the significant advancements demonstrated in recent studies, there remains a critical need to further refine and integrate multimodal approaches for enhancing survival predictions in brain tumor patients. While existing research has made substantial progress by incorporating diverse data types, including imaging, molecular, and clinical data, the integration of diffusion-weighted MRI (DWI) with other modalities presents an underexplored area with considerable potential. This study leverages a multimodal approach that integrates MRI embeddings from various MRI sequences and diffusion metrics with detailed clinical data to improve the accuracy of glioma mortality prediction. By combining these advanced techniques, we aim to provide a more nuanced understanding of tumor biology and patient prognosis, ultimately contributing to more effective and personalized treatment strategies in oncology.

3 MATERIALS AND METHODS

3.1 Dataset

In this paper, we leverage a multi-input approach to predict mortality using various types of brain MRI scans as shown in Figure 1, including T1, T2, T2/FLAIR, DWI, susceptibility-weighted (SWI), segmentation, 2D 55-direction HARDI, 3D arterial spin labeling (ASL), T1 Gad, and T1 Gad Seg [23]. This method integrates the diverse information provided by these different MRI modalities to enhance the accuracy and robustness of the prediction model.

In the experimental phase, we utilized the UCSF-PDGM dataset from The Cancer Imaging Archive [23], which consists of MRI scans and clinical data from 495 subjects with histopathologically proven diffuse gliomas. The dataset includes a variety of MRI types (refer to Table 1), such as T2-weighted, T2/FLAIR-weighted, SWI, DWI, pre- and post-contrast T1-weighted images, ASL perfusion images, and HARDI (see Figure 1). Each MRI type provides unique insights into the brain's structure and pathology.

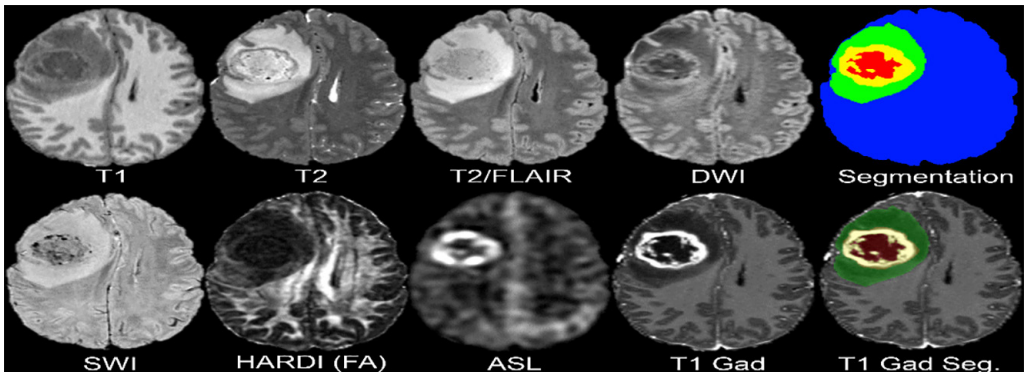

Fig. 1. MRI modalities and tumor segmentation from preoperative imaging using a 3.0 tesla scanner [23]

For instance, T2-weighted and T2/FLAIR images are instrumental in identifying edema and glioma infiltration, while SWI is valuable for detecting microhemorrhages and calcifications. DWI captures variations in water diffusion, highlighting areas of high cellularity typical of aggressive tumors. ASL perfusion imaging offers non-invasive measurements of cerebral blood flow, providing insights into tumor vascularity. The pre- and post-contrast T1-weighted images visualize anatomical details and blood-brain barrier integrity, with post-contrast images revealing areas of abnormal vascular permeability. HARDI provides detailed mapping of white matter tracts, elucidating tumor infiltration and brain connectivity.

Additionally, the UCSF-PDGM dataset includes diffusion MRI metrics such as Eddy_FA, Eddy_L1, Eddy_L2, Eddy_L3, and Eddy_MD, which provide quantitative data reflecting the microstructural properties of tissue (refer to Table 1). These metrics are derived from advanced diffusion imaging techniques and offer detailed insights into the integrity and organization of brain tissue, contributing valuable information for mortality prediction.

