Deep Learning Guided Radiogenomic Signatures for Prognostic Stratification in Glioblastoma Multiforme

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Abstract: Glioblastoma multiforme (GBM) is the most aggressive and lethal primary brain tumor, with an average survival of no more than 15 months despite advances in surgery, chemotherapy, and radiotherapy. Linking imaging phenotypes with genomic frameworks can improve personalized prognosis and treatment planning. This study develops a deep learning-based radiogenomic framework that integrates high-dimensional imaging features extracted from multiparametric MRI using a convolutional neural network (CNN) with key molecular biomarkers, including EGFR amplification, IDH mutation, and MGMT promoter methylation. A multiomics fusion module combined imaging-derived features with genomic alterations to enable stratified survival prediction. The publicly available datasets were used to train and validate the framework, i.e., TCIA and TCGA-GBM. The CNN-based radiogenomic model was more successful than the traditional radiomic and dictionary learning -based approaches, with high prognostic accuracy. Survival stratification into high- and low-risk groups showed significant differences, as confirmed by Kaplan–Meier analysis, C-index, and AUC metrics. The radiogenomic markers based on the model obtained biologically meaningful information on tumor heterogeneity and a better predictive outcome than the traditional methods. Radiogenomic signatures based on deep learning make it possible to prognosticate GBM accurately, non-invasively, and biologically in a manner that is precise, relevant, and now more useful in the field of neuro-oncology. The next step in research involves future multi-institutional validation, explainable AI integration, and adding more omics data to make prognostics more accurate and clinically applicable.

Keywords: CNN, Deep Learning, Glioblastoma Multiforme, Image Feature, MRI, Prognostic Stratification, Radiogenomic, Survival Prediction, TCGA.

INTRODUCTION

Glioblastoma multiforme (GBM) is the most threatening and frequent form of initial brain cancer, which grows aggressively, is resistant to treatment, and progresses clinically swiftly. It is not just a simple malignant neoplasm, and the disease exhibits an extensive infiltrative pattern as well as clinical relevance of the cellular proliferation not only in the tumor margins but also in the normal surrounding brain. GBM has an anatomical expression as shown in Figure **1**.

This picture demonstrates the part of the brain that is impacted by GBM, and this shows how invasive and disunited the tumor is.

The Cancer Genome Atlas (TCGA) was the first type of cancer that has been comprehensively described in terms of its key genetic alterations and driver mutations, thus showing how highly complicated its genomic picture is [1]. In accordance with the existing classifications, the GBM is split into two groups according to the isocitrate dehydrogenase (IDH) status: IDH-wild and IDH-mutant. Though certain other studies cited in this analysis were published before the latest update of the WHO classification, and thus continue to use the former nomenclature of secondary GBM to denote the IDH-mutant tumors.

Radiogenomic signatures are genetic patterns of the tumor associated with non-invasive imaging characteristics, and the radiogenomic signatures are needed to provide accurate and personalized prognosis. It enhances more accurate cancer management through better decision-making in oncology and helps in evaluating the tumor biology comprehensively. It will also minimize the constraints of invasive surgical sampling, improve early diagnostic processes, and enable better characterization of the tumors. Radiomics is a quantitative method of MRI and

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other imaging technologies that identifies the small imaging features and foci of interest that cannot be seen with the naked human eye, resulting in the enhancement of clinical knowledge and prognostic stratification of GBM [17].

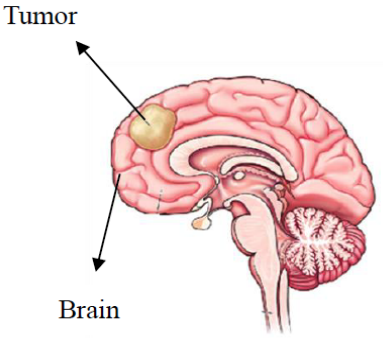

Figure 1: Anatomical Representation of Glioblastoma Multiforme (GBM).

