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Review

Artificial Intelligence in Glioma Diagnosis: A Narrative Review of Radiomics and Deep Learning for Tumor Classification and Molecular Profiling Across Positron Emission Tomography and Magnetic Resonance Imaging

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Academic Editor: Hisham Daoud

Received: 9 August 2025
Revised: 25 September 2025
Accepted: 1 October 2025
Published: 3 October 2025

Citation: Christodoulou, R.C.; Pitsillos, R.; Papageorgiou, P.S.; Petrou, V.; Vamvouras, G.; Rivera, L.; Papageorgiou, S.G.; Solomou, E.E.; Georgiou, M.F. Artificial Intelligence in Glioma Diagnosis: A Narrative Review of Radiomics and Deep Learning for Tumor Classification and Molecular Profiling Across Positron Emission Tomography and Magnetic Resonance Imaging. *Eng* **2025**, *6*, 262. https://doi.org/10.3390/eng6100262

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Abstract

Background: This narrative review summarizes recent progress in artificial intelligence (AI), especially radiomics and deep learning, for non-invasive diagnosis and molecular profiling of gliomas. **Methodology**: A thorough literature search was conducted on PubMed, Scopus, and Embase for studies published from January 2020 to July 2025, focusing on clinical and technical research. In key areas, these studies examine AI models' predictive capabilities with multi-parametric Magnetic Resonance Imaging (MRI) and Positron Emission Tomography (PET). **Results**: The domains identified in the literature include the advancement of radiomic models for tumor grading and biomarker prediction, such as Isocitrate Dehydrogenase (IDH) mutation, O6-methylguanine-dna methyltransferase (MGMT) promoter methylation, and 1p/19q codeletion. The growing use of convolutional neural networks (CNNs) and generative adversarial networks (GANs) in tumor segmentation, classification, and prognosis was also a significant topic discussed in the literature. Deep learning (DL) methods are evaluated against traditional radiomics regarding feature extraction, scalability, and robustness to imaging protocol differences across institutions. **Conclusions**: This review analyzes emerging efforts to combine clinical, imaging, and histology data within hybrid or transformer-based AI systems to enhance diagnostic accuracy. Significant findings include the application of DL to predict cyclin-dependent kinase inhibitor 2A/B (CDKN2A/B) deletion and chemokine CCL2 expression. These highlight the expanding capabilities of imaging-based genomic inference and the importance of clinical data in multimodal fusion. Challenges such as data harmonization, model interpretability, and external validation still need to be addressed.

Keywords: gliomas; deep learning; radiomics; MRI; PET; diagnosis: molecular profile; artificial intelligence

1. Introduction

Gliomas, a complex and heterogeneous group of primary brain tumors, present a substantial challenge within neuro-oncology. These tumors vary from indolent, low-grade types such as oligodendroglioma to highly aggressive, high-grade variants like glioblastoma, which accounts for 41% of gliomas and exhibits the poorest prognosis with a survival rate of around 7% in five years. Despite extensive research on glioma etiologies, knowledge of definitive risk factors remains limited, with ionizing radiation being the most well-studied [1]. In 2021, the World Health Organization (WHO) revised its classification of central nervous system (CNS) tumors, highlighting the necessity of moving beyond histological criteria for glioma classification. This transition towards more accurate differentiation based on genetically heterogeneous markers, such as Isocitrate Dehydrogenase (IDH) mutation, 1p/19q codeletion, and O6-methylguanine-DNA methyltransferase (MGMT) promoter methylation, marks a significant advancement in the field [2].

Glioma diagnosis mainly relies on magnetic resonance imaging (MRI), which provides high-resolution anatomical detail of the brain, and it is considered the primary imaging technique for initial assessment and ongoing monitoring [3]. Standard MRI sequences routinely used in radiological evaluations include T1-weighted, T2-weighted, and Fluid Attenuated Inversion Recovery (FLAIR) sequences, each offering vital information about mass effect, vasogenic edema, and tumor contrast enhancement patterns [4]. A significant challenge for neuroradiologists involves distinguishing treatment-related changes, such as radiation necrosis, from actual tumor progression. In such cases, advanced MRI techniques—like diffusion-weighted imaging (DWI), perfusion-weighted imaging (PWI), and MRI spectroscopy- are often used to support diagnosis [5,6].

Nuclear medicine modalities, such as Positron Emission Tomography (PET), have also become highly valuable in evaluating gliomas, offering functional and molecular insights that complement the structural detail provided by the MRI [7]. Several advancements in nuclear medicine have been reported in recent years in the diagnosis and treatment of brain tumors, enabling disease detection and monitoring and the potential use of the same tracers as therapeutic agents [8]. Some of the main radiotracers currently utilized in PET imaging for the detection and characterization of gliomas include ^{18}F-FDG, which detects the increased metabolic state of the malignant cells, and amino-acid tracers (^{11}C-MET and ^{18}F-FET), which enable a more targeted tumor identification through their adhesion to specific cell receptors [9].

Even though imaging modalities provide valuable information regarding the tumor pathology, tissue biopsy remains essential for a definitive diagnosis and grading, since imaging features lack sufficient specificity [10,11]. Tissue biopsy allows direct histopathological examination of tumor cells, assessment of cellular morphology, mitotic activity, and necrosis, as well as molecular and genetic profiling, which are critical for accurate classification and treatment planning. Molecular profiling specifically improves histopathology by including IDH mutations, MGMT promoter methylation testing, and 1p/19q co-deletion status; factors that are now included in the WHO 2021 classification, as previously mentioned [2]. These molecular markers serve diagnostic and prognostic purposes; for instance, IDH-mutant gliomas generally are linked to better clinical outcomes due to their responsiveness to targeted therapies, such as vorasidenib. Similarly, MGMT promoter methylation predicts sensitivity to temozolomide [12,13].

While histopathology and molecular profiling are currently the gold standards, they are invasive, time-consuming, and can be limited by sampling bias, especially in heterogeneous tumors like glioblastoma multiforme [14]. At the same time, stereotactic biopsies may not fully capture the molecular heterogeneity of gliomas, which can lead to under- or misdiagnosis [15]. It is also important to note that the delay between imaging biopsy and obtaining molecular results can slow early therapeutic decisions, particularly in rapidly progressing high-grade gliomas [16,17]. AI-assisted imaging has the potential to overcome these challenges by providing non-invasive, whole-tumor analysis. It can identify regions of highest molecular heterogeneity for targeted biopsy, predict molecular markers from imaging features, and accelerate preliminary diagnostic insights, complementing and guiding tissue sampling.

Although biopsy and related procedures pose limitations, imaging techniques also exhibit challenges. The variability between readers in MRI interpretation remains a significant issue, especially with borderline or ambiguous cases [12,18]. Radiologists can interpret small imaging details differently, potentially affecting treatment choices. Imaging methods like spectroscopy or perfusion MRI often lack reproducibility across different institutions, limiting their standalone diagnostic utility [19,20]. PET imaging in glioma detection also presents various challenges that affect the accuracy and reliability of the modality. Key limitations include the decreased tumor-to-background contrast when utilizing ^{18}F-FDG, owing to the naturally high-glucose uptake of the normal brain tissue, the potential for false-positive findings due to tumor inflammation or treatment-related effects, and the heterogeneous tracer uptake observed across different tumor types and grades [21–23].

