

The role of radiomics and deep learning in glioma MRI: Advances, challenges, and LMIC-tailored opportunities for precision medicine

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Abstract

Glioma is the most common primary malignant central nervous system tumour in adults, with limited access to advanced molecular diagnostics in low- and middle-income countries, like Pakistan. Radiomics and deep learning offer cost-effective, non-invasive alternatives for glioma magnetic resonance imaging characterisation, but their clinical translation remains unoptimised for resource-constrained settings. A structured literature search from January 2018 to October 2025 was conducted across PubMed, Embase, Web of Science, Cochrane Library and Chinese biomedical databases with focus on radiomics and deep learning for glioma magnetic resonance imaging endpoints. Of the 2,132 initial records, 41(1.92%) studies were analysed. The narrative review synthesised advances in radiomics and deep learning for glioma magnetic resonance imaging segmentation, like convolutional neural networks, generative adversarial networks and transformer architectures, preoperative grading (area under the curve: 0.85-0.90), molecular typing, survival stratification and post-radiotherapy response differentiation. Key limitations included small cohorts, lack of external validation, and non-standardised imaging protocols. Radiomics and deep learning enhance glioma precision medicine, but face barriers in terms of standardisation and workflow integration. Prioritising lightweight models and multicentre validation from low- and middle-income countries will accelerate adoption in resource-limited settings, like Pakistan.

Keywords: Glioma, Magnetic resonance imaging, Radiomics, Deep learning, Low- and middle-income countries.

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Introduction

Magnetic resonance imaging (MRI) is a non-invasive tool for glioma diagnosis and management, as it reflects tumour histology, functional metabolism and dynamic changes.¹ In low- and middle-income countries (LMIC), like Pakistan, only 15% of neuro-oncology centres have access to next-generation sequencing.² Radiomics, a quantitative imaging analysis method driven by artificial intelligence (AI), mines image features to construct clinically meaningful tumour models and improve diagnostic accuracy. Deep learning (DL), a neural network-based machine learning paradigm, autonomously extracts high-dimensional features from MRI data with superior performance compared to traditional methods.³

The current narrative review was planned to summarise recent advances in radiomics and DL for glioma MRI segmentation, preoperative grading, molecular typing, overall survival (OS) prediction, and post-radiotherapy treatment response evaluation — framing these tools as complements for neuroradiologists — and to highlight LMIC-adapted challenges and opportunities for these technologies in glioma precision medicine.

Methods, Results and Discussion

The current narrative review comprised a structured literature search to identify studies on radiomics and DL applications in glioma MRI. The search covered PubMed, Embase, Web of Science Core Collection, and Cochrane Library for articles published between January 2018 and October 2025, with supplementary searches of Chinese core databases [China National Knowledge Infrastructure (CNKI), Wanfang) for region-specific research for which English translations were obtained.

Database-adapted key word combinations used included ("glioma" OR "brain tumour") AND ("MRI" OR "magnetic resonance imaging") AND ("radiomics" OR "deep learning" OR "convolutional neural network" OR "transformer" OR "radiogenomics").

Studies were included if they focussed on radiomics/DL-based glioma MRI analysis; reported original research, systematic reviews, or meta-analyses with clear methodology; addressed key clinical endpoints (segmentation accuracy, grading, molecular marker

prediction, survival stratification, or treatment response); and provided sufficient validity-assessable data.

Studies were excluded if they were non-empirical (conference abstracts, case reports, editorials); focussed on non-MRI modalities; had duplicated data; or lacked core outcome metrics (area under the curve [AUC], accuracy, sensitivity/specificity).

Two reviewers with neuroimaging and AI-in-medicine expertise independently screened titles, abstracts and full texts, with discrepancies resolved by a third senior reviewer via consensus. A total of 2,132 records were identified, and 41 (1.92%) studies met the inclusion criteria.

The included studies were appraised for methodological quality using the Joanna Briggs Institute (JBI) critical appraisal tool for diagnostic test accuracy studies, with focus on cohort representativeness, validation rigour, and reporting of imaging protocols.⁴

Accurate, automated glioma segmentation from MRI scans underpins quantitative analysis and surgical planning, with radiomics and DL models — including convolutional neural networks (CNN), generative adversarial networks (GAN) and transformer-based architectures — delivering higher accuracy and robustness than conventional methods.