A radiogenomic study is an integrative study of imaging characteristics and molecular data that has been used to study tumor biology and clinical outcomes. The genomic model identifies the modification of DNA in the tumor and connects it to the radiomic to come up with predictive forms. Radiogenomics is able to foretell molecular subtypes, aggressive tumor behavior, and patient survival through direct imaging data by correlating radiomic landscapes with genomic patterns [18]. Such analysis is conducted in a systematic way of work with many steps, which is illustrated in Figure **2**.

This visual representation shows the process of the radiogenomic study, beginning with the acquisition of multiparametric MRI, feature extraction using CNN, the combination of genomic data, and ending with predictive modeling of molecular subtypes and patient survival.

Artificial intelligence (AI) has many subfields, one of them being deep learning, a technology that has revolutionized the analysis of medical data [19]. Deep learning is not based on handcrafted features as compared with traditional machine learning methods. Convolutional Neural Networks (CNNs), one of the most popular deep learning models in the industry, can be applied to raw data to learn hierarchical representations and produce structured and supervised representations. Deep learning has proven useful in healthcare by being able to identify the ability to capture complex spatiotemporal relationships across cross-sections of medical images. Medical imaging is one area where it is capable of identifying the patterns that are challenging or even indescribable through traditional methods [20].

Multiparametric MRI provides heterogeneous information as to the morphology of the tumor, cellular density, necrosis, and vascularity. Using such imaging data, CNNs are able to find delicate patterns that reflect relevant genetic modifications (EGFR amplification, MGMT promoter methylation, and IDH mutation). Together with genomic data, this can form a radiogenomic framework that transcends basic correlation, permitting predictive patient outcome modeling [2].

Deep learning technologies are still changing the paradigm of the radiogenomics of glioblastoma (GBM). It combined both imaging and molecular information to enhance survival projections, give customized treatment advice, enhance the comprehension of tumor heterogeneity, and advance the effects of precision medicine [16].

LITERATURE REVIEW

The article [7] applies a deep learning-based model on scientific and radiomic features to divide early treatment of glioblastoma patients. It was also used on 76 patients with early prediction of glioblastoma disease and improved the disease after chemoradiotherapy treatment [8]. The outcome was established through a follow-up of up to six months after chemoradiotherapy. Constructed models included clinical variables, MGMT promoter methylation status, and 307 quantitative imaging features derived from early post-chemoradiotherapy T1-weighted contrast-enhanced, T2-weighted, and Apparent Diffusion Coefficient (ADC) imaging related to enhancing disease and perilesional oedema masks. Recursive feature elimination augmented with bootstrapped cross-validation was used for feature selection.

The result includes that Age, MGMT promoter methylation status, three radiomic characteristics from the enhancing disease mask on ADC, two shape-based features from the enhancing disease mask, and one radiomic feature from the perilesional oedema mask were among the top features chosen on T2WI. The accuracy of the model obtained after this was 73.7%, the sensitivity of 78.2%, the specificity of 66.7%, and the area under the receiver operating characteristic curve (AUC) was 0.80 [10].

The research background [9] incorporates the whole-exome sequencing (WES) and somatic copy number alteration (SCNA) data, which can use prognostically significant molecular subtypes of wild-type glioblastoma of IDH1/2 that were not identifiable

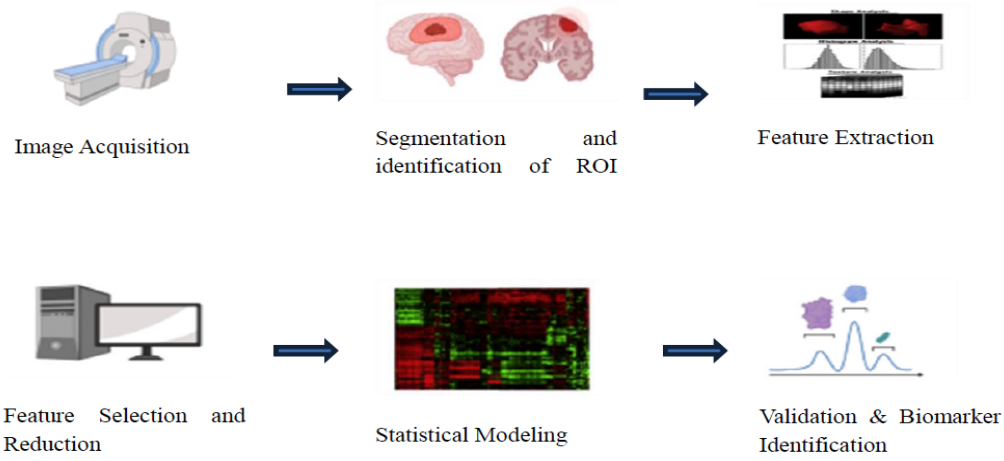

Figure 2: Workflow of Radiogenomic Analysis in GBM.