In addition to the comprehensive imaging data, the UCSF-PDGM dataset includes detailed clinical information for each subject (refer to Table 1). This encompasses demographic data such as age and sex, tumor genetic testing results such as IDH status and MGMT methylation, WHO CNS tumor grade, and the final pathologic

diagnosis per the 2021 WHO classification. Furthermore, the dataset includes information on the extent of resection (biopsy, subtotal resection, or gross total resection), overall survival, and survival status, which are crucial for mortality prediction.

Table 1. Overview of clinical data and MRI modalities/metrics used for multimodal mortality prediction in GBM patients

Data Type	MRI Modality or Metric	Description
Standard MRI Sequences	T1	T1-weighted imaging provides detailed anatomical information, highlighting normal brain structures and abnormalities.
	T2	T2-weighted imaging enhances fluid-filled spaces, making it ideal for identifying edema and glioma infiltration.
	FLAIR	Fluid-Attenuated Inversion Recovery (FLAIR) suppresses the effects of fluid to highlight lesions near cerebrospinal fluid.
	SWI	Susceptibility-Weighted Imaging (SWI) emphasizes magnetic susceptibility effects, useful for detecting microbleeds and calcifications.
Diffusion MRI Metrics	DWI	Diffusion-Weighted Imaging (DWI) captures water diffusion properties, highlighting areas of restricted diffusion typical of high cellularity.
	Eddy FA	Fractional Anisotropy (FA) measures the degree of directional water diffusion, reflecting white matter tract integrity.
	Eddy L1, Eddy L2, Eddy L3	These are eigenvalues representing diffusion along the principal axes of the diffusion tensor, providing detailed directionality of water diffusion.
	Eddy MD	Mean Diffusivity (MD) is the average diffusion in all directions, providing a general measure of water diffusion in tissue.
	ASL	Arterial Spin Labeling (ASL) is a perfusion MRI technique that measures cerebral blood flow non-invasively.
	HARDI	High Angular Resolution Diffusion Imaging (HARDI) captures complex diffusion patterns, enabling detailed white matter tractography.
Clinical Data	Demographic Data	Includes age, sex, and other demographic details of the patients.
	Genetic Markers	Includes IDH status, MGMT methylation, and other tumor genetic testing results.
	WHO CNS Grade	The WHO classification grade of the tumor, ranging from low to high grade.
	Extent of Resection	Information on whether the tumor resection was a biopsy, subtotal, or gross total resection.
	Survival Data	Overall survival time and status (alive or deceased) of the patients.

This combination of multi-parametric MRI scans and rich clinical data enables a thorough analysis of the factors influencing patient outcomes, enhancing the robustness and accuracy of our predictive model. By leveraging the diverse and complementary information from different MRI modalities and integrating detailed clinical variables, our study aims to provide a nuanced understanding of glioma pathology and its impact on patient prognosis.

