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Brain Tumor Radiogenomic Classification Using AI Approaches: Research Area Review

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Abstract

A malignant tumor in the brain is a life-threatening condition. It is known as glioblastoma, it's the most common form of brain cancer in adults and the one with the worst prognosis, with a median survival of less than a year. This article is an extensive review of the basic background, technique and clinical applications of artificial intelligence (AI) and radiomics in the field of tumor neuroclassification. This survey provides a comprehensive review of recent advancements in brain tumor detection and MGMT promoter methylation status prediction using machine learning, deep learning, radiomic, and topological data analysis techniques. It encompasses a wide array of studies that utilize diverse datasets, such as TCGA, BraTS, RSNA, and Kaggle, showcasing the evolution of non-invasive diagnostic approaches. The reviewed research demonstrates significant improvements in diagnostic accuracy, often exceeding 90%, highlighting the potential of these methodologies to enhance early detection, classification, and personalized treatment planning in neuro-oncology. The survey emphasizes the importance of leveraging large, heterogeneous datasets and advanced algorithms to bridge the gap between research and clinical application. Future directions include validation across broader populations and integration into clinical workflows to realize the full potential of AI-driven brain tumor diagnostics.

Keywords: Glioblastoma; Magnetic Resonance Imaging Scans; AI; Tumor Classification; MGMT Methylation Status; CNN.

1 | Introduction and Background

Glioblastoma multiforme (GBM), one of the most common brain tumors, accounts for about 45% of all malignant types of central nervous system tumors and is more likely to develop as preliminary GBM [1]. Despite some advancements in classic multimodal therapy, including surgical resection heeded by adjuvant chemo radiotherapy and adjuvant chemotherapy, the median survival of patients remains pretty low, at only 14–16 months[2, 3]. GBM is considered a lethal disease with a poor prognosis due to its biological complexity, high frequency of chemotherapeutic resistance, and frequent recurrence after surgical treatment[4]. The common chemotherapeutic agent for GBM treatment is temozolomide (TMZ), an alkylating drug that makes cells more sensitive to radiation [5]. This agent exerts its cytotoxic marks through methylating O6-methylguanine, which in turn causes DNA damage leading to cell death [6, 7].

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Therefore, the main barrier to the successful therapy of GBM is ingrained and/or acquired chemo resistance to TMZ regulated by an enzyme called O6-methylguanine-DNA methyltransferase (MGMT), which is a highly evolutionarily conserved DNA repair enzyme that removes alkylated guanine remains at the DNA level, thereby antagonizing the effects of alkylating therapeutic agents[8]. Owing to the reduction of MGMT transcription induced by CpG island methylation in the MGMT promoter region [9], it could be a possible predictive biomarker for TMZ resistance and poor progression-free survival. It is thus essential to determine the MGMT methylation status to have an accurate therapy strategy and enhance success rates for GBM treatment. In current years, some radiological research has extended radiomics models for predicting survival rates, distant metastasis, and characterizations of molecular characteristics [10]. As the MGMT methylation status is regarded as an important predicting biomarker for guiding GBM treatment decisions, several computational models were also developed to preoperatively predict the MGMT methylation status based on magnetic resonance imaging (MRI) [11].

1.1 | Brain MRI Scans

One of the most popular medical imaging procedures is brain MRI. It allows medical professionals to use alternative MRI sequences, such as T1w, T2w, or FLAIR, to focus on distinct regions of the brain and investigate their anatomy and disease. MRI is used to diagnose some clinical diseases, such as cerebrovascular accidents, and to examine the structure of the brain. Magnetic resonance imaging, or head MRI, is a non-invasive medical treatment that generates high-definition images of the internal components of the head, primarily the brain. MRI creates these finely detailed images by using radio waves, a computer, and a big magnet [12]. Radiation is not used in it.

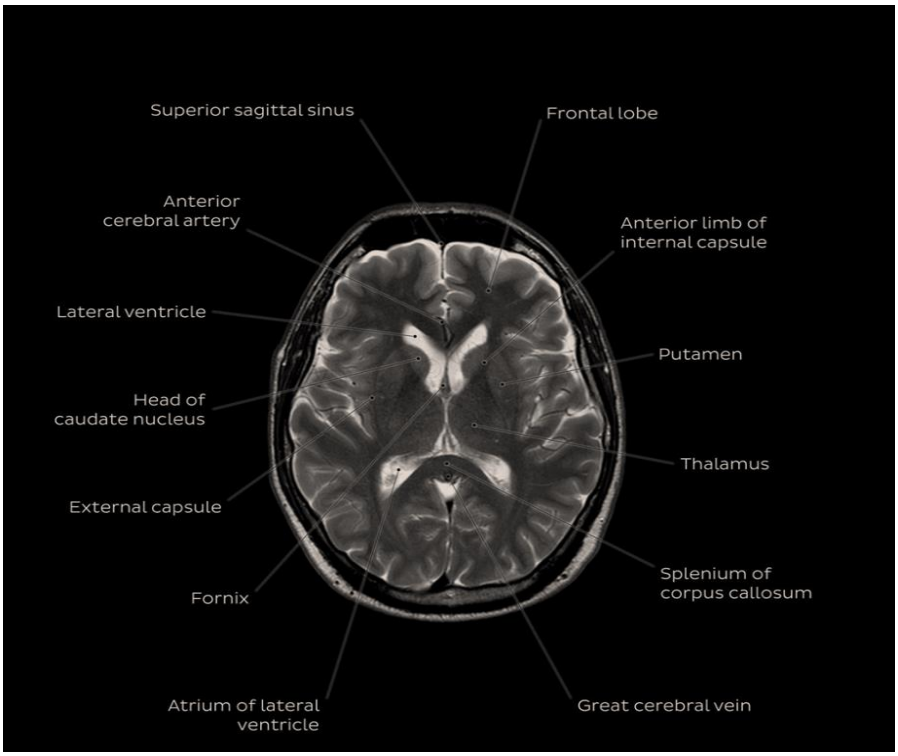

Figure 1. Brain MRI (T2-weighted) at the Thalamic Level.