by epigenetic or clinical values. Radiologic features of these molecular subtypes have not yet been determined, as 46 multisequence, pre-operative magnetic resonance imaging (MRI) scans of IDH1/2-wildtype glioblastoma patients in The Cancer Imaging Archive (TCIA) were analyzed based on their radiologic features (n = 35,340), and each of them had a corresponding WES/SCNA data [23]. Their feature choice comparison method was with the variance thresholding feature selection method, recursive feature elimination, and least absolute shrinkage and selection operator (LASSO) feature selection applied in training six standard machine learning classifiers to distinguish between a mixture of molecular subtypes.

Consistency of us based on two prognostic subtypes to distinctly classify glioblastomas. This was consistent with an area under the curve of 0.80 (±0.03) on the ridge logistic regression on the PCA (15-dimensional) embedding of the feature set produced by our whole feature selection procedure [24]. They contain characteristics that can be used to provide the outlines of the two T2 signal abnormality regions and T2-weighted fluid-attenuated inversion recovery (FLAIR) MRI sequences characterizations that can perhaps be the best in describing the two populations and have to be considered [12].

The past few decades have seen significant advancements in genomic methodology and computational medicine [11]. These innovations have sparked interest in potential therapeutic targets accessible for the treatment of glioblastoma. Nevertheless, prognosis and targeted treatment efficacy for glioblastoma patients are dismal at best [25]. Glioblastoma is very heterogeneous in both time and space. The presence of different genetic subpopulations in glioblastoma tumors increases the adaptability of the tumors to the changing environmental factors. As a result, there is a lack of effective therapeutic response in glioblastoma patients, as treatment strategies remain agnostic to the different genetically defined regions of the tumor. Genomic modifications within the tumor give rise to distinct phenotypic patterns observable through medical imaging.

In this context, the role of magnetic resonance imaging is crucial in glioblastoma, as it helps define different biologically and phenotypically distinct regions to derive the molecular signatures of the tumor. As mentioned in previous sections, genomics encompasses a host of analyses for tumor characterization and assessment of tumor response during therapy that are non-invasive and global in scope. The review tries to describe the different opportunities of utilizing radiogenomic methods to categorize patients with regard to the distinct characteristics of tumors in an effort to construct specific therapies.

This study aims to construct an ICI-related prognostic biomarker to assess the prognostic relevance of glioblastoma patient radiomic landscapes, as well as evaluate related features of ICI in GBM patients. Three databases provided the gene expression and survival information of GBM patients. Based on the ICI pattern identified by the CIBERSORT and ESTIMATE algorithms, a unique ICI score was created for every GBM patient and independently verified. Quantitative radiomic characteristics were also taken out of the peritumoral and intratumoral areas. Due to this, the association between the medical images and the ICI scores was developed in the group, which had genetic and image data using machine

learning [13]. The prognostic value of the identified radio genomic model was examined using the imaging and survival data on another dataset [14].

METHODOLOGY

Data Sources and Multimodal Input Acquisition

In this study, a radiogenomic model is used to conduct prognostic studies in glioblastoma using multiparametric MRI features and genomic biomarkers. T1, T1CE, T2, and FLAIR imaging images were acquired via The Cancer Imaging Archive (TCIA), whereas the corresponding genomic features (EGFR amplification, IDH mutation, and MGMT promoter methylation) were acquired in the TCGA-GBM dataset [3]. Such multimodal inputs formed the principles of the radiological and molecular togetherness under one predictive system.