3.2 Methodology

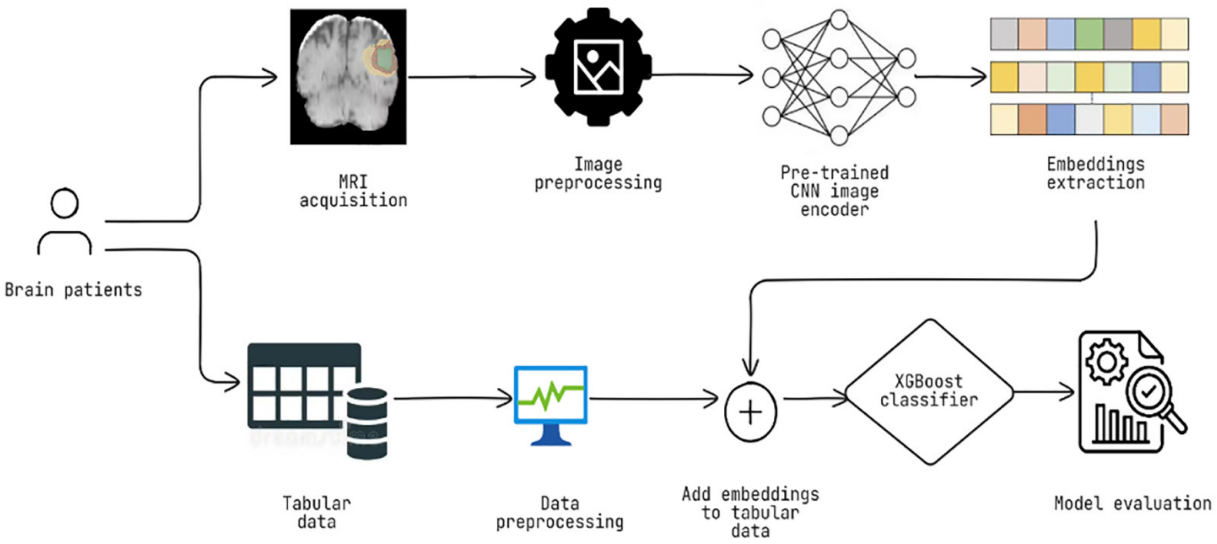

Fig. 2. Workflow of multi-modal data integration using image embeddings and clinical data for predictive modeling

The proposed approach deviates from traditional methods by leveraging multiple MRI types for each patient, enhancing the predictive accuracy for patient survival. Specifically, we followed a structured methodology comprising several key steps (see Figure 2):