1.2 | Radiomics

Radiomics is a recently developed translational field that uses radiological pictures to extract several qualities, including geometry, strength, and texture, to capture various imaging patterns. These patterns may be applied to the subtyping, grading, and staging of tumors. Additionally, Radiomics is typically applied to systems with various variations for prognosis, monitoring, and evaluation of therapy response [13].

Radiomics can be broadly classified into two categories: feature-based and deep learning-based. These clinical evaluations that are impacted by the human readers yield less consistent, accurate, and repeatable outcomes than these.

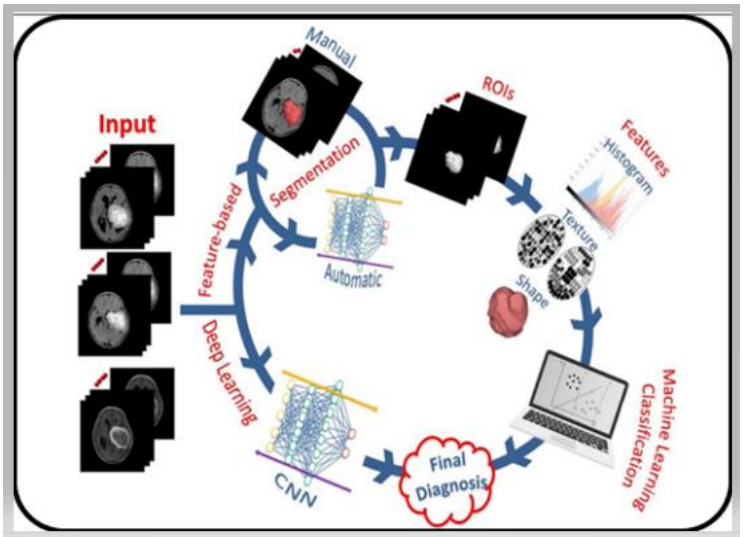

Figure 2. Overview of the Radiomics Workflow.

1.3 | MGMT(O6-methylguanine DNA Methyltransferase)

is an enzyme that repairs DNA damage, contributing to resistance against alkylating drugs used in chemotherapy [14]. The methylation status of the MGMT promoter is a crucial biomarker for predicting chemotherapy response in glioblastoma patients. This methylation can inhibit the MGMT gene, making tumor cells more susceptible to treatment by preventing DNA repair. In glioblastoma, where MGMT is active, chemotherapy efficacy is reduced because the enzyme fixes guanine nucleotides, counteracting the intended effects of alkylating agents [15]. convolutional neural networks (CNNs) employ to analyze radiological images combined with molecular data to predict MGMT methylation status. CNNs are particularly effective in medical imaging due to their ability to automatically learn features from input data without manual feature engineering. By training on large datasets of MRI scans, CNNs can identify complex patterns associated with brain tumors, such as shape, texture, and location [16]. This survey discusses how to improve the accuracy and reliability of determining MGMT methylation status which aiding in treatment strategy decisions. For glioblastoma patients, exploring clinical trials and innovative treatments is vital. Clinical trials provide opportunities for accessing cutting-edge therapies beyond standard care, which include surgery, radiation, and chemotherapy.

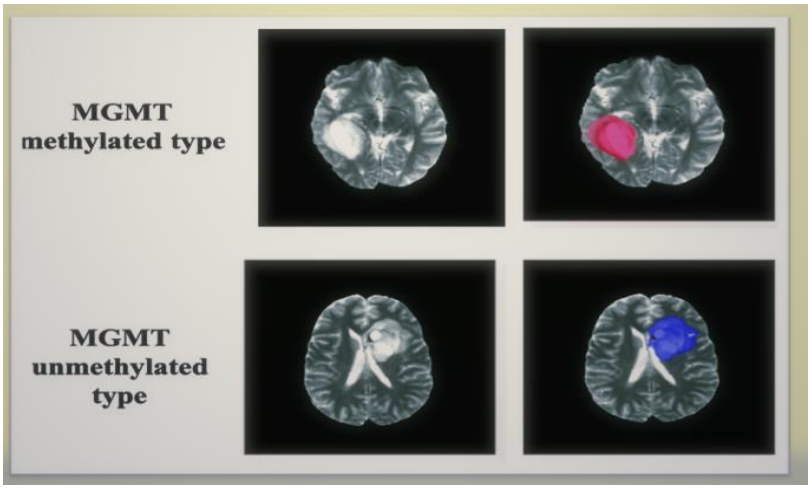

Figure 3. The methylation status of MGMT.

2 | Materials and Methods

The survey article's approach used different deep learning techniques for Brain Tumor Radiogenomic Classification. The survey models attempted to predict the genetic subtype of glioblastoma. Using MRI (magnetic resonance imaging) scans, they try to train and test their models to look for MGMT promoter methylation and enhance glioblastoma patient diagnosis and treatment planning. Magnetic Resonance Imaging (MRI) is a crucial tool in diagnosis and treatment planning for gliomas. It provides essential information that helps with surgical planning and postoperative monitoring. Accurate image segmentation is vital as it can significantly impact treatment outcomes and potentially improve survival rates by aiding precise surgical interventions and ongoing assessment.