Artificial intelligence (AI) is changing how glioma diagnoses are made by providing non-invasive, automated tumor detection, grading, and molecular analysis methods. Using algorithms that learn from large imaging datasets, AI tools, especially those based on radiomics and deep learning (DL), can identify subtle, multi-dimensional patterns in MRI and PET scans that are often invisible to the human eye [3]. Radiomics techniques allow quantification of tumor morphology, texture, and intensity features from standard MRI sequences, or texture and tracer-uptake patterns when applied in PET imaging, which may subsequently be linked to histopathological or molecular labels [24,25]. For instance, machine learning models trained on radiomic features have shown strong predictive ability for MGMT promoter methylation and IDH mutation status, two vital biomarkers in glioma classification [26,27]. In parallel, DL techniques like convolutional neural networks (CNNs) and attention-based models, such as transformers, have demonstrated impressive ability to segment tumor subregions and predict genetic alterations directly from raw MRI images, eliminating the need for handcrafted feature extraction [10,28]. Beyond these AI-driven methods, integrating biomechanical and oncophysics-based models -which capture tumor growth dynamics, tissue mechanics, and microenvironment interactions- may enhance predictive accuracy and support personalized therapy planning.

By providing non-invasive insights into tumor characteristics and behavior, AI-based imaging tools can help guide treatment planning and monitor therapy response across various interventions, including surgery, radiotherapy, chemotherapy, targeted therapies such as temozolomide, and immunotherapy. Predictive models may support timely therapeutic decisions, optimize treatment sequencing, and help personalize interventions according to tumor aggressiveness and molecular profile.

These models offer the potential for fast, consistent, and scalable diagnostic tools, especially in centers with limited access to molecular testing. Recent studies have also begun exploring large language models and generative pre-trained transformer (GPT)-based platforms to combine radiologic and genomic data [29]. This emerging approach marks a new frontier in personalized neuro-oncology.

As the body of literature exploring AI applications in glioma imaging grows, the rationale for this review is to provide a comprehensive summary of recent advances and their translational potential in clinical neuro-oncology. Specifically, we highlight how radiomics and DL models are currently used for tumor classification and grading, with increasing success in distinguishing gliomas solely based on imaging [15]. Notably, recent studies demonstrate promising results in the non-invasive prediction of molecular features like IDH mutation, MGMT promoter methylation, and 1p/19q codeletion, which are critical for treatment decisions and prognosis [5,30]. This review aims to examine studies containing DL and/or radiomics pipelines for glioma characterization, underscore their clinical relevance, and identify future research opportunities. This is the first narrative review to systematically integrate radiomics and DL-based approaches across PET and MRI modalities for glioma diagnosis and molecular profiling. This includes models based on transformer architectures, multimodal fusion frameworks, and explainable Artificial Intelligence systems designed for neuro-oncology applications [16,31].

2. Materials and Methods

To provide a thorough and current literature review, we performed a narrative analysis of peer-reviewed studies published from January 2020 to July 2025. We systematically searched three electronic databases PubMed, Scopus, and EMBASE using a combination of Boolean operators and keywords: ("glioma" OR "brain tumor" OR "glioblastoma") AND ("radiomics" OR "machine learning" OR "deep learning" OR "convolutional neural network" OR "transformer") AND ("classification" OR "segmentation" OR "grading" OR "molecular profiling") AND ("IDH" OR "MGMT" OR "1p/19q") AND ("PET" OR "Nuclear Medicine" OR "MRI"). Filters for English-language studies and human subjects were applied whenever possible. Inclusion criteria encompassed studies that (1) investigated AI-based methods for glioma imaging, classification, or molecular prediction, and (2) reported performance metrics such as accuracy, AUC, or F1-score. Priority was given to studies utilizing publicly available datasets (TCIA/NIH) or real-world institutional cohorts. The quality of the included studies was assessed by taking into account where was feasible parameters as the sample size, performance metrics reports (AUC/F1-score, etc.) and transparency in methodology (explainability, radiomics features reproducibility, code availability) This review emphasizes radiomics-driven machine learning and deep learning architectures, including hybrid pipelines and explainable AI models, while also addressing their limitations, clinical application status, and future research directions.

3. Results

This narrative review references 103 articles, including those providing clinical and technical background. These were grouped thematically into seven main areas: (1) radiomics analysis of gliomas, (2) challenges and limitations of radiomics in gliomas (3) deep learning in glioma imaging, (4) challenges and limitations of deep learning in gliomas, (5) integrating imaging modalities with genomics and clinical data, (6) clinical translation and real-world application, and (7) future directions. These categories highlight the ongoing integration of computational imaging, machine learning, and neuro-oncology, aiming for a more personalized, non-invasive diagnosis and biomarker evaluation of gliomas. The principal utilities of radiomics and deep learning are briefly mentioned in Table 1, and extensively described in the following sections, focusing on their roles in tumor segmentation, prognosis assessment, and molecular profile prediction (Figure 1).

Table 1. Key features of Radiomics and DL technologies in neuro-oncology.

Domain	Radiomics	Deep Learning
Feature Extraction	Relies on handcrafted features (e.g., shape, texture, intensity) extracted from imaging data	Learns features automatically from raw imaging data, without prior handcrafted design
Interpretability	More transparent; features can be linked to biological or pathological processes	Often considered a "black box" with limited interpretability unless explainable AI is applied
Data Requirements	Can be applied to smaller datasets with careful feature selection and robust modeling	Requires large, annotated datasets for effective training and generalization
Flexibility	Well-suited for combining imaging with clinical or genomic data	Highly adaptable to multimodal inputs and end-to-end tasks (e.g., segmentation + classification)
Performance	Good predictive performance but may plateau with highly complex tasks	Demonstrates superior accuracy in segmentation, classification, and molecular prediction
Reproducibility	Affected by differences in feature extraction protocols across centers	Model performance may vary with architecture, training data and preprocessing pipelines

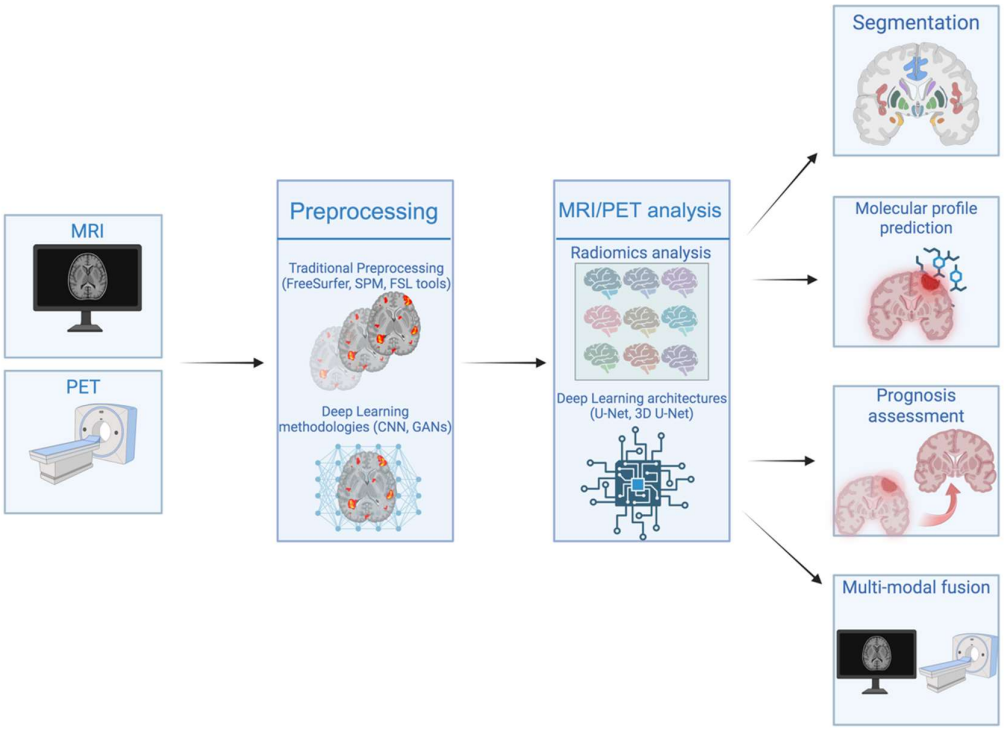


Figure 1. MRI or PET imaging as input data, undergoing traditional or deep learning-based preprocessing. In this figure it is highlighted how radiomics and deep learning architectures are used for tumor segmentation, prognosis assessment, and molecular profile prediction. The pipeline supports multi-modal data fusion, enabling comprehensive glioma characterization.