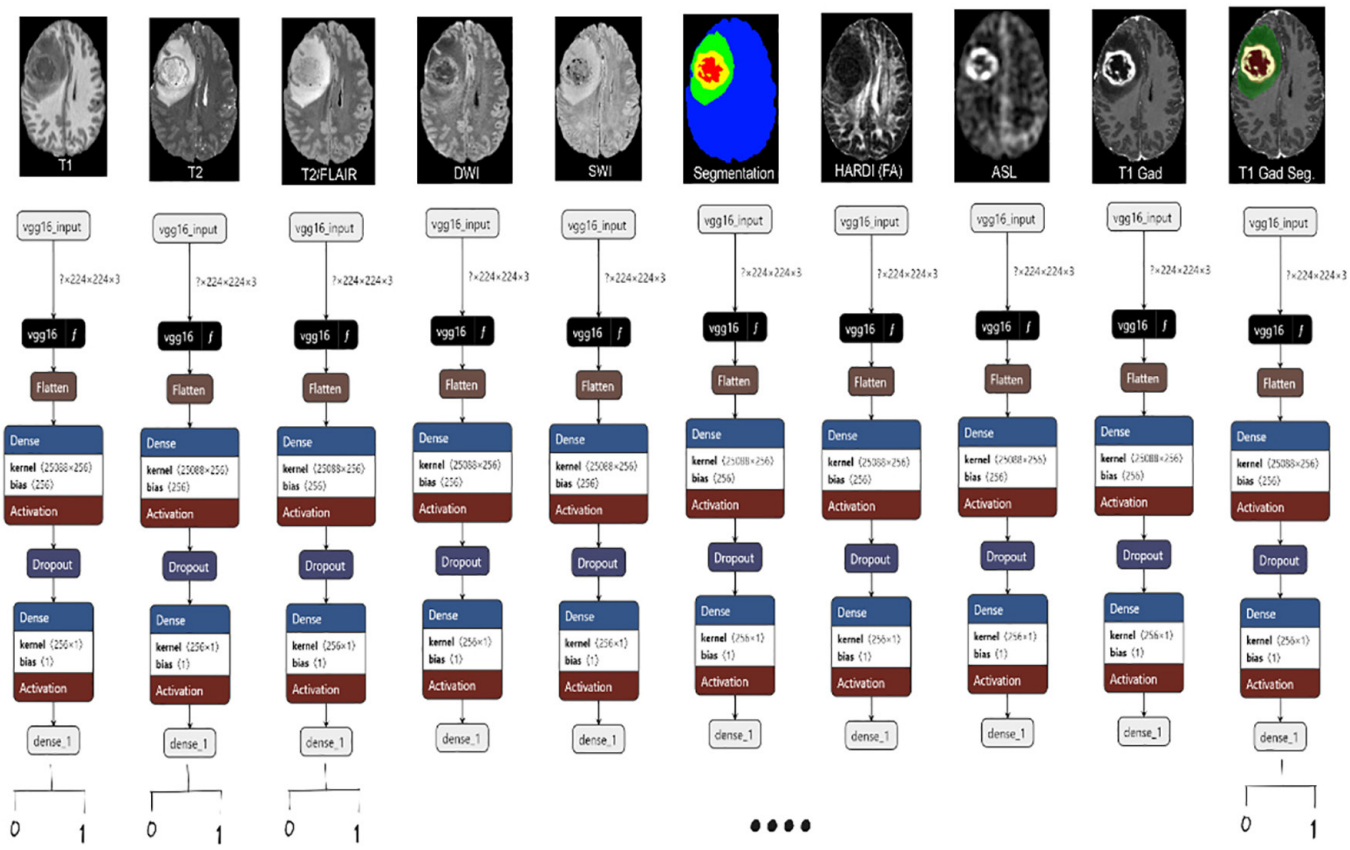

Fig. 3. Training VGG16 classifier on the extracted images

Model training on MRI types: For each MRI modality (*e.g.,* T2, T1, FLAIR, and diffusion MRI), we trained a VGG16 model to predict the binary outcome of patient survival (dead or not dead) (see Figure 3). Each type of MRI scan was carefully preprocessed to ensure consistency, which involved normalization and resizing of the images. In addition to standard MRI sequences, the VGG16 model was also trained on specific diffusion MRI metrics derived from advanced diffusion imaging techniques such as HARDI. The preprocessed images were then fed into the pre-trained VGG16 model, which was initially trained on the ImageNet dataset, to extract relevant features. This feature extraction process involved flattening the 2D feature maps obtained from the convolutional layers into 1D vectors, making them suitable for input into the subsequent fully connected layers.

Dense and dropout layers: The flattened 1D feature vectors were passed through a series of dense (fully connected) layers. The first dense layer typically comprised a substantial number of neurons, such as 256, and employed the ReLU (rectified linear unit) activation function to introduce non-linearity, thereby enabling the network to learn complex patterns. To prevent overfitting, dropout layers were employed after the dense layers, randomly dropping a fraction of the neurons during training to ensure the model generalizes well to unseen data.

Multi-input model architecture: Each MRI scan type underwent the aforementioned steps independently, resulting in multiple separate pipelines. The outputs of these pipelines—each representing the extracted features from a specific MRI scan type—were then concatenated into a single comprehensive feature vector. This combined vector integrated the diverse information captured from the different MRI modalities, providing a holistic representation of the input data.

Generating embeddings and combining with clinical data: Once the VGG16 models were trained, we generated embeddings for each MRI image, capturing the essential features learned by the models. The embeddings from all MRI types for each patient were concatenated. These concatenated embeddings were then combined with the tabular clinical data, resulting in a rich feature set that included both imaging and clinical information. The clinical data encompassed demographic details, tumor genetic testing results, and other relevant clinical variables, enhancing the predictive power of the model.

Training XGBoost model: Finally, we trained an XGBoost model using the combined feature set (embeddings + clinical data) to predict patient survival. The XGBoost model, known for its robustness and efficiency in handling large datasets with heterogeneous features, utilized the rich feature set to produce accurate mortality predictions. The final model outputted a probability score between 0 and 1, indicating the likelihood of mortality, with higher values suggesting a greater risk.