Despite extensive efforts by researchers, accurately segmenting brain tumors continues to pose significant challenges. These difficulties stem from issues like uncertain tumor locations, variable shapes, low-contrast images, biases in annotations, and imbalanced datasets. However, the advent of powerful deep learning techniques has shown promising results. Many of these approaches automatically teach feature representations, leading to more precise and reliable brain tumor segmentation performance.

2.1 | Classification Algorithms

Due to their robustness in capturing complicated interactions between individual features and across feature combinations as well as their capacity to handle high-dimensional information, ML approaches are gaining popularity in radiomics investigations as a means of developing efficient prognostic/predictive models. In this study, binary classification between MGMT methylation and unmethylated classes in GBM patients was carried out using supervised ML models, such as RF, XGBoost, and SVM. Ensemble learning methods like The XGBoost, and RF algorithms gather individual outcome predictions from multiple weak learners.

2.2 | U-NET Technique

The UNET architecture is a specialized form of neural network designed to enhance the capabilities of Fully Convolutional Networks (FCN) for biomedical image segmentation tasks. It is characterized by its distinctive U-shaped structure, which integrates both an encoder and a decoder network[17].

The encoder, or contracting path, systematically applies pairs of convolutional layers, each followed by a rectified linear unit (ReLU) and a max pooling layer. This sequence effectively compresses spatial information while amplifying feature information. Conversely, the decoder, or expansive path, employs up-sampling operations. These operations are enriched by incorporating high-resolution features from the encoder via skip connections, which help restore spatial details lost during the encoding process.

2.3 | Deep Convolutional Neural Networks (CNNs)

Deep Convolutional Neural Networks (CNNs) have gained significant popularity and proven effectiveness in segmenting brain MRI images. These networks excel at image analysis because they automatically learn layered feature representations directly from raw data, making them highly suitable for such tasks[18].

Typical deep CNNs are composed of several types of layers, including convolutional, pooling, and fully connected layers. For segmentation purposes, models like U-Net are frequently employed. U-Net features an encoder-decoder framework that effectively captures both local details and broader context, which is essential for accurate segmentation. Training: Developing a CNN for brain MRI segmentation requires a labeled dataset with known ground truth segmentation labels[19]. During training, the network learns to translate input scans into precise segmentation masks by optimizing a loss function, such as cross-entropy or Dice loss, to enhance prediction accuracy. Commonly used datasets, such as the Brain Tumor Segmentation (BRATS) collection, serve as benchmarks for training and testing CNN models. These datasets include diverse MRI scans with various tumor types, aiding in the development of more resilient models. Even with their effectiveness, CNNs encounter obstacles like class imbalance, where certain tumor

types may be underrepresented in the training data. To address this, techniques such as data augmentation and transfer learning are often implemented to improve model robustness[20]. Besides tumor segmentation, CNNs are employed in other brain-related domains, including the detection of structural abnormalities and the analysis of brain activity through functional MRI (fMRI) data.

2.4 | ResNet Model

Using a ResNet model for brain tumor MRI segmentation typically involves adapting the standard architecture into a segmentation framework, such as a U-Net-like structure, where ResNet serves as the encoder (feature extractor). This enhances feature representation while preserving spatial information crucial for segmentation[21]. ResNet-based Segmentation for Brain Tumors: Encoder: ResNet (e.g., ResNet-50 or ResNet-101) extracts hierarchical features from MRI images. Decoder: A symmetrical decoder expands the features back to the original image size, enabling pixel-level segmentation. Skip Connections: Connect encoder layers with corresponding decoder layers to preserve spatial details (as in U-Net).

Typical Workflow:

Preprocess MRI scans: Normalize intensities, resize, and augment data. Feature extraction: Use a ResNet backbone to capture rich features. Upsampling & decoding: Use transposed convolutions, upsampling, or interpolation layers to produce segmentation masks. Loss functions: Use dice coefficient, cross-entropy, or combined loss to optimize the model. Training & validation: Fit the model with annotated MRI scans.

3 | Literature Survey

Eman Abdel-Maksoud et al. in (2021) present an efficient image segmentation approach using the K-means clustering technique integrated with the Fuzzy C-means algorithm. To enable accurate brain tumor identification, it is followed by thresholding and level-set segmentation stages. The proposed technique can benefit from K-means clustering for picture segmentation in terms of computing time [22].

Dhamea A. Jasm et al. in (2021), the steps of the image mining method are provided, as well as an in-depth description of employing image mining to classify brain tumors. In addition, analysis of the latest techniques which have been used to classify the brain tumors with comparison to the training groups and the amount of accuracy that was obtained from the analysis. The high published accuracy claims to be 98% which was obtained using the deep convolutional neural network (DCNN) [23].

Emrah Irmak et al. in (2021) try to make multiclassification of brain tumors for early diagnosis purposes using a convolutional neural network (CNN). Three different CNN models are proposed for three different classification tasks. Using the first CNN model, brain tumor detection is 99.33% accurate. With an accuracy of 92.66%, the second CNN model can categorize brain tumors into five types: normal, glioma, meningioma, pituitary, and metastatic. The third CNN model can classify brain tumors into three grades Grade II, Grade III, and Grade IV with an accuracy of 98.14% [24].