4. Discussion

4.1. Radiomics in Glioma Diagnosis and Molecular Profiling

Radiomics is an expanding field that converts standard medical images into high-dimensional data through advanced feature extraction techniques. The typical radiomics process includes image acquisition, tumor segmentation, feature extraction, and modeling

with statistical or Machine Learning (ML) methods [32]. A single MRI scan can produce hundreds to thousands of quantitative features encompassing shape, intensity, texture, and wavelet domains, which may non-invasively reflect the tumor's biological properties [33]. Similarly, PET imaging yields quantitative data by capturing the uptake of radioligands in target cells, offering non-invasive insights into tumor metabolism, molecular profiles, intratumoral heterogeneity, and potential aggressiveness. Segmentation, whether manual, semi-automated, or fully automated, is crucial in radiomics workflows, as the accuracy of subsequent feature extraction depends on precise tumor boundary delineation. After segmentation, radiomic features are normalized, selected, and used in classification or regression models to predict clinical or molecular outcomes [34,35]. These models can assist radiologists by highlighting subtle subvisual imaging patterns, such as complex spatial or textural features that may not be readily apparent to the human eye. For example, in glioma imaging, AI has been used to suggest regions potentially associated with IDH mutation status on MRI, supporting radiologists in identifying imaging biomarkers that might otherwise go unnoticed. This collaborative approach can enhance diagnostic confidence, inform prognosis, and guide treatment planning. Some of the most representative MRI and PET radiomics studies published in the last five years are demonstrated in Table 2, highlighting the model used and the application of this model for glioma diagnosis.

Using standard MRI sequences or PET imaging, radiomics has shown significant potential in distinguishing low-grade gliomas (LGG) from high-grade gliomas (HGG) [36–38]. Radiomic-based ML classifiers can effectively distinguish tumor grades by analyzing texture variability, intensity patterns, and tumor boundaries, achieving performance comparable to experienced clinicians [39]. These techniques are essential in uncertain or equivocal classification cases where visual evaluation alone is insufficient. Several studies have examined radiomics-based grading in line with the WHO classification, explicitly targeting the differentiation between grade II, III, or IV gliomas. For example, structural and diffusion tensor imaging (DTI) radiomics models have demonstrated high AUC scores in predicting tumor aggressiveness and invasive capacity [19]. Furthermore, incorporating multi-parametric MRI data such as T1, T2, FLAIR, and contrast-enhanced sequences has improved classification accuracy by capturing detailed anatomical and physiological tumor characteristics [40]. In some cases, combining imaging-derived features with germline genetic profiles has further enhanced glioma subtype stratification [41,42]. These classification models are typically validated through cross-validation on public datasets or institutional cohorts, encouraging broader use of radiomics in glioma grading [13]. An essential advantage of radiomics is its ability to leverage routinely acquired clinical imaging, making it widely applicable across institutions. Nevertheless, its reliance on handcrafted features and variability in extraction protocols remain key limitations, underscoring the need for standardization and integration with DL approaches to achieve more robust and generalizable performance.

Regarding radiomics in nuclear medicine, several studies aimed to employ such models to extract valuable insights about glioma grading—not based on anatomy but on their metabolic and functional characteristics [43]. By quantifying tracer uptake and metabolism, PET-based radiomics can provide functional information that complements structural MRI findings. However, its application is still influenced by differences in tracer availability and technical protocols across centers. An essential radiomics study of ^{11}[C]-Methionine PET/CT features, conducted by Russo G. et al. in 2021, described developing a machine learning-based model trained to differentiate low-grade from high-grade tumors. The model achieved 0.85 accuracy in grade prediction, suggesting the feasibility of 11[C]-MET-PET radiomics for supporting clinical decision-making, even though its use remains limited to specialized centers with on-site cyclotron capabilities [44].

Beyond grading, radiomics play a crucial role in the noninvasive prediction of glioma molecular markers, such as IDH mutation, MGMT promoter methylation, 1p/19q codeletion, and, more recently, ATRX loss [45]. These markers have essential diagnostic, prognostic, and therapeutic implications. Radiomics models have been employed to determine IDH mutation status directly from MRI scans by analyzing features like tumor shape, boundary sharpness, and intratumoral heterogeneity [46]. For instance, studies using multicontrast MRI sequences in a two-stage training framework demonstrated high accuracy in predicting IDH status, even when trained on relatively small datasets [47]. Other models incorporate perfusion and diffusion imaging, such as dynamic susceptibility contrast MRI and diffusion tensor imaging, to enhance molecular prediction sensitivity [48]. A more recent study by Zhou W. et al. 2024 developed and validated radiomics models using preoperative ^{11}[C]MET PET/CT imaging to predict IDH mutation status and WHO grade in diffuse gliomas. Using data from 178 patients, models based on PET, CT, and combined features were tested. The combined PET/CT model, integrated with clinical variables in a nomogram, achieved high predictive accuracy of IDH status, with an AUC reaching 88%, and reasonable differentiation of WHO-grades in IDH-wildtype patients [49].

Radiomic pipelines utilizing super-resolution reconstruction techniques on PET and MRI have enhanced the prediction of MGMT methylation by improving image quality and texture analysis [50]. Models that combine clinical information with advanced imaging features have achieved AUC scores above 0.85 for MGMT prediction [51]. These noninvasive profiling tools could speed up treatment choices, lessen the need for invasive biopsies, and broaden access to molecular diagnostics in areas with limited pathology resources. Multi-parametric radiomic models, including the T2-FLAIR mismatch sign, have greatly enhanced the 1p/19q codeletion prediction in IDH1-mutant gliomas. This imaging sign, characterized by a hyperintense signal on T2 images with relative FLAIR signal suppression and a surrounding hyperintense rim, is a specific imaging biomarker associated with IDH-mutant, 1p/19q non-codeleted astrocytomas [52]. Similarly, PET-based radiomics has been applied to predict IDH mutation and 1p/19q codeletion status in gliomas. A notable 2022 study evaluated radiomic features extracted from ^{18}F-FDOPA PET scans in 72 newly diagnosed glioma patients. Machine learning models were developed and validated using these features, achieving area under the curve (AUC) values of 0.831 for IDH mutation prediction and 0.724 for 1p/19q codeletion [53].