CNN-based segmentation methods

CNNs excel at high-dimensional data processing and feature extraction for glioma segmentation. Zhou et al. proposed a three-dimensional (3D) cavity convolution CNN to enhance differentiation of tumours of varying sizes,⁵ while Noori et al. improved 2D U-Net performance via attention mechanisms and multi-view fusion.⁶ This technical optimisation addresses the clinical challenge of blurred tumour-oedema boundaries in low-grade glioma MRI, enabling more precise delineation of tumour margins to support intraoperative navigation. Tian et al. integrated axial attention into CNNs and addressed data imbalance with deep supervision and hybrid loss models, boosting segmentation precision for multi-modal MR glioma images.⁷

GAN-based segmentation methods

GANs are valued for their generalisability and multimodal synthesis capacity in glioma segmentation. Khanh's 3D-GAN combined multi-scale architectures with 3D visualisation tools to improve accuracy.⁸ Cui's GAN-segNet incorporated autoencoders and focal loss-based functions for precise glioma segmentation.⁹ However, GANs face limitations, like training instability and poor convergence.¹⁰

Transformer-based segmentation methods

Transformers, originally developed for natural language processing, have gained traction in MRI segmentation due to strong contextual modelling capabilities.¹¹ This capability is particularly valuable for clinical glioma imaging, where it can capture the spatial correlation between the primary tumour and peritumoural infiltration zones that conventional CNNs often overlook. Jiang et al.'s Swin Brain Tumour Segmentation (BTS) used a 3D Swin Transformer encoder and enhanced feature modules for robust glioma segmentation.¹² The model's strong global contextual modelling ability solves the clinical problem of segmenting infiltrative gliomas with scattered lesions, reducing under-segmentation of micro-invasive tumour foci that are critical for surgical resection planning. Liang's BTSwin-UNet, a 3D U-shaped Swin Transformer network, leveraged self-supervised learning to mitigate data scarcity.¹³ Yang et al.'s D2-Net captured modality-region correlations to segment gliomas with missing MR modalities.¹⁴

Current challenges and future opportunities

GANs offer low training data dependence and easy neural network integration, but suffer from training difficulty, overfitting, and high computational costs. Transformers outperform CNNs and GANs in global information modelling and parallel computing, making them ideal for large-scale brain tumour data processing. Future research shall prioritise Transformer integration and lightweight network construction to advance clinical translation of high-precision glioma segmentation.¹³ Additionally, interobserver variability in tumour segmentation represents the largest real-world barrier to radiomics' clinical adoption, as inconsistent segmentation directly compromises feature reliability and model reproducibility.

Prediction of preoperative grading

Conventional MR has limited precision for glioma grading, whereas advanced MR sequences [Dynamic Susceptibility Contrast (DSC) perfusion, Diffusion Weighted Imaging (DWI), Amide Proton Transfer (APT), Magnetic Resonance Spectroscopy (MRS)] achieve moderate-to-high accuracy for subtype differentiation. A Multiecho DWI and its Apparent Diffusion Coefficient (ADC) maps assess tumour water molecule diffusion restriction — not just cellular density. This imaging phenotype is jointly regulated by factors like cellular density, extracellular matrix fibrosis, intratumoural oedema, membrane integrity, and cellular arrangement, underpinning its value for glioma subtype differentiation. While DSC perfusion is a mainstream reference for assessing tumour vascularity, it is susceptible to artifacts from blood-brain barrier disruption and contrast leakage in high-grade lesions. MRS, which supplies

metabolic data for glioma grading, has key pitfalls: spectral peak overlap, high sensitivity to magnetic field inhomogeneity and head motion, and low spatial resolution that impairs metabolite quantification in small/ill-defined tumours. Preoperative glioma grading [per 2021 World Health Organization (WHO) Central Nervous System (CNS) tumour classification, grades 1-4] is critical for surgical and treatment planning, and radiomics/DL enables non-invasive grading prediction.¹⁵ As outlined in Johnson et al.'s radiological interpretation guide for the 2021 WHO CNS tumour classification, molecular biomarkers have become core determinants of glioma grading, and radiomics/DL models must be calibrated against these molecular-radiological correlation standards to ensure their grading predictions align with clinical diagnostic gold standards.¹⁶

Wang et al.'s multi-sequence radiomics nomogram yielded consistency indices of 0.97 (training) and 0.96 (validation) for grading 85 glioma patients.¹⁷ Gutta et al.'s CNN model, trained on 237 patients' MR data, reached 0.87 grading accuracy, outperforming imaging-histology feature-only models.¹⁸ Lin et al.'s combined model (age + multiparametric MR radiomics) achieved an AUC of 0.97, 94% sensitivity and 91% specificity for grading.¹⁹