N Saranya et al in (2021) bring out the Convolution Neural Network algorithm, image processing and data augmentation to say the brain images are cancerous and which are not cancerous [25].

Abd El Kader et al. in (2021) proposed a differential deep CNN model to classify abnormal or normal MR brain images, the experimental results showed that the proposed model achieved an accuracy of 99.25% [26].

Xiaoqing Gu et al. in (2021) proposed a brain tumor MR image classification method using convolutional dictionary learning with local constraint (CDLLC). To investigate discriminative information, their method incorporates multi-layer dictionary learning into a convolutional neural network (CNN) structure. Two therapeutically relevant multi-class classification tasks on the Cheng and REMBRANDT datasets are constructed for the experiment [27].

In October 2021 Beomseok Sohn et al [28], built binary relevance (BR) and ensemble classifier chain (ECC) models for multi-label classification and compared their performance. In the classifier chain, they calculated the mean absolute Shapley value of input features. IDH mutation status was predicted with the highest AUCs of 0.964 (BR) and 0.967 (ECC). The ECC model showed higher AUCs than the BR model for ATRX (0.822 vs. 0.775) and MGMT promoter methylation (0.761 vs. 0.653) predictions. The mean absolute Shapley values suggested that previous classifier predictions were important for improving subsequent predictions along the classifier chains. They developed a radiomics-based multiple gene predictions chained model that incorporates mutual information of each genetic alteration in glioblastoma and grade 4 (astrocytocytoma), IDH-mutant, and outperforms a simple bundle of binary classifiers using the prediction probability of prior classifiers.

In June 2022 Sixuan Chen et al [29], trained a residual network (ResNet) to give a binary prediction of MGMT promoter methylation status. Instead of using images as an input, as in existing research, our research extracted radiomics features from a selected region of interest (ROI) in different modalities of MR images and used them as the input of the model. Based on the ROI of the whole tumor, the predictive capacity of the T1CE and ADC model achieved the highest AUC value of 0.85. Based on the ROI of the tumor core, the T1CE and ADC model gained the most elevated AUC value of 0.90. After comparison, the T1CE combined with the ADC model based on the ROI of the tumor core exhibited the best performance, with the highest average accuracy (0.91) and AUC (0.90) among all models. The deep learning method using MRI radiomics has excellent diagnostic performance with a high accuracy in predicting MGMT promoter methylation in diffuse gliomas.

After image preprocessing and feature extraction, Fei Zheng et al [30] built and compared the performance of two types of machine-learning (ML) models in June 2022. The first type was established utilizing all MRI sequences (T1WI, T2WI, contrast enhancement (CE), FLAIR, DWI_b_high, DWI_b_low, and ADC), while the second type was established using single MRI sequences as described above. Results The Maximum Relevance and Minimum Redundancy technique was used to determine 7 radiomic features for the ML model based on all sequences. The predictive accuracy was 0.993 and 0.750 in the training and validation sets, respectively, and the area under curves (AUCs) were 1.000 and 0.754 in the two sets respectively. For the ML model based on single sequences, the numbers of selected features were 8, 10, 10, 13,9, 7, and 6 for T1WI, T2WI, CE, FLAIR, DWI_b_high, DWI_b_low, and ADC, respectively, with predictive accuracies of 0.797~1.000 and 0.583~0.694 in the training and validation sets respectively, and the AUCs of 0.874~1.000 and 0.538~0.697 in the two sets, respectively. In the independent validation set, the T1WI-based model performed best, whereas the CE-based model performed worst.

In august 2022, Duyen Thi Do et al. [31] the radiomics features extracted from multimodal images from magnetic resonance imaging (MRI) had undergone a two stage feature selection method, including an eXtreme Gradient Boosting (XGBoost) feature selection model followed by a genetic algorithm (GA)-based wrapper model for extracting the most meaningful radiomics features for predictive purposes. According to the cross-validation results, the GA-based wrapper model performed well in predicting the MGMT methylation status in GBM, with a sensitivity of 0.894, specificity of 0.966, and accuracy of 0.925. Application of the extracted GBM radiomics features on a low-grade glioma (LGG) dataset also achieved a sensitivity 0.780, specificity 0.620, and accuracy 0.750, indicating the potential of the selected radiomics features to be applied more widely on both low- and high-grade gliomas.

In September 2022 Shingo Kihira et al. [32] developed a symmetric Deep Learning-based U-Net framework based on FLAIR's 512 _ 512 segmented maps as the ground truth mask. Their findings: The final group included 208 patients with an average _ standard deviation of age (years) of 56 _ 15 and an M/F ratio of 130/78.The DSC of the generated mask was 0.93. Prediction of IDH-1 and MGMT status achieved AUCs of 0.88 and 0.62, respectively. Survival prediction of <18 months demonstrated an AUC of

0.75. Their deep learning-based framework can detect and segment gliomas with excellent performance for the prediction of IDH-1 biomarker status and survival.

Shahzad Ahmad Qureshi1 et al. in 2023 propose a novel two-stage MGMT Promoter Methylation Prediction (MGMT-PMP) system that extracts latent features fused with radiomic features predicting the genetic subtype of glioblastoma. A novel fne-tuned deep learning architecture, namely Deep Learning Radiomic Feature Extraction (DLRFE) module, is proposed for latent feature extraction that fuses the quantitative knowledge to the spatial distribution and tumorous structural size by radiomic characteristics (GLCM, HOG, and LBP). The novice rejection method was shown to be highly effective in picking and isolating negative training cases from the original dataset. The fused feature vectors are then employed by k-NN and SVM classifiers for training and testing. The highest classification performance is (96.84 0.09%), (96.08 0.10)%, and (97.44 0.14)% for detecting MGMT methylation status in patients with glioblastoma[16].