Beyond binary mutation prediction, radiomics has also been employed to visualize and quantify the spatial heterogeneity of biomarkers such as IDH1 within gliomas. A recent study utilized voxel-wise radiomic mapping to measure regional differences in IDH1 expression, allowing for in vivo assessment of intratumoral heterogeneity [54].

Radiomics has demonstrated potential in rare, aggressive tumor subtypes like diffuse midline gliomas, with MRI-based radiomic signatures yielding as prognostic markers. These signatures assist in stratifying patient risk and determining treatment intensity [55]. In contrast to static MRI-based radiomics used for risk stratification, this study demonstrated the applicability of delta radiomics from dynamic ^{18}F-FDOPA PET in predicting progression-free survival in high-grade glioma patients. By analyzing longitudinal changes in PET-derived radiomic features, the delta-absolute model significantly outperformed conventional and single-time-point approaches, even in small cohorts, highlighting its robustness and potential in rare disease settings [56].

Radiomics in PET imaging has also contributed to identifying and differentiating early tumor progression from the post-therapy pseudoprogression, a term used to describe the initial increase in tumor size after immunotherapy or radiation therapy [57]. A study in 2020 evaluated the use of FET PET radiomics in the differentiation of the two entities in glioblastoma patients following chemoradiation. The authors used data from 34 patients

and utilized advanced radiomic modeling. Their approach achieved 100% sensitivity and negative predictive value in identifying pseudoprogression, outperforming conventional PET metrics like TBRmax, a feature that reflects the peak tracer uptake intratumoral compared to the normal brain tissue uptake [58]. These findings underscore the potential of FET PET radiomics in assessing post-treatment changes, offering valuable support for clinical decision-making and validation.

Table 2. Key radiomics studies from 2020 to 2025 regarding MRI or PET in glioma classification, molecular markers' prediction, or diagnosis.

Authors	Imaging Modality	Application of Radiomics	Model Type	Performance Metrics	Clinical Utility	Reference
Sun X. et al. (2024)	Conventional MRI	Prediction of glioma subtype based on automatic segmentation	3D U-Net based CNN	Accuracy: up to 0.909	Non-invasive glioma molecular characterization	[39]
Nakase T. et al. (2025)	Conventional MRI	IDH mutation status prediction	Elastic Net Neural Network	Accuracy: 0.86	Non-invasive glioma profiling	[41]
Mora N. et al. (2023)	T1w, T2w, FLAIR MRI	ATRX mutation status prediction	Lasso Regression	Accuracy: 0.746	Non-invasive glioma molecular classification	[42]
Russo G. et al. (2021)	11[C]-MET PET/CT	Prediction of tumor grading	Discriminant Analysis	Accuracy: 0.85	Aid clinical decisions and non-invasive grading	[44]
Meng L. et al. (2022)	T1w, T2w, FLAIR, ADC MRI	ATRX mutation status prediction	LASSO + Support Vector Machine (SVM)	Accuracy: 0.88	Non-invasive genetic profiling	[45]
Truong N. et al. (2024)	Preoperative MRI	IDH mutation status prediction	Random Forest, XGBoost ensemble	Accuracy: up to 0.95	Non-invasive glioma molecular classification	[47]
Minh T. et al. (2023)	Conventional MRI, DTI	MGMT methylation status prediction	Multi-stage ML model	Accuracy: 0.80	Non-invasive therapy stratification in GBM	[48]
Zhou W. et al. (2024)	11[C]-MET PET/CT	IDH mutation status and WHO prediction	LASSO + ML (SelectKBest, Spearman)	AUC (IDH): 0.87 and (WHO): 0.77	Non-invasive molecular and grade stratification	[49]
Zhang C. et al. (2024)	Diffusion MRI (DTI)	IDH mutation status and glioma grade prediction	GAN-based super resolution	AUC (IDH): 0.88 and (grade): 0.81	Non-invasive molecular status and tumor grading	[50]
Du P. et al. (2023)	Preoperative T1w, T2w MRI	Non-invasive prediction of diffuse astrocytic glioma, IDH-wildtype with GBM features (DAG-G)	Multiple ML classifiers (RF, SVM, etc.)	AUC: 0.89–0.91 in external validation	Aid treatment planning by identifying aggressive gliomas preoperatively	[51]

Table 2. *Cont.*

Authors	Imaging Modality	Application of Radiomics	Model Type	Performance Metrics	Clinical Utility	Reference
Zaragori et al. (2022)	^{18}F-DOPA PET	Predict IDH mutation and 1p/19q co-deletion status	Logistic Regression (IDH), SVM with RBF kernel (1p/19q)	AUC (IDH): 0.831 (1p/19q): 0.724	Non-invasive glioma molecular characterization	[53]
Ahrari S. et al. (2024)	L-[18F]-fluoro-phenylalanine PET	Predict progression-free survival using delta radiomics	SVM + Recursive Feature Elimination + ElasticNet + GB-Linear	C-Index: 0.783 (Accuracy or AUC not provided)	Prognosis prediction in rare HGG	[56]
Lohman P. et al. (2020)	O-2-[18F]-fluoroethyl-L-tyrosine (FET) PET	Discriminate pseudoprogression from early tumor progression	Random Forest classifier + RFE (4 features)	Accuracy: 0.70	Differentiation of pseudoprogression from tumor progression	[58]
Zhang L. et al. (2023)	[18F]-FDG PET + Multi-modal MRI	Predict ATRX mutation status in IDH-mutant LGG	Random Forest integrated with clinical Radiomics	AUC: 0.975 in validation	Non-invasive ATRX mutation prediction in LGGs	[59]
Bai J. et al. (2025)	^{18}F-FET PET/MRI (FLAIR, T1, ADC)	Prediction of molecular genotypes (IDH, TERT, MGMT)	Naïve Bayesian classifier	AUC (IDH): 0.97, (MGMT): 0.86	Preoperative molecular genotype prediction in adult-type diffuse gliomas	[60]

Radiomics analysis has also focused on ATRX mutation, a key molecular dysfunction in astrocytic glioma formation. Leveraging multiparametric MRI features for ATRX prediction broadens the scope of noninvasive molecular phenotyping and illustrates the potential of radiomics to uncover markers that are otherwise accessible only through biopsy. Recent studies prove that multiparametric MRI-based models can accurately predict ATRX loss, further expanding the scope of noninvasive molecular phenotyping [59].

Radiomics in glioma imaging has also evolved to integrate MRI modalities and PET imaging for identifying tumor characteristics [59,60]. A representative study published in 2025 evaluated the use of radiomics. Features from multiparametric ^{18}F-FET PET/MRI to predict molecular genotypes (IDH, TERT, MGMT) in adult-type diffuse gliomas. ML models—Naive Bayes with five-fold validation—were trained on 994 extracted features across PET and MRI modalities, significantly outperforming single-modality and MRI-only models, achieving AUCs of 0.97 for IDH, 0.90 for TERT, and 0.86 for MGMT prediction. These results suggest that integrated PET/MRI radiomics enable accurate genotype prediction, supporting more personalized treatment for glioma patients [60]. While MRI- and PET-based radiomics provide valuable insights, each has strengths and limitations. MRI radiomics offers broad access and high resolution and captures structural, diffusion, and perfusion features, which are helpful for tumor grading and molecular markers like IDH or MGMT. However, MRI features can vary due to scanner type, protocols, and segmentation, affecting reproducibility [12]. PET radiomics reflects metabolic activity, distinguishing progression from pseudoprogression and providing functional markers like amino acid uptake. Its drawbacks include higher costs, tracer availability, radiation, and lower spatial resolution than MRI [21,44].