Imaging Preprocessing and Tumor Subregion Segmentation

All MRI sequences were preprocessed using standardized methods to minimize inter-scanner variability and provide the spatial consistency of all subjects. All MRI sequences were skull-stripped, spatially co-registered to a standard set of anatomical templates, and intensity normalized. A 3D U-Net CNN with PyTorch was trained in the segmentation of tumor subregions, such as enhancing tumor core, necrotic core, and peritumoral edema, which was fully automated. In order to be accurate, all segmentations were then manually inspected and corrected by a board-certified radiologist with 10 years of experience in neuro-oncology, who confirmed the limits of the tumor and corrected areas of necrosis or edema accordingly. This methodology guaranteed an accurate definition of regions of interest to be used in the robust extraction of downstream features and radiogenomic integration [15].

CNN Architecture for Radiomic Feature Extraction

A specialized Convolutional Neural Network (CNN) was created to obtain latent radiomic embeddings of the multiparametric MRI sequences. The network was a conventional 2D convolutional network with four consecutive convolutional blocks. They all had a convolutional layer with a kernel of 3 x 3, Rectified Linear Unit (ReLU) activation, batch normalization, and a 2 x 2 max-pooling process. The convolutional blocks had 32, 64, 128, and 256 filters and, thus, enlarged the representational capacities of the model gradually, decreasing the spatial resolution by downsampling. This convolutional stem was then followed by a flattening layer and two fully connected layers with 512 and 128 neurons that were both ReLU activated, and dropout regularized with a dropout rate of 0.3. The output layer produced a 128-dimensional radiomic embedding, which was the reduced feature representation of every patient [4].

To be reproducible, all CNN parameters (Hyperparameters such as layer arrangements, filter sizes, activation functions, optimizer parameters, learning rate schedule, batch size, epochs, and regularization methods) are listed in a Table **1**. Another Table **2**) details all radiomic features extracted from each tumor subregion, including first-order, texture, and shape features, along with their definitions and units.

All MRI slices were resized to 224×224 pixels and normalized before being fed into the model. The CNN was trained by setting the learning rate to 0.0001 using the Adam optimization algorithm and reducing this rate by half after every ten epochs. The categorical cross-entropy loss function was employed to optimize survival-related class separation. A stratified sampling strategy was used to divide the dataset into training (70%), validation (15%), and independent testing (15%) to retain the class distribution in the survival labels. Up to 100 epochs with a 16-size batch were trained, and early stopping on the validation loss was used to avoid overfitting.

The subjects had their CNN-derived radiomic signature recovered after the training, which was a 128-dimensional radiomic signature of the final combined layer, and the final fully connected layer was discarded. These embeddings represented high-order morphological and textural patterns of tumor subregions, such as necrotic irregularity and edema distribution, which are not easily quantifiable using hand-engineered radiomic descriptors. The resulting feature vectors were then combined with genomic biomarkers in the multiomics fusion module.

Genomic Biomarker Encoding and Multiomics Integration

Simultaneously with imaging-based feature extractions, binary encodings were constructed to indicate the occurrence or lack of significant genomic changes. The biomarkers that were selected were: EGFR, IDH, and MGMT, and were selected based on the proven clinical relevance of each in the prognosis of GBM, and also the treatment response of the

Table 1: CNN Architecture and Hyperparameters for Radiomic Feature Extraction

Parameter	Specification
Model Type	2D Convolutional Neural Network (CNN)
Input Size	224 × 224 × 3 (resized MRI slices, normalized)
Layer Arrangement	Conv(32, 3×3) → ReLU → BatchNorm → MaxPool(2×2) → Conv(64, 3×3) → ReLU → BatchNorm → MaxPool(2×2) → Conv(128, 3×3) → ReLU → BatchNorm → MaxPool(2×2) → Conv(256, 3×3) → ReLU → BatchNorm → MaxPool(2×2) → Flatten → Dense(512) → ReLU → Dropout(0.3) → Dense(128) → ReLU → Dropout(0.3) → Output: 128-dimensional embedding
Filter Sizes	3 × 3 for all convolutional layers
Number of Filters	32, 64, 128, 256 progressively
Activation Functions	ReLU for hidden layers, linear output for embedding
Optimizer	Adam
Optimizer Parameters	β1 = 0.9, β2 = 0.999, ε = 1e-08
Learning Rate Schedule	Initial LR = 0.0001, reduced by 50% every 10 epochs
Batch Size	16
Epochs	Up to 100 with early stopping on validation loss
Loss Function	Categorical cross-entropy
Regularization Methods	Dropout (0.3), early stopping, batch normalization
Data Augmentation	Rotation ±15°, horizontal flip, zoom ±10%, shift ±10%
Validation Strategy	Stratified sampling: training 70%, validation 15%, testing 15%
Software / Hardware	PyTorch framework, NVIDIA GPU