Numan Saeeda et al. in April 2023 [33] proposed that Deep learning algorithms were used to analyze brain MRI scans of tumors to detect the MGMT promoter methylation status. Researchers predicted the methylation status of the MGMT in glioblastoma tumors using deep learning algorithms and a sizable open MRI dataset containing 585 patients. The Grad-CAM technique, filtration sensitivity, data feature graphical representations, and trained loss topography were the methods they used to evaluate these models. The largest mean AUC and the largest Area Under Curve by fold are determined. At 0.69, the average AUC achieves saturation.

Dapeng Cheng et al. in November 2023[34] emphasized EAV-UNet, a technology for accurately detecting lesion locations. Optimizing feature extraction, detecting abnormal regions with automated segmentation techniques, and strengthening the structure. The method implements the VGG-19 encoder in place of the U-Net encoder. They enhanced the decoder's feature details by including a Channel and Spatial Attention Mechanism (CBAM) module. To obtain crucial edge properties from the stream, they integrated an edge identification component into the encoder. This strategy obtained an F1 score of 96.1%.

Mohannad Barakat et al. in December 2023[35] offered an innovative approach to multi-modal glioma segmentation that combines a voting network and (SAM) the Segment Anything Model. We can fine-tune SAM with bounding box-guided prompts (SAMBA) to better fit African data. Trials on the BraTS-Africa dataset produced satisfactory results, demonstrating the promise of the technique. SAM attained a Dice value of 86.6 for binary segmentation and 60.4 for multiclass segmentation.

Anton François et al. in January 2024 [36] explained that the new method for MRI image segmentation, (TDA) Topological Data Analysis, offers number of advantages over conventional machine learning techniques. The process involves three steps: automatic thresholding to show the entire object, recognizing a distinct subset with predetermined topology, and deducing segmentation components. The final segmentation of the running model, displaying the Dice score of 0.94.

Amr Mohamed et al. in January 2024 [37] proposed that the 3D Vision Transformer (ViT3D) with a 32x32x32 patch size and simple averaging ensemble outperformed other deep learning frameworks in glioblastoma MGMT biomarker status prediction, reaching a testing AUC of 0.6015. Exception outperformed EfficientNet-B3 and ResNet50, with a testing AUC of 0.61745.

Yongqi He et al. in February 2024 focuses on predicting the methylation status of the MGMT (O-6-methylguanine-DNA methyltransferase) promoter in glioblastoma using weakly supervised learning and transformer-based models [38] . The methylation status of MGMT is important for treatment and prognosis, but its detection remains challenging. The authors employed a weakly supervised learning approach, which allows the model to learn from the data with limited labeling. This was achieved using two transformer-based models, which are known for their effectiveness in handling complex image data. Accuracy and AUC (Area Under the Curve) scores were used to evaluate model performance. TCGA dataset: accuracy = 0.79, AUC = 0.86. Independent dataset (Beijing Tiantan Hospital): Accuracy = 0.76, AUC = 0.83.

Shenbagarajan et al. (February 2024) present a method to enhance brain tumor detection in MRI scans using advanced machine learning and deep learning techniques [39] . Their approach preprocesses MRI images with the Adaptive Contrast Enhancement Algorithm and median filtering. The classification of tumor regions is performed using a novel Ensemble Deep Neural Support Vector Machine (EDN-SVM) classifier. The model achieved outstanding performance, with 97.93% accuracy, 92% sensitivity, and 98% specificity, highlighting its potential as a reliable tool for accurately detecting abnormal and normal brain tissues in MRI scans.

Seong-O Shim in March 2024 applied the ResNet101 deep learning model with transfer learning for analyzing the 2021 Radiological Society of North America (RSNA) Brain Tumor Challenge dataset [40] . For determining MGMT methylation state in glioma patients, the model achieved an accuracy of 85.48%, sensitivity of 80.64%, and specificity of 90.32%. Conversely, for classifying cases with no tumor, the model yielded an accuracy of 85.48%, sensitivity of 90.32%, and specificity of 80.64%.Additionally, 74 radiomic features were computed and optimized using an ensemble Bagged Tree classifier combined with the Relief feature selection method, which reduced the feature set to 30. This enhanced approach improved validation accuracy to 84.3% and gave a result for the area under curve (AUC) equal 0.9038 for detecting MGMT promoter methylation status.

Mahmoud Khaled Abd-Ellah proposes in April 2024 an automatic brain tumor diagnosis system [41] for the detection, classification, and segmentation of glioblastomas using convolutional neural networks (CNNs). The system utilizes MRI images to diagnose and segment brain tumors, specifically gliomas (including glioblastomas). It is composed of two main stages: tumor detection and classification and tumor segmentation. The system achieved 99% accuracy in tumor detection and classification, demonstrating high precision in differentiating between normal and glioma categories. The segmentation stage exhibited strong results, with the Dice score, sensitivity, and specificity metrics indicating high effectiveness in accurately identifying tumor regions.