3.3 Data preprocessing and integration

To ensure robust model training, we implemented a comprehensive preprocessing pipeline for both imaging and clinical data. For MRI data, steps included addressing scanner variations, standardizing spatial orientation, and maintaining image quality. Intensity normalization was performed using z-score standardization to minimize scanner-related variability, followed by skull stripping with FSL's Brain Extraction Tool (BET) to isolate brain structures. Spatial alignment was standardized to the MNI152 template (1 mm^3 resolution), and quality control measures eliminated artifacts, ensuring consistent dataset orientation.

Clinical data preprocessing included handling missing values via multiple imputation, encoding categorical variables with one-hot encoding, and normalizing

continuous variables to a [0, 1] range to prevent disproportionate feature influence. Highly correlated features (correlation > 0.85) were removed to reduce redundancy and multicollinearity.

Integrating imaging and clinical data posed challenges due to their heterogeneity. A two-stage strategy was employed: first, extracting 4096-dimensional embeddings from the VGG16 network's final layer, and second, concatenating these embeddings with processed clinical features through a custom fusion layer to leverage complementary information. See the appendix for the GitHub repository with the study code.

Choice of VGG16 architecture: We selected VGG16 for feature extraction after extensive testing against alternatives such as ResNet50 and EfficientNetB0. VGG16 outperformed others, achieving 2–3% higher validation accuracy on our dataset. Its simple sequential architecture captured subtle tissue contrasts effectively and facilitated easier modification and interpretability—key for clinical applications. Additionally, VGG16 required less memory during inference, making it more practical for resource-limited clinical settings. While EfficientNet often excels in natural image tasks, VGG16's demonstrated effectiveness in capturing MRI tissue variations solidified its selection.

4 EXPERIMENTAL RESULTS

The obtained results are presented in three parts: the performance of individual VGG16 models on different MRI types (refer to Table 2), the performance of the XGBoost model trained on concatenated embeddings from all MRI types, and the performance of the XGBoost model trained on combined embeddings and clinical data (refer to Table 3). By integrating multi-parametric MRI data with detailed clinical information, our approach provides a comprehensive analysis of the factors influencing patient outcomes, thereby enhancing the robustness and accuracy of mortality prediction in diffuse glioma patients.

4.1 Performance of VGG16 models on different MRI types

The performance metrics of the individual VGG16 models trained on various MRI types are summarized in Table 2. The metrics include accuracy, precision, recall, and F1 score.

Table 2. Performance metrics of VGG16 for different MRI types

MRI Type	Accuracy	Precision	Recall	F1 Score
Bias	0.905	0.921	0.887	0.903
Eddy FA	0.891	0.929	0.847	0.886
Eddy L1	0.875	0.884	0.863	0.873
Eddy L2	0.885	0.837	0.956	0.893
Eddy L3	0.848	0.910	0.774	0.837
Eddy MD	0.881	0.880	0.883	0.881
Misc	0.883	0.928	0.831	0.877
Parenchyma Segmentation	0.895	0.908	0.879	0.893
Segmentation	0.909	0.895	0.927	0.911

The individual VGG16 models showed high performance across various MRI types, with accuracy ranging from 0.848 to 0.909 and F1 scores ranging from 0.837 to 0.911. The highest accuracy and F1 score were achieved by the segmentation MRI type, indicating its superior ability to predict patient survival.

4.2 Performance of XGBoost models

The performance of the XGBoost models trained on different feature sets is summarized in Table 3. The first set of results corresponds to the XGBoost model trained on concatenated embeddings from all MRI types. The second set of results pertains to the XGBoost model trained on combined embeddings and clinical data.

Table 3. Performance metrics of XGBoost models

Model	Accuracy	Precision	Recall	F1 Score
XGBoost on Combined Embeddings (All MRI)	0.733	0.655	0.844	0.738
XGBoost on Combined Embeddings + Clinical Data	0.865	0.837	0.905	0.870

The XGBoost model trained on concatenated embeddings from all MRI types demonstrated moderate performance with an accuracy of 0.733 and an F1 score of 0.738. The high recall value of 0.844 indicates the model's effectiveness in identifying positive cases, although the precision was relatively lower at 0.655. The inclusion of clinical data along with the embeddings significantly enhanced the performance of the XGBoost model. This model achieved an accuracy of 0.865 and an F1 score of 0.870, demonstrating a balanced performance in both identifying positive cases and maintaining precision. The recall value of 0.905 indicates a high sensitivity to detecting positive survival outcomes, while the precision of 0.837 reflects the model's reliability in predicting true positives.