4.2. Challenges and Limitations of Radiomics in Gliomas

These tools can accelerate treatment decisions, minimize reliance on invasive biopsies, and broaden molecular access in resource-limited settings. Despite their potential, radiomics in glioma diagnosis encounter significant challenges that limit their use in clinical settings. These can be grouped into common challenges shared with DL and radiomics-specific issues. These challenges can be categorized into key points: (1) dependence on precise tumor segmentation, (2) lack of standardized imaging protocols, (3) small sample sizes and limited validation, and (4) variability introduced by preprocessing methods and reporting practices.

Radiomics-specific challenges largely stem from dependence on precise tumor segmentation, which is often manual or semi-automatic. For instance, the BraTS challenge datasets require expert manual segmentation of gliomas across multiple MRI sequences to enable consistent radiomic feature extraction. Similarly, studies applying radiomics to [^{11}C]-MET PET for glioma grading often depend on manual delineation of metabolic tumor volumes to ensure accurate texture and intensity-based feature computation. This process can cause variability between observers, resulting in inconsistent feature extraction and affecting model accuracy [61].

Another significant challenge is the lack of standardization in imaging protocols among different institutions and scanners. Variations in resolution, sequence settings, and magnetic field strength can significantly impact the radiomic features extracted, a challenge shared with deep learning models [62].

Small sample sizes limited external validation, and overfitting further impacts reproducibility, especially when models are trained and tested on the same datasets [63]. Such methodological inconsistencies highlight the need for standardized pipelines and multicenter collaborations to ensure robust, reproducible, and generalizable performance across clinical settings.

Furthermore, radiomics features are often influenced by subtle image noise and preprocessing techniques, and many published models lack transparent reporting or open-source code, issues also relevant to deep learning [64].

4.3. Deep Learning Approaches in Gliomas

DL, especially CNNs, have transformed medical imaging by enabling end-to-end learning directly from raw data. Unlike radiomics, which relies on handcrafted features and manual segmentation, CNNs recognize hierarchical spatial patterns through multiple convolutional layers [65]. In glioma imaging, CNNs are often used for tumor segmentation, classification, and molecular profiling from MRI data, offering the advantage of handling complex multi-parametric inputs and reducing reliance on manual annotations [6]. A significant benefit of deep learning is its scalability. These models can be trained on multiple parametric MRI sequences and frequently surpass traditional classifiers when large annotated datasets are accessible [66]. However, they may be sensitive to small sample sizes and heterogeneous imaging protocols, affecting generalizability. Fully convolutional networks also enable pixel-level segmentation and probabilistic biomarker maps, overcoming the limitations of radiomics, which depend on precise tumor delineation [20]. A concise summary of some representative studies of DL is presented in Table 3.

Tumor segmentation remains the most well-established use of DL in neurooncology. Architectures like U-Net effectively identify tumor subregions in multi-modal MRI scans, including necrosis, enhancement, and edema, with high spatial accuracy [65]. U-Net architectures have also been trained on PET images, aiming to segment the tumor on a metabolic scale, rather than anatomically. A 2023 study by Gutsche R. et al. demonstrated a deep learning-based method for fully automated metabolic tumor volume (MTV) segmentation

on ^{18}F-FET PET scans, leveraging a modified U-Net architecture. The model was trained and tested on PET scans of patients with glioma, achieving high accuracy and agreeing strongly with expert assessments. These automated MTV changes were significantly associated with survival outcomes, confirming the model's clinical utility for treatment response assessment [67]. A different study of 2023 developed and validated a multi-label CNN, 3D U-Net architecture, for automatic detection and segmentation of gliomas using ^{18}F-FET PET scans, scoring 88.9% (sensitivity and 96.5% precision in scan classification, with DSC ~74.6% for lesion segmentation [68]. Together, these developments reflect how deep learning steadily transforms tumor segmentation in neuro-oncology—from improving consistency in imaging interpretation to offering practical support for clinical decision-making across anatomical and metabolic imaging modalities.

CNNs also classify gliomas by grade and subtype, achieving high diagnostic accuracy [6]. Vision transformer models and hybrid CNNs have recently started incorporating MRI and PET imaging data with clinical or histopathological information, further improving their generalizability [69]. For molecular profiling, CNNs identify key biomarkers such as IDH mutation, MGMT promoter methylation, and 1p/19q codeletion directly through imaging. An end-to-end system segments tumors automatically and simultaneously, predicts tumor grade and its molecular status [70]. In IDH prediction, GANs enhanced morphological variability and improved model generalization [71]. Additionally, models trained on GBM cohorts accurately discriminated between IDH-mutant and wild-type cases [72]. Likewise, deep learning models have been applied in PET imaging to accurately predict gliomas' molecular features in patients. A recent study developed a DL approach using an assistance training (AT) scheme to predict H3K27M mutation status in midline gliomas from ^{11}C-MET or ^{18}F-FET PET scans. The AT method enabled mutual learning between the two tracers while requiring only one as input during prediction. This model achieved an AUC of 0.943 for MET and 0.8619 for FET in internal cross-validation, demonstrating clinical relevance by aligning with multidisciplinary decisions in pathology-uncertain cases [73].

Emerging applications go beyond traditional markers. One study noninvasively predicted CCL2 expression levels, a vital immunologic biomarker, using MRI in high-grade gliomas, providing insights into tumor microenvironment imaging [74]. Another deep learning model accurately identified CDKN2A/B homozygous deletion status in IDH-mutant astrocytoma, aiding preoperative genomic risk assessment [75]. These approaches demonstrate the advantage of integrating imaging with molecular characterization, enabling noninvasive prediction of key biomarkers.

Deep learning demonstrates impressive results in predicting MGMT methylation, with AUCs exceeding 0.85 in certain studies [76]. Using standardized methylation tests also achieves high accuracy in IDH-wildtype gliomas [77]. Furthermore, cross-institutional research confirms the stability of these models despite variations in scanners or protocol [78]. Finally, systematic reviews validate the reliability of CNNs for glioma segmentation and prognosis [79], emphasizing the increasing success of deep learning in molecular subtype classification, especially with multimodal and semi-supervised methods [80].

These results signify that deep learning models offer an effective way to develop noninvasive, image-based diagnostic workflows that can predict structure, grade, and genotype status, laying the groundwork for precision neuro-oncology.

Table 3. Key deep learning studies from 2020 to 2025 regarding MRI or PET in glioma classification, molecular markers' prediction or diagnosis.