Krishnan (June 2024) introduces (RViT) the Rotation Invariant Vision Transformer, a deep learning model designed to improve brain tumor classification from the MRI scans [42]. The model made use of rotating patch embeddings, to improve its accuracy in detecting brain cancers. Evaluation on Kaggle's Brain Tumor MRI Dataset showed outstanding performance: F1-score gave a result of 0.984, Matthew's Correlation Coefficient (MCC) equal 0.972 and Overall model accuracy was 0.986. This study highlights the potential of RViT's rotational invariance approach to advance the complex medical imaging tasks and brain tumor detection.

Shaz Mumtaz Khan et al. (September 2024) presents an effective and innovative approach to brain tumor detection and classification, integrating deep learning with advanced feature selection methods to improve precision and efficiency in medical imaging [43]. Geometric features and four texture attributes were extracted, optimized through a step-by-step process using a Genetic Algorithm (GA). The proposed method achieved a high accuracy of 96% in identifying and classifying brain tumors. The model's performance and novelty were rigorously compared with established techniques, demonstrating superior results.

Pavan Nathani et al. in November 2024 presented a Radiogenomic model for predicting Methylguanine DNA Methyltransferase (MGMT) promoter hypermethylation in Glioblastoma Multiforme (GBM) using multimodal MRI data and the EfficientNet deep learning architecture [44]. Since MGMT status is critical for determining temozolomide sensitivity and improving prognosis, a non-invasive prediction method is essential to reduce the need for biopsies. The study utilized MRI sequences from the Brain Tumor Segmentation (BraTS) 21 dataset, including T1-weighted, T1-weighted contrast-enhanced, T2-weighted, and FLAIR scans, focusing on preprocessing techniques for cross-modal alignment. The EfficientNet-B0 model, pre-trained on ImageNet and fine-tuned for binary classification of MGMT methylation status, achieved a moderate validation score of 0.62393.

Mahmoud Ragab in November 2024 presents a new model, Brain Tumor Recognition using an Equilibrium Optimizer with a Deep Learning Approach (BTR-EODLA), to automatically detect and classify brain tumors in MRI scans [45]. The main objective of this research is to enhance diagnostic accuracy and help in treatment strategies. The model's parameters are fine-tuned using the Equilibrium Optimizer (EO), which is designed to enhance the accuracy of the deep learning model. A series of trials validated the system's effectiveness in detecting brain tumors from MRI scans. The proposed system achieved emotional accuracy of 98.78, overpassing existing models in terms of performance.

İlker Özgür Koska et al. in January 2025 aimed to develop a robust classifier for predicting MGMT methylation status in glioblastoma using multiparametric MRI [46]. By utilizing a subset of the BRATS 2021 dataset with MGMT labels and segmentation masks, researchers created a comprehensive mask fusion approach that identified relevant tissue areas, including those that appear disease-free yet contain pathology. They built a 3D ROI-based custom CNN classifier, which outperformed single-sequence classifiers, achieving accuracies of 0.88 with a multiparametric approach using T1 contrast-enhanced and FLAIR images, and 0.81 with all four MRI sequences. The best model also achieved a ROC AUC of 0.90.

Sumaiya Fazal in March 2025 introduces ADAPT (Adaptive Sparse Autoencoders), an innovative method for determining MGMT methylation status in glioblastoma patients using MRI images [47] . ADAPT offers a promising advancement for personalized treatment plans in glioblastoma by improving the accuracy of MGMT methylation status prediction. Its high performance in terms of accuracy, specificity, and sensitivity suggests strong potential for clinical application, enhancing both diagnosis and treatment response predictions for glioblastoma patients. The ADAPT method achieves 95% accuracy, 93% specificity, and 94% sensitivity. These results highlight the method's high diagnostic precision.

Arash Hekmat in March 2025 presents a novel approach for improving the classification accuracy of brain tumor MRI images using a hybrid model [48] called Attention-Fused MobileNet-LSTM. This model integrates features from two widely recognized pre-trained convolutional neural networks (CNNs), MobileNetV1 and MobileNetV2, along with Long Short-Term Memory (LSTM) networks, to enhance diagnostic performance and reduce the challenges inherent in MRI image analysis. The Attention-Fused MobileNet-LSTM model offers a robust and highly accurate solution for classifying brain MRI images and distinguishing between normal and malignant tumors. Its 98.66% accuracy and high AUC suggest that it has strong potential as a reliable diagnostic tool in the medical field, addressing challenges related to image complexity, noise, and feature extraction. This model not only enhances diagnostic accuracy but also provides transparency through visualization techniques like Grad-CAM, which could support clinicians in understanding model decisions.

4 |Comparison Results of the Literature Survey Research

In this part, we discuss and analyze the results of the literature survey papers. Compared to earlier surveys, several recent studies on brain tumor segmentation have been published in the past few years. In our work, we provide an overview of these latest surveys, including their detailed insights and key highlights, summarized in Table 1.

Table 1. Comparison results of the literature survey research.