In summary, the derived results underscore the effectiveness of integrating multiple MRI modalities, including advanced diffusion metrics, with comprehensive clinical data for predicting patient survival. The combined approach, which employs XGBoost on both imaging-derived embeddings and clinical variables, demonstrated superior performance compared to models relying solely on imaging or clinical data. These findings highlight the transformative potential of multimodal integration, advancing the accuracy and reliability of survival predictions and paving the way for more personalized and informed treatment strategies in glioma care.

5 DISCUSSION

The central problem addressed by this study is the challenge of accurately predicting glioma patient mortality using non-invasive imaging techniques. Gliomas, being highly heterogeneous brain tumors, present significant variability in terms of prognosis, even within the same tumor grade. Traditional diagnostic tools often rely on isolated imaging modalities or clinical factors, which may not fully capture the complexity of the disease. This research aims to overcome these limitations by employing a multimodal approach, integrating MRI sequences and diffusion metrics with detailed clinical data. By leveraging deep learning models

like VGG16 for feature extraction and combining them with machine learning algorithms such as XGBoost, the study seeks to enhance the precision and reliability of mortality prediction for glioma patients. This method addresses the need for more comprehensive and personalized tools in neuro-oncology to improve patient outcomes.

The results of this study underscore the critical importance of integrating both MRI-derived embeddings and clinical data to enhance the prediction of patient survival in diffuse gliomas. The analysis was conducted in three stages: evaluating individual VGG16 models trained on different MRI modalities, assessing the performance of an XGBoost model on concatenated embeddings from these MRI modalities, and examining the impact of incorporating clinical data into the XGBoost model alongside the MRI embeddings.

The VGG16 models trained on individual MRI types showed strong performance, with accuracies ranging from 0.848 to 0.909 and F1 scores from 0.837 to 0.911, highlighting the unique features captured by each modality. The segmentation-based model achieved the highest scores, excelling in survival outcome distinction. However, combining embeddings from all MRI types in an XGBoost model yielded moderate results (accuracy: 0.733, F1: 0.738), likely due to high dimensionality and redundancy. Adding clinical data improved performance significantly (accuracy: 0.865, F1: 0.870), balancing precision (0.837) and recall (0.905). High recall, essential in medical contexts, ensures the identification of at-risk patients, minimizing missed cases and enhancing timely interventions.

Table 4. Comparison of glioma survival/mortality prediction methods using different datasets and approaches

Study	Dataset	Approach	Accuracy
Our study	UCSF PDGM	XGBoost on MRI embeddings + clinical data	86.5%
Manjunath et al. [31]	BraTS 2020	Machine learning models (KNN, SVM, etc.) on MRI radiomic features + clinical data	64.4% (KNN)
Shboul et al. [32]	BraTS 2017 & 2018	Survival regression with MRI features and clinical data	68%
Islam et al. [33]	BraTS 2018	ANN regression on extracted MRI and clinical features	67.9%

The comparison in Table 4 underscores the superiority of our proposed approach over existing methods in glioma survival prediction. Unlike prior studies that predominantly rely on publicly available datasets such as BraTS, our study benefits from the UCSF-PDGM dataset, which provides richer and more diverse clinical data, enabling a more comprehensive analysis. Furthermore, our multimodal approach, which integrates MRI embeddings derived from advanced deep learning models such as VGG16 and diffusion metrics with detailed clinical data, demonstrates a significant improvement in accuracy. Specifically, by combining these embeddings with XGBoost, our model achieves an accuracy of 86.5%, substantially outperforming previous methods such as the KNN-based approach by Manjunath et al. (64.4%) [31] and the regression-based techniques by Shboul et al. (68%) [32] and Islam et al. (67.9%) [33]. This highlights the effectiveness of combining deep learning and machine learning within a multimodal framework to enhance prediction performance and emphasizes the critical role of integrating diverse data modalities for advancing glioma prognosis.