disease. These genomic variables were curated and preprocessed before integration. A multiomics fusion module combined the CNN-derived radiomic embeddings with the genomic biomarker encodings to form a comprehensive feature space capable of capturing tumor morphology, tissue heterogeneity, and molecular state [5].

Radiogenomic Integration Workflow

The entire workflow of the proposed radiogenomic integration framework is shown in Figure 3 [11]. It commences with the quantitative features of multiparametric MRI sequences extraction, such as structural, diffusion, and perfusion modalities. Simultaneously, molecular data, i.e., gene expression measures and noteworthy genomic changes, are ready to be incorporated. The imaging-derived features and molecular features are then fed through a multiomics fusion module, which matches and fuses the heterogeneous data together into a latent representation. This combined feature space is then used to train a survival prediction model which approximates the overall survival and classifies the patients into the low- and high-risk categories. Radiologic and genomic information are also combined to capture tumor heterogeneity and enhance the accuracy of prognostic information, which is essential to highlight in the workflow.

This figure illustrates the complete radiogenomic workflow, starting from multiparametric MRI feature extraction and genomic data preparation, proceeding through multiomics fusion, and ending with survival prediction and risk stratification into low- and high-risk patient groups.

MGMT Methylation Interpretation in the Prognostic Framework

MGMT is a DNA repair gene responsible for correcting alkylation damage. Temozolomide causes lesions in DNA, such as O6-methylguanine, that induce tumor cell apoptosis. The MGMT promoter is also methylated, which silences the expression of the gene, and the lesion cannot be repaired, thereby increasing the treatment resistance. About 40-50% of GBM patients show MGMT promoter methylation, which is a powerful outcome predictor of patient survival and response rates toward temozolomide and radiotherapy. But heterogeneity of tumors makes it difficult to dictate that only one biopsy can give a picture of the whole tumor mass. The point of radiogenomic modeling is to infer MGMT status (non-invasively) using MRI, which is a difficult but clinically important task in itself [21,22].

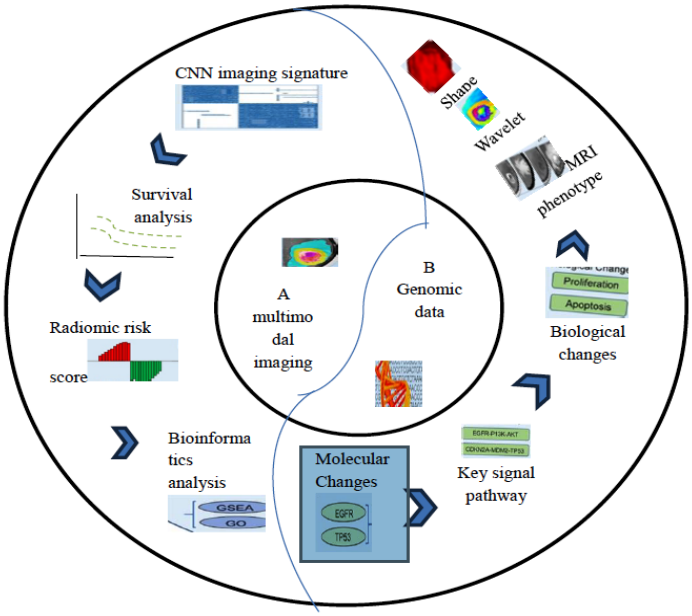

Figure 3: Workflow of the Proposed Radiogenomic Integration Framework for GBM Survival Prediction.