Name of researcher	Date of publishing	Objectives (outcomes)	The used dataset	Accuracy rate	Used technique
Duyen Thi Do et al.[31]	august 2022	Results of this paper showed that the used methodology could noninvasively predict the MGMT methylation status.	the Cancer Genome Atlas (TCGA)-GBM Dataset	Accuracy= 0.925	The GA-RF based wrapper model which combines Genetic Algorithms (GA) with Random Forests (RF)
Fei Zheng et al[30]	June 2022	Applying radiomics techniques to forecast the methylation status of (MGMT) promoters in patients with	215 patients who were pathologically	accuracy = 0.993	two kinds of machine-learning (ML) models: (model based on seven

		newly diagnosed glioblastoma, while also evaluating and comparing the effectiveness of various MRI sequence types.	confirmed as GBM after surgical resection or biopsy		different single MRI sequences), (model based on the combination of all sequences)
Shingo Kihira et al.[32]	September 2022	The deep learning-driven framework is capable of accurately identifying and segmenting gliomas, demonstrating strong effectiveness in predicting IDH-1 biomarker status and patient survival outcomes.	Training and validation were performed on dataset collected from Mount Sinai Hospital (MSH). Testing models' performance using datasets from the University of California, Los Angeles (UCLA).	Accuracy= 0.93	Deep learning-based U-Net framework
Sixuan Chen et al[29]	June 2022	predicting (MGMT) promoter methylation status in diffuse gliomas by developing a deep learning framework using MRI radiomics	Patients' data from the Affiliated Drum Tower Hospital of Nanjing University Medical School between 2018 and 2020.	accuracy =0.91	a residual network (ResNet model)
Beomseok Sohn et al [28]	October 2021	Create a radiomics-driven multi-gene prediction framework that integrates mutual information among various genetic mutations present in glioblastoma and grade IV astrocytoma, specifically focusing on IDH-mutant cases.	Dataset was supported by Research Institute of Radiological Science and Center for Clinical Image Data Science (471 patients from medical records)	AUCs of 0.964 (BR) and 0.967 (ECC).	binary relevance (BR) and ensemble classifier chain (ECC) models
Emrah Irmak et al. [24]	2021	focuses on multi-class brain tumor classification to facilitate early diagnosis using convolutional neural networks (CNNs). Three distinct CNN models are developed, each tailored to a specific classification task.	Four different datasets (RIDER dataset, REMBRANDT dataset, TCGA-LGG data collection, Another brain tumor dataset	Accuracy= 99.33%	Three different convolutional neural network (CNN) models are proposed for three different classification tasks.
Abd El Kader et al. [26]	2021	classify different types of brain tumors, including abnormal and normal magnetic resonance (MR) images.	Normal and abnormal MR brain images collected from Tianjin Universal Center of Medical	Accuracy= 99.25%	deep convolutional neural network (DCNN)

			Imaging and Diagnostic (TUCMD)		
Shahzad Ahmad Qureshi1 et al. [16]	2023	propose a novel two-stage MGMT Promoter Methylation Prediction (MGMT-PMP) system that extracts latent features fused with radiomic features predicting the genetic subtype of glioblastoma. Deep Learning Radiomic Feature Extraction (DLRFE) module, was proposed for latent feature extraction that fuses the quantitative knowledge to the spatial distribution and the size of tumorous structure through radiomic features: (GLCM, HOG, and LBP)	The 2021 RSNA Brain Tumor challenge dataset (BraTS-2021)	Accuracy= 97.44%	Deep Learning Radiomic Feature Extraction (DLRFE) module
Numan Saeeda et al. [33]	April 2023	employing deep learning models and one of the largest public MRI datasets to predict the methylation status of the MGMT promoter in glioblastoma tumors using MRI scan	The 2021 RSNA Brain Tumor challenge dataset (BraTS-2021)	mean AUC = 0.69	Deep learning algorithms
Dapeng Cheng et al. [34]	November 2023	EAV-UNet is a specialized system developed to precisely identify lesion areas. It enhances feature extraction, employs automatic segmentation methods to detect abnormal regions, and reinforces its structural design. The primary focus is on segmenting lesion regions, particularly in cases where tumor borders are unclear or blurred.	Dataset 1: Cancer Genome Atlas (TCGA) Dataset 2: brain tumor dataset. Dataset 3: BraTS 2021 dataset	F1 score = 96.1%.	medical image segmentation network called EAV-UNet. EAV-UNet is an improved version of the U-Net design
Mohannad Barakat et al. [35]	December 2023	To develop and evaluate an innovative multi-modal glioma segmentation approach specifically adapted for the challenges of African datasets (characterized by limited access to high-quality imaging) by combining a fine-tuned Segment Anything Model (SAMBA) with a voting network ensemble strategy.	the Brain Tumor Segmentation (BraTS) Challenge Africa (BraTS-Africa) dataset	Dice coefficient of 86.6 for binary segmentation and 60.4 for multi-class segmentation	the Segment Anything Model (SAM) and a voting network
Anton François et al. [36]	January 2024	introduce and describe a new general method for MRI image segmentation based on Topological Data Analysis (TDA), which offers advantages such as reduced dependence on large annotated datasets, interpretability, stability, and adaptability, by leveraging topological features and their localization to accurately identify various anatomical structures without relying on deep learning.	three datasets :the myocardium in ACDC, glioblastoma in BraTS 2021 and cortical plates in STA	Accuracy= 0.94	Topological Data Analysis (TDA-based module) and U-Net
Amr Mohamed et al. [37]	January 2024	predicting MGMT promoter status from mpMRI data and contributing to the ongoing efforts in precision medicine	RSNA MICCAI dataset on Kaggle	AUC= 0.6174	Deep learning approach (the Exception model ,EfficientNet-B3 and ResNet50)
Sumaiya Fazal et al. [47]	March 2025	Assess the methylation status of the MGMT promoter gene using features extracted from MRI image signatures. This method involves generating synthetic MRI images through iterative processes and then applying a	RSNA-MICCAI brain tumor Radiogenomic dataset	Accuracy = 95%	ADAPT (Adaptive Sparse Autoencoders) model