Authors	Imaging Modality	Application of Deep Learning	Model Type	Performance Metrics	Clinical Utility	Reference
Iqbal MS. et al. (2025)	Multimodal MRI	Non-invasive MGMT promoter status classification in GBM	3D Residual U-Net for segmentation + 3D ResNet10 for classification	AUC: 0.66	Support treatment planning by predicting MGMT status	[65]
Koska I. et al. (2025)	Multiparametric MRI (T1w, T2w, FLAIR)	Non-invasive MGMT promoter status prediction in GBM	3D-ROI-based custom CNN	Accuracy: up to 0.88	Preoperative prognostic biomarker for treatment planning	[66]
Gutsche R. et al. (2023)	^{18}F-FET PET	Automated metabolic tumor volume segmentation in glioma patients	Artificial Neural Network	Sensitivity: 0.93 and F1 score: 0.92	Evaluation and response assessment in glioma patients	[67]
Rahimpour M. et al. (2023)	^{18}F-FET PET	Automatic glioma detection, segmentation and Tumor-to-Background ratio estimation	Multi-label CNN and single-label CNN	Sensitivity: 0.89	Tumor delineation and uptake quantification, reducing inter-reader variability	[68]
Waghmare P. et al. (2021)	Multiparametric MRI (T1w, T2w, FLAIR)	Prediction of multiple glioma molecular markers (IDH, MGMT, 1p/19q, grade)	Semi-supervised hierarchical multi-task CNN	Accuracy: 0.823	Non-invasive genomic profiling for treatment planning	[69]
Decuyper M. et al. (2021)	Preoperative MRI (T1w, T2w, FLAIR)	Glioma segmentation and prediction of grade, IDH and 1p/19q co-deletion status	3D U-Net + multi-task CNN	AUC (grade): 0.93, (IDH): 0.94, (1p/19q): 0.82	Non-invasive preoperative molecular marker prediction for prognosis and therapy planning	[70]
Park J. et al. (2021)	T1w-FLAIR MRI	Synthetic image generation for data augmentation and IDH mutation prediction in GBM	GAN for synthetic generation + diagnostic CNN model	Diagnostic accuracy: 0.90–0.93	Improved training data and diagnostic accuracy for IDH mutation	[71]
Napolitano A. et al. (2021)	Multiparametric MRI (T1w, T2w, FLAIR)	GBM-specific IDH mutation prediction	4-block 2D CNN	Accuracy: up to 0.83	Non-invasive IDH status prediction in GBM	[72]
Li J. et al. (2023)	T2w MRI data	Automatic segmentation and prediction of H3K27M in diffuse midline gliomas	nnU-Net architecture	Accuracy: 0.85–0.92	Prediction of H3K27M status for prognosis and treatment stratification	[73]

4.4. Model Selection in Deep Learning

CNNs remain the core method for glioma imaging because of their excellent performance in segmentation and molecular prediction [68–70]. They excel at extracting local spatial features, making them dependable for classification and delineating tumor boundaries. However, their effectiveness can be hindered by dependence on extensive annotated datasets and a limited capacity to capture long-range contextual information.

On the other hand, GANs are especially useful when data availability is limited or imbalanced. They can enhance datasets and generate super-resolution images, thereby boosting the accuracy of molecular marker and grade assessments [50,71]. Their key benefit lies in tackling small sample sizes and improving image quality. However, they can face challenges such as training instability and the risk of producing synthetic images that may not fully represent the accurate biological picture [71].

Lastly, Transformers are equipped with self-attention mechanisms, which make them excel at modeling long-range dependencies and multimodal data integration. This makes them highly effective for genomic subtyping and molecular profiling [15]. Their main limitations are the need for large datasets and high computational resources, which can restrict their use in smaller research environments.

4.5. Challenges and Limitations of Deep Learning in Gliomas

Despite the promising results of deep learning in glioma diagnosis and biomarker prediction, several key challenges must be addressed to be widely adopted in clinical practice. These challenges can be broadly summarized as: (1) limited interpretability of DL models, (2) risk of overfitting and lack of external validation, (3) domain shift due to variability in imaging protocols, and (4) insufficient prospective and clinically oriented studies. Some challenges, such as limited sample sizes, lack of external validation, and variability in imaging protocols, are shared with radiomics.

A primary DL-specific concern is deep neural networks' 'black-box' nature. Most CNN and transformer models offer limited interpretability, decreasing physician trust and complicating clinical decision-making, particularly when AI predictions influence treatment choices. Although explainable AI (XAI) techniques like Grad-CAM and SHAP can partially visualize decision processes, their application in glioma imaging remains inconsistent, poorly understood, and undocumented.

Another major challenge is the overfitting that happens when models memorize noise or dataset-specific patterns instead of learning general features. This problem appears commonly in glioma datasets with limited samples or class imbalance, where models achieve high internal accuracy but struggle with new data. Without external validation, these models can be unreliable in real-world clinical settings [81]. Domain shift presents a significant challenge: variations in MRI acquisition protocols, scanner brands, field strengths, and preprocessing methods can significantly impact model performance across different institutions. A recent study revealed that radiomic and deep features remained highly sensitive to input changes even after intensity normalization, highlighting the need to develop robust preprocessing pipelines [82]. This specific issue was highlighted in a comprehensive systematic review and meta-analysis, where it has been shown that DL models achieved high diagnostic accuracy for glioma molecular markers in single-center studies, with their performance dropping notably during external validation or when used across different datasets [83]. The review stressed the urgent importance of standardization, larger datasets, and prospective trials before these tools can be reliably used in clinical settings. Multi-institutional datasets, cross-site harmonization, and inclusion of clinical metadata can mitigate these issues, but achieving robust generalizability remains difficult.

Furthermore, only a few models undergo prospective validation, and even fewer are developed with user-friendly interfaces or regulatory compliance in mind. Until DL models become explainable, externally validated, and resilient to real-world variability, their application will mainly stay within academic and research settings.

4.6. Integrating Imaging Modalities with Genomics, Biomechanical, and Clinical Data

A key emerging area in glioma research involves combining multimodal data such as PET and MRI, clinical metadata, histopathology, and genomics within integrated deep learning frameworks. Unlike traditional methods that depend only on imaging features, these multimodal models utilize complementary data sources, resulting in more accurate tumor behavior and molecular subtype predictions (Figure 2). A comparison between the traditional methods and AI-assisted diagnosis is provided in Table 4.

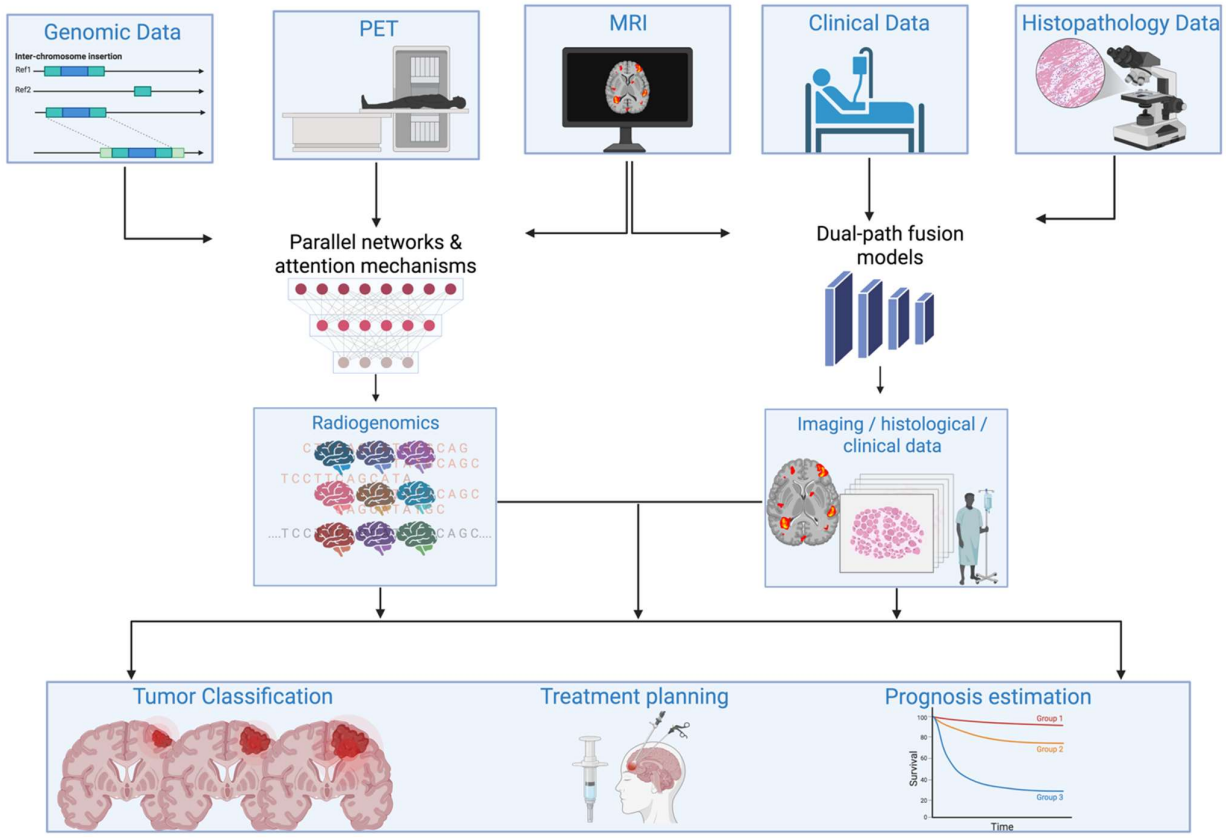


Figure 2. Multimodal fusion framework integrating imaging data (MRI/PET), histopathological features, and clinical/genomic information. By combining these diverse data sources, the model enhances tumor classification, prognosis assessment, and treatment monitoring. This integrative approach supports more accurate, personalized decision-making in glioma management.

Table 4. Comparison of traditional methods and AI-based tools in glioma diagnosis, characterization and decision-making.

Aspect	Traditional Methods (Histopathology and Imaging)	AI-Based Approaches (Radiomics and Deep Learning)
Invasiveness	Biopsy is required for definitive diagnosis; invasive and carries procedural risks [10,11]	Non-invasive, based on MRI and PET imaging features [3]
Time Efficiency	Histopathology and molecular profiling are time-consuming and can delay treatment decisions [16,17]	Rapid predictions generated directly from imaging data [3]

Table 4. *Cont.*

Aspect	Traditional Methods (Histopathology and Imaging)	AI-Based Approaches (Radiomics and Deep Learning)
Sampling Bias	Biopsies may not capture tumor heterogeneity, leading to under- or misdiagnosis [14,15]	Analyzes the entire tumor volume, accounting for spatial heterogeneity [46]
Specificity	Imaging features alone lack sufficient specificity; overlap with treatment-related changes; biopsy considered a highly specific method [10,11]	Captures subtle, multidimensional patterns invisible to the human eye [3,24]
Reproducibility	Imaging interpretation varies across readers and institutions, limiting reproducibility [18–20]	Algorithms provide consistent and scalable outputs when trained on heterogeneous datasets and undergo external validation [63]
Molecular Insight	Requires histopathology and genetic testing for markers like IDH, MGMT, 1p/19q [2,12,13]	Can non-invasively predict molecular features such as IDH mutation, MGMT promoter methylation, and 1p/19q codeletion [26,27]

Recent studies indicate that fusion architectures, such as parallel networks and attention mechanisms, can effectively combine radiologic and genomic data to improve glioma patient stratification. For example, radiogenomic models utilizing MRI and DNA-methylation data have identified distinct molecular clusters of gliomas with similar imaging characteristics, emphasizing meaningful genotype-phenotype connections [84]. Novel network architectures like MDPNet, a dual-path fusion model, have been created to simultaneously combine clinical data and imaging features. This approach enhances model generalizability and biomarker prediction [85]. These models employ separate pathways for radiologic and tabular data, which are subsequently merged through late fusion and optimized jointly.

Furthermore, multi-task learning has become a valuable approach in glioma modeling. One study developed a single-stage multi-task deep network that can simultaneously perform segmentation, grading, and molecular subtype classification, significantly decreasing computational cost and training time while maintaining accuracy [86].

These innovations represent a significant transition from models with a single input and output to comprehensive, end-to-end multimodal systems that are clinically relevant. By capturing the complexity of real-world neuro-oncology decisions, such systems can offer great potential for personalized diagnostics, prognosis estimation, and treatment planning, especially when combined with explainable features and validated through multiple institutions.

In addition to multimodal data integration, predictive modeling of glioma therapy outcomes can be further enhanced by incorporating biomechanical and oncophysics-based models. While AI-driven radiomics and DL excel at identifying patterns and classifying tumors, tumor growth dynamics, tissue mechanics, and microenvironment interactions captured by biophysical models provide mechanistic insight. These biomechanical models have evolved in recent years due to the rapid growth of computational technologies and tools. Such approaches build on advances in cellular and tissue-level modeling, where continuous, discrete, and hybrid biophysical models have been used to simulate cell behavior and interactions, providing a framework for integrating AI-driven imaging features with mechanistic predictions [87]. Integrating these models with imaging and genomic features offers a promising avenue for more accurate treatment response and disease progression prediction, complementing the capabilities of purely AI-based approaches.

4.7. Clinical Translation and Real-World Application

While deep learning and radiomics models for glioma diagnosis show promise in retrospective studies, their clinical adoption remains limited. Many developed with curated datasets and consistent protocols are rarely used in practice. Moving from research to real-world application requires addressing workflow integration, model interpretability, regulatory approval, and validation. A significant challenge is the lack of prospective validation; few models have been tested in real settings or shown to impact decision-making or patient outcomes. For instance, a CNN model predicting MGMT methylation lost accuracy outside controlled environments [81]. Federated learning frameworks can overcome the lack of validation and testing by integrating AI software into PACS and model evaluation on tumor boards to demonstrate clinical impact.

Variability in imaging protocols across institutions further hampers implementation, as shown by reduced performance when combining data from multiple hospitals [88], a problem known as domain shift. Incorporating AI into radiology workflows, like PACS and multidisciplinary discussions, is essential for usability and trust. Models must provide transparent, interpretable predictions facilitating team communication [89]. Trust is crucial, mainly since black-box models often are not used if they lack explanations or clinical context [90]. Another practical limitation lies in cost and access. Institutions may face substantial licensing fees, infrastructure demands (e.g., GPU servers, cloud storage), and personnel training costs as these tools evolve into commercial products. Resource-limited settings or smaller centers may not be equipped to implement or maintain such AI systems, potentially widening disparities in care. Furthermore, while freely available, open-source tools often require technical expertise for customization and deployment, another barrier to real-world adoption.

High implementation costs can be reduced through cloud-based deployment, open-source frameworks, and academic–industry partnerships, reducing infrastructure burdens and widening accessibility [91]. Regulatory hurdles, including compliance with HIPAA or GDPR, also limit AI adoption, with few systems receiving FDA clearance or proven benefits in neuro-oncology [64]. Overcoming these barriers requires collaboration among data scientists, radiologists, and regulators to develop trustworthy AI tools. Interpretability is key; models like CNNs often produce accurate but opaque results, raising safety concerns. Explainable Artificial Intelligence techniques, such as Grad-CAM or SHAP, help visualize decision influences, increasing clinician trust [92]. Transparency, auditability, and human-AI collaboration are vital for acceptance [93]. Ethical issues, data security, and accountability notably influence clinicians' perceptions, with concerns about regulation, responsibility, and bias [94]. Trust in physicians and transparency are vital for safe AI use, particularly in critical decisions. Multidisciplinary teams rely on interpretability to communicate findings effectively. Ethical and legal issues, including liability for AI errors and data privacy laws, complicate deployment [95].