Patient Cohorts and Clinical Characteristics

This involved 112 confirmed cases of glioblastoma clinically, with 50 females and 62 males. The discovery cohort was comprised of 75 patients obtained through the TCGA database, and the validation cohort is made up of 37 patients from China University. MRI images of the validation cohort were obtained on 3.0 Tesla scanners with standardized imaging parameters such as T1-weighted, T1-weighted contrast-enhanced, T2-weighted, and FLAIR with slice thickness of 1-5 mm and in-plane resolution of 0.5-1 mm. Ethical approval was obtained for all imaging and data acquisition procedures, and all methods adhered to institutional and international guidelines. Inclusion criteria required early-stage GBM treatment and complete pre-treatment MRI studies. Exclusion criteria included patients who were already undergoing treatment or who did not have survival data. Survival time was computed from initial pathological diagnosis to patient death or censoring. Demographic and clinical characteristics are summarized in Table **1** [6].

Multi-Layered Survival Prediction Model

The integrated radiogenomic feature space was used to construct a multi-layered survival prediction model. Patients were stratified into high-risk and low-risk groups based on the model output. Standard clinical measures such as Area Under the Curve (AUC), concordance index (C-index), and Kaplan-Meier survival curves were used to evaluate the performance of the survival prediction. These analyses showed that the framework was effective in generating clinically meaningful prognostic stratification.

Overall Methodological Framework

As outlined in Figure **3**, the methodology involves starting with multimodal data collection, then continuing with preprocessing, CNN-based representation learning, genomic biomarker integration, multiomics fusion, and risk categorization and survival prediction. This method is a step toward a more precise, interpretable, and clinically relevant radiogenomic predictor of glioblastoma prognosis by integrating radiomic signatures derived with deep learning with genomic biomarkers.

RESULT

The outlined radiogenomic framework, which utilizes CNN, is more effective than traditional radiomics and those based on dictionary learning approaches for prognostic stratification of GBM patients. In order to categorize high- and low-risk survival groups, the integrated model that correlated mpMRI from the TCIA cohort with genomic data from TCGA-GBM obtained a C-index of 0.78 and an AUC of 0.82. The model's clinical confidence was increased when Kaplan-Meier survival analysis revealed a statistically significant difference between the two groups (log-rank test, $p < 0.01$). This validates the predictive ability of combined genomic biomarkers and radiomic signals produced from deep learning for GBM outcomes.

Table 2: Demographic and Scientific Landscapes of Patients in the Validation Data Set and the Discovery Dataset

Patient characteristics	Discovery Set	Validation Data Set
Number of patients	75 (67%)	37 (33%)
Female	19	18
Male	43	32
Age ranges	19 to 84	10 to 78
Mean	54.990	53.950
Median	57	55
OS ranges	30 to 1642	77 to 1870
Mean	495.160	494.220

Based on the convincing outcomes in prognostic stratification of GBM patients, the proposed framework, which collaborates deep learning with guided radiogenomics, showed great efficacy. The model was developed on the discovery cohort (n=75, TCGA/TCIA) and was subsequently validated on an independent cohort (n=37, China University). The model was comparatively better on the discovery and independent cohort sets. The Kaplan-Meier estimator is used to estimate the probability of survival, as shown in equation 1.

$$S(t) = \prod_{ti \le t}\left(1 - \frac{d_i}{n_i}\right) \quad (1)$$

Where n_i is the number of people at risk prior to time t_i, d_i is the number of fatalities at time t, and t_i is the time of the event (death). Patients with more promising radiogenomic characteristics who show a greater S(t) over time are highlighted in the low-risk category. The high-risk group has a reduced chance of surviving and dies more quickly. The statistical significance of the change between these two curves is confirmed by the long-rank test (p=0.0000).

Figure **4** shows the Kaplan-Meier survival curves for CNN-based radiogenomic stratification in glioblastoma patients. The prognostic evaluation of glioblastoma patients with CNN-genomic derived signatures, as demonstrated with Kaplan-Meier survival analysis, indicates that the green curve identifies patients classified as low-risk. In contrast, the red curve signifies the high-risk group as defined by the model. The patients classified as low-risk appear to have a considerably higher survival rate throughout the follow-up period than the high-risk group, whose probability of survival declines steeply.