This study highlights that integrating MRI-derived embeddings with clinical data provides a comprehensive approach to predicting outcomes in diffuse gliomas. The combined model outperforms single-modality approaches, leveraging clinical variables such as age, sex, genetic markers, and WHO CNS grade to enhance the interpretability of MRI data. This synergy captures complex interactions, improving predictive accuracy, recall, and patient prognosis, enabling more personalized treatment strategies. The findings of the study align with prior research emphasizing the importance of multimodal data integration in medical prognosis. Studies have shown that combining imaging, radiomic, clinical, and genetic features enhance predictions of glioblastoma molecular subtypes and survival outcomes [24] [25]. The inclusion of radiomic signatures alongside genetic factors, such as IDH mutations and clinical risk variables, has further improved survival predictions in high-grade gliomas [26]. Additionally, integrating radiologic, histopathologic, and epigenetic markers has proven effective for robust survival risk stratification in glioma patients [17]. This study introduces key innovations in glioma survival prediction by leveraging diverse MRI sequences, including standard modalities (T1, T2, FLAIR) and advanced diffusion metrics from HARDI (e.g., Eddy_FA, Eddy_MD). Using a pre-trained VGG16 model for feature extraction, we generated modality-specific embeddings enriched with detailed clinical data. The inclusion of advanced diffusion metrics, offering unique insights into tissue microstructure, marks a novel contribution to multimodal survival prediction. Integrating these data into an XGBoost model created a robust pipeline that improves predictive accuracy and addresses the limitations of single-modality approaches. This framework highlights the clinical potential of multimodal strategies for personalized treatment, though challenges like data integration and model interpretability remain.

The transition from development to deployment presented several challenges, particularly in computational resources, processing time, and data handling. Processing large 3D MRI scans required significant memory, which we addressed through several optimizations: enabling memory growth for GPUs, implementing parallel processing with multiprocessing pools, batch processing of images, and converting 3D scans to 2D slices with averaging to reduce memory demands. The pipeline, encompassing multiple steps such as image extraction, preprocessing, feature extraction, and classification, posed challenges for real-time predictions due to preprocessing overhead. To mitigate this, we employed parallel processing techniques, such as using ThreadPoolExecutor in the image extraction stage, to improve efficiency. Data handling also required solutions for managing missing or corrupted scans, addressing variations in image quality and formats, and ensuring consistent preprocessing across different MRI types. These optimizations were crucial to adapting the model for practical, real-world clinical use. In summary, the deployment of AI models in clinical practice necessitates careful consideration of hardware limitations, workflow integration, and data heterogeneity. Our work provides a roadmap for addressing these challenges, bridging the gap between research and real-world implementation. To enable widespread adoption in healthcare settings, future efforts should focus on further optimizing and standardizing these approaches while expanding the scope of predictive models. This includes incorporating additional data types, such as genomic and proteomic profiles, to enhance predictive power and clinical utility. Longitudinal studies are essential to evaluate the long-term effectiveness of these models in practice, and developing interpretable frameworks will be critical to ensure predictions are both understandable and trusted by medical professionals.

6 CONCLUSION

In conclusion, the integration of multi-parametric MRI data with detailed clinical information presents a powerful approach for predicting patient survival in diffuse gliomas. Future work should explore the inclusion of additional data types, such as genomic and proteomic profiles, to further enhance the predictive power and clinical utility of these models. Additionally, the development of interpretable models will be crucial for clinical adoption, ensuring that predictions can be understood and trusted by medical professionals. The high recall achieved in this paper underscores the critical importance of such integrative approaches in ensuring no at-risk patient is missed, thus enhancing patient care and treatment outcomes.

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8 APPENDIX

The code used for feature extraction, data integration, and model training is publicly available at GitHub Repository.

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