		specialized sparse autoencoder, which includes an adaptive sparsity constraint, to accurately predict the MGMT methylation state.			
İlker Özgür Koska et al [46]	January 2025	build a robust classifier for the MGMT methylation status of glioblastoma in multiparametric MRI.	The BRATS 2021 dataset	AUC= 90%	3D ROI-based custom CNN classifier
Pavan Nathani et al.[44]	November 2024	proposes the Radiogenomic model for predicting the status of MGMT Promoter methylation in glioblastoma patients based on the multi-modal MRI data and the EfficientNet Deep Learning Architecture.	The BRATS 2021 dataset	AUC-ROC score = 0.62393	The EfficientNet-B0 model
Shaz Mumtaz Khan et al.[43]	September 2024	Proposes a distinctive method for identifying and classifying brain tumors by integrating an improved U-Net model with ensemble learning strategies.	The BRATS 2021 dataset	Accuracy = 96%	An enhanced U-net algorithm combined with ensemble learning techniques.
Seong-O Shim et al.[40]	March 2024	analyzes mpMRI imaging to predict MGMT promoter methylation status	The 2021 (RSNA) Brain Tumor challenge dataset	Accuracy = 85.48%	ResNet101 deep learning model
Yongqi He et al. et al. [38]	February 2024	Accurately predicts the methylation status of the MGMT promoter in glioblastoma and demonstrates a certain level of generalization across different datasets.	The TCGA database and H&E-stained Whole slide images (WSI) of Beijing Tiantan Hospital	Accuracy= 79%	supervised learning and transformer-based models
Shenbagarajan et al.[39]	February 2024	propose and validate a novel deep learning and machine learning-based method for accurate detection and classification of brain tumors in MRI images, utilizing preprocessing, segmentation, feature extraction, and an ensemble classifier to improve diagnostic accuracy.	RSNA MICCAI dataset on Kaggle.	Accuracy= 97.93%	ensemble deep Neural Support Vector Machine (EDN-SVM)model

5 | The Contributions of the Survey

This survey aims to serve as a comprehensive resource amid the numerous deep learning-based approaches to brain tumor segmentation that have demonstrated encouraging outcomes. Our work offers an in-depth and analytical overview of the latest methods in this field. We expect that this review will provide valuable guidance and technical perspectives for researchers and industry practitioners alike. The key contributions of this survey can be summarized as follows:

- We provide a detailed review categorizing and structuring various deep learning techniques for brain tumor segmentation, including a taxonomy that highlights key technical innovations.
- The survey summarizes the advancements in deep learning approaches for brain tumor segmentation, and prediction of the MGMT methylation status.
- We conduct an extensive comparison of existing methods based on their performances on publicly available challenges and datasets providing critical evaluations and insightful discussions.

6 |The Limitations of this survey

- **Dataset Heterogeneity:** The studies utilize diverse datasets with varying image qualities, sizes, and annotations, which can affect the comparability and generalizability of the reported results.
- **Limited External Validation:** Many models are validated on specific datasets without extensive testing across independent or multi-center datasets, raising concerns about their robustness and clinical applicability.
- **Variability in Techniques:** The wide range of algorithms and feature extraction methods makes it challenging to identify a universally best approach and may lead to inconsistent performance benchmarks.
- **Sample Size Disparities:** Several studies rely on relatively small datasets, which can limit statistical power and might lead to overfitting, reducing real-world effectiveness.
- **Lack of Standardization:** Differences in evaluation metrics, model architecture, and preprocessing protocols hinder direct comparison and comprehensive assessment of model performance.
- **Clinical Translation Gap:** Despite high reported accuracy and AUC scores, few studies address integration into clinical workflows, interpretability, and real-world validation necessary for practical adoption.
- **Focus on Specific Tumor Types:** Some studies target particular genetic markers or tumor subtypes, which may not encompass the full spectrum of brain tumor heterogeneity seen clinically.
- **Limited Longitudinal Data:** Most studies focus on static image analysis without considering temporal changes or treatment response, which are vital for comprehensive prognosis.

These limitations highlight the need for larger, diverse, multicenter datasets and standardized evaluation protocols to enhance the reliability and clinical readiness of AI-based brain tumor diagnostics.

7 |Conclusions

Nonetheless, in the last few decades, AI in Radiogenomics has introduced unique answers to existing clinical issues in cancer treatment, as well as beneficial results for individualized prognosis and treatment planning. As previously discussed, it is being used extensively in much cancer research such as survival prediction, progression-free survival, cancer heterogeneous analysis, and so on in the era of precision medicine. This compilation of recent research studies highlights diverse and advanced approaches for brain tumor detection and MGMT promoter methylation status prediction, utilizing various datasets and machine learning, deep learning, and topological data analysis techniques. The reported high accuracy, sensitivity, and AUC scores across these studies demonstrate significant progress in non-invasive brain tumor diagnostics and genomic prediction, emphasizing the potential of AI-driven methods to enhance clinical decision-making and personalized treatment strategies in neuro-oncology. Continuous development and validation on large, diverse datasets are essential for translating these models into routine clinical practice. But we have observed that certain research has been made with insufficient funding and a lack of (i) multi-institutional data, (ii) proper cross-validation analysis, (iii) generalizable results, and (iv) robustness, posing additional challenges and shaking oncologists' confidence in its use in routine clinical practice. In the near future, we believe that additional research will focus on overcoming the current limitations of AI in Radiogenomic and improving their AI.

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Conflicts of Interest

The authors declare that there is no conflict of interest in the research.

Ethical Approval

This article does not contain any studies with human participants or animals performed by any of the authors

Data Availability

There is no data used in this study.

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