This separation is confirmed by the log-rank test to have statistical significance with a value of p = 0.0000, meaning the difference between the two survival distributions is extremely significant. This indicates that the deep learning–based frameworks for radiogenomics proposed in this paper do classify patients into distinctly different risk groups with distinct clinical outcomes. The radiomic signature is employed to categorize patients as high-risk and low-risk patients. The vertical line is the 95 percent assurance interval.

To compare the CNN-based radiogenomic model with the traditional model, the accuracy, precision, F1 Score, recall, and AUC formula are used.

For accuracy,

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN} \quad (2)$$

To calculate precision,

$$\text{Precision} = \frac{TP}{TP + FP} \quad (3)$$

For Recall,

$$\text{Recall} = \frac{TP}{TP + FN} \quad (4)$$

To measure F1 Score,

$$\text{F1 Score} = 2 \text{ X } \frac{Precision\ X\ Recall}{Precision + Recall} \quad (5)$$

To calculate the area under the ROC curve (AUC),

$$\text{AUC} = \int_0^1 TPR\ (FPR) dFPR \quad (6)$$

where FPR is the false positive rate, TPR is the true positive rate (equivalent to Recall), and TP, TN, FP, and FN represent true positives, true negatives, false positives, and false negatives, respectively.

Per-class performance and confusion matrix

To provide a more detailed evaluation, a confusion matrix was computed for high- and low-risk

classifications. In the discovery group (n = 75), the model was accurate on 34 out of 36 low-risk patients (sensitivity 94.4%) and 136 out of 39 high-risk patients (specificity 92.3%), and the cumulative accuracy was 93.3%. In the independent validation cohort (n = 37), 15/16 low-risk patients and 19/21 high-risk patients were accurately categorised (sensitivity 93.8% and specificity 90.5% respectively). The F1 scores were 0.94 for low-risk and 0.91 for high-risk patients. This per-class breakdown confirms that the model discriminates effectively between risk groups without bias toward one group.

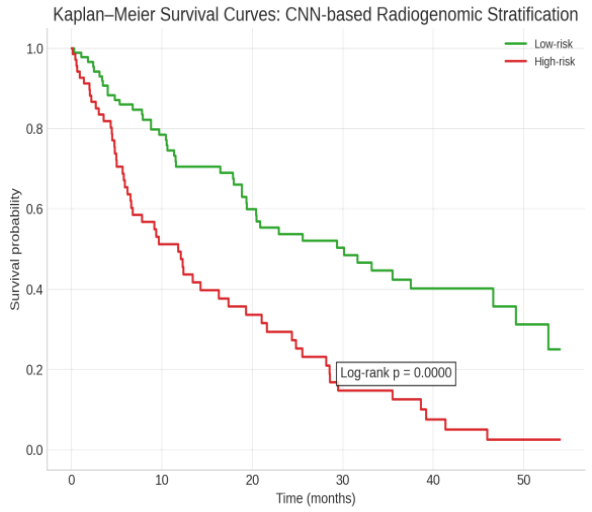

Figure 4: Kaplan–Meier survival curves for CNN-based radiogenomic stratification.

Figure **5** shows the comparison of performance metrics of the CNN-based radiogenomic model and the traditional model. The CNN-based model surpassed all traditional approaches to calculating radiomics on all measures of class (accuracy, precision, recall, F1 score, and AUC), which demonstrates the possibility of applying the model to stratified glioblastoma prognosis.

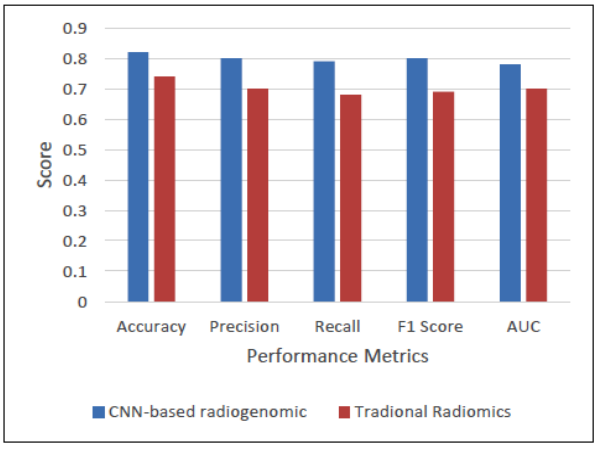

Figure 5: Performance comparison between CNN-based radiogenomic and traditional radiomics models.