To address these challenges, co-developing AI with clinicians and ethicists ensures technical reliability and ethical alignment. Without interpretability and legal clarity, AI use in glioma care remains cautious. Transitioning AI from research to clinic requires prospective validation, robust external testing, and regulatory approval based on accuracy, safety, and transparency [96,97]. Seamless integration into existing workflows, with user-friendly interfaces, is also essential. Radiologists and oncologists will be crucial for the successful implementation.

4.8. Future Directions

The upcoming advances in glioma AI focus on developing models that are more scalable, interpretable, and capable of collaboration across different institutions. One promising

approach is federated learning, which allows decentralized model training while maintaining patient privacy, significantly increasing training datasets, particularly for rare subtypes and pediatric tumors.

Equally transformative is the rise of multimodal AI models that combine MRI features with genomics, pathology, clinical history, and treatment data to produce detailed personalized diagnostic and prognostic insights. Recent developments include fusion models that merge imaging with methylation and gene expression data, enabling more precise patient stratification and treatment guidance [98,99].

Another key development concerns the integration of explainability directly into AI architectures, shifting from post hoc methods to transparent-by-design systems. These models are being developed alongside clinical end users to ensure they are easy to interpret and to foster trust from the outset [92].

These efforts build upon foundational work in knowledge-based deep learning, where integrating domain-specific clinical insights into model structures enhances performance and helps prevent overfitting on small datasets [100].

Finally, experiments with federated learning in large cohorts demonstrate that cross-site models can perform as well as those trained on centrally pooled data, challenging traditional beliefs about data centralization [101].

As AI advances, its effectiveness will rely on technical precision, fairness, transparency, and collaborative development to promote an equitable global influence in neuro-oncology.

Only a few AI models in glioma management have been prospectively validated, which is essential for real-world use. A significant multicenter study of GBM patients utilized MRI-based deep learning to forecast survival after radiotherapy, achieving an AUC of 0.93 in an external validation cohort, highlighting the importance of robust, forward-looking trials [55]. Nonetheless, a comprehensive meta-analysis indicated that most models still lack such validation, which limits their clinical applicability [83]. Interestingly, to address this gap, several trials conducted between 2024 and 2025 are starting to examine AI in clinical neuro-oncology to bridge this gap. For instance, the PEAR-GLIO trial (NCT06038760) is prospectively testing AI tools in adult gliomas, while the NCT06036381 study is gathering a large multimodal imaging cohort (MRI, CT, PET) for radiomics and deep learning research. Despite being at various planning and implementation stages, these trials demonstrate ongoing efforts to advance from retrospective studies to clinically relevant validation [102,103].

Regulators like the FDA now mandate that AI systems show reliable performance in different environments, provide clear explanations, and demonstrate real-world impact as outlined in the SaMD Action Plan. Successfully incorporating AI tools into clinical workflows, such as through PACS or EHR systems, depends on their ability to deliver transparent, contextualized results that support doctors in making better decisions.

5. Limitations of the Study

Although this review emphasizes recent progress in using AI for glioma imaging, certain limitations must be acknowledged. Many referenced studies involve small sample sizes, retrospective data, or are from single centers, which restricts their broader applicability. Hence, the generalizability of the results must be considered with caution. This highlights the need for larger, prospective, and multicenter studies to ensure that findings are robust and representative of diverse clinical settings.

It is also important to note that the lack of prospective studies raises concerns about the integration and performance of these AI tools in real-world clinical workflows. Most existing studies rely on retrospective datasets, often failing to capture routine practice's variability, image quality issues, and time constraints.

The absence of standardized imaging protocols and multicenter validation further complicates generalization. Variability in scanner hardware, acquisition parameters, and image preprocessing workflows can lead to model performance inconsistencies, hindering direct comparability and reproducibility across studies. Without harmonized protocols and independent validation cohorts, there is a significant risk that models trained in one setting may fail to replicate their accuracy when applied to broader clinical populations.

Finally, a further limitation of this study is the possibility of selection bias in the studies included. Despite efforts to capture the most relevant and recent literature, some potentially valuable studies may have been excluded due to publication language barriers or database restrictions.

6. Conclusions

Artificial intelligence has greatly improved glioma imaging, allowing for more accurate tumor classification, molecular analysis, and treatment strategies. Techniques like radiomics and deep learning demonstrate promising capabilities in predicting genetic markers without invasive procedures, assessing risk levels, and supporting clinical decision-making. However, challenges such as limited interpretability, lack of prospective validation, and difficulties integrating into clinical workflows still hinder widespread adoption. Future progress will depend on transparent model design, regulatory alignment, and collaborative development across institutions. As innovation continues and practical validation advances, AI can significantly transform how personalized and efficient care is provided to glioma patients.

Author Contributions: Conceptualization, R.C.C. and M.F.G.; methodology, R.C.C.; software, R.C.C.; validation, R.C.C., M.F.G. and R.P.; formal analysis, R.C.C.; investigation, R.C.C., R.P. and V.P.; resources, M.F.G.; data curation, R.C.C.; writing—original draft preparation, R.C.C., L.R., R.P., P.S.P., G.V. and V.P.; writing—review and editing, R.C.C., P.S.P., S.G.P. and E.E.S.; visualization, R.C.C.; supervision, M.F.G.; project administration, R.C.C. and M.F.G. All authors have read and agreed to the published version of the manuscript.

Funding: This research received no external funding.

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: No new data were generated.

Acknowledgments: The authors have reviewed and edited the output and take full responsibility for the content of this publication.

Conflicts of Interest: The authors declare no conflicts of interest.

Abbreviations

AI	Artificial Intelligence
MRI	Magnetic Resonance Imaging
PET	Positron Emission Tomography
CNN	Convolutional Neural Network
GAN	Generative Adversarial Network
IDH	Isocitrate Dehydrogenase
MGMT	O6-methylguanine-DNA methyltransferase
1p/19q	1p/19q Codeletion
WHO	World Health Organization
AUC	Area Under the Curve

FLAIR	Fluid Attenuated Inversion Recovery
DTI	Diffusion Tensor Imaging
DWI	Diffusion Weighted Imaging
PWI	Perfusion Weighted Imaging
ML	Machine Learning
SVM	Support Vector Machine
ADC	Apparent Diffusion Coefficient
CT	Computed Tomography
TBR	Tumor-to-Background Ratio
SHAP	SHapley Additive exPlanations
Grad-CAM	Gradient-weighted Class Activation Mapping
XAI	Explainable Artificial Intelligence
EHR	Electronic Health Record
PACS	Picture Archiving and Communication System
HIPAA	Health Insurance Portability and Accountability Act
GDPR	General Data Protection Regulation
SaMD	Software as a Medical Device
MTV	Metabolic Tumor Volume
ROI	Region of Interest
TPR	True Positive Rate
FET	Fluoroethyltyrosine
FDG	Fluorodeoxyglucose
MET	Methionine
CCL2	C-C Motif Chemokine Ligand 2
CDKN2A/B	Cyclin Dependent Kinase Inhibitor 2A and 2B
ATRX	Alpha Thalassemia/Mental Retardation Syndrome X-Linked
TERT	Telomerase Reverse Transcriptase

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