The CNN was able to capture intricate visual elements, and this was an improvement over the traditional handcrafted measures. It was found that the heterogeneity of edema and necrotic core was highly predictive of the survival outcome based on the visualization of the feature importance. Moreover, these imaging signals and genomic alterations were biologically significant and had a correlation. Agnostic as to the hallmark invasive patterns associated with EGFR-driven GBMs, the peritumoral edema features also showed links to EGFR amplification. This crossroad of the genetic pathways and phenotype imaging highlights the radiogenomic domain and the crossroad of tumor biology and imaging.

DISCUSSION

The CNN-based radiogenomic method was more precise and generalized against previous models, such as those made with the help of logistic regression or a combination of dictionary learning and sparse regression. The methods of dictionary learning showed dependence on features that had to be hand-selected, and this gave them an insufficiency to effectively represent the heterogeneity of tumors using DTI and mpMRI data. Comparatively, CNNs were capable of learning more complex pattern imaging, along with integrating complementary molecular biomarkers that were more predictive with higher interpretability.

Though these are the strengths, there are several limitations that ought to be considered. To begin with, the researchers utilized retrospective datasets that can lead to selection bias and reduce control over confounding factors. Second, differences in MRI-acquisition settings between institutions and scanners may have an impact on reproducibility and generalizability of radiomic features, ultimately impacting the performance of models in clinical practice. Third, the small set of biomarkers (dominated by EGFR, IDH, and MGMT) might not be able to reflect the entire molecular heterogeneity of glioblastoma. The inclusion of transcriptomic and epigenomic data has the potential to enhance the prognostic capabilities and biological relevance of the model. To optimize the clinical translation, there is a need to have multi-institutional validation using a larger and more diverse cohort to represent the differences in the imaging protocols and the patient population. In addition to explainable AI approaches, interface attention maps, and saliency visualizations should be taken into consideration in future research to increase model transparency and allow their interpretation by clinicians.

Overall, the results represent an excellent basis for the clinical relevance of DGL radiogenomics in clinical prognosis. The combination of CNN-based imaging properties with that of molecular biomarkers, besides providing a significant predictive value of patient outcomes, can also provide a biologically significant insight into the complexity of the tumor. This highlights the possibility of the creation of precision medicine in neuro-oncology by employing radiogenomic frameworks.

CONCLUSION

This article proves that a combination of deep learning with radiogenomic techniques should be used to improve prognostic stratification in glioblastoma multiforme (GBM). The usage of a convolutional neural network (CNN)-based multiparametric MRI and key molecular biomarkers, such as EGFR amplification, IDH mutation, and MGMT promoter methylation, in combination effectively characterizes the heterogeneity of tumors, besides the model offering biologically sound reasons as to why outcome stratification is possible at both population and individual patient level. Such a hybrid approach is superior to the conventional radiomic and dictionary learning shapes, evidenced by increased C-index, AUC, and concordant Kaplan-Meier separation of survival in risk groups. The framework also contains equations that compute the performance measures that enable the predictive accuracy to be measured reproducibly. Radiogenomic signatures developed based on deep learning are a significant breakthrough towards precision medicine in GBM, with the ability to be used to accurately, non-invasively, and biologically meaningfully predict prognostication. These strategies have the potential to increase more strategic clinical outcome-based and clinical decision-making in neuro-oncology. The CNN-based model is also more generalized and precise than the earlier models, e.g., sparse regression or dictionary learning. In order to practice in the future, one must take into consideration the possibility of the multi-institutional cohort validation to ensure the strength of different groups of patients and imaging regimens. Besides, explainable AI techniques, such as attention maps and saliency visualizations, will be included to enhance the transparency of the models and assist a clinician in interpreting the model. It can be improved further by adding other forms of omics data to the model, including transcriptomic and epigenomic, which can add precision to prognostics and a better biological perspective of the heterogeneity of GBM. Such refinements will be continuous, and they will be employed in countering the unintended prognostic biases of retrospective analyses and will make them more valid in clinical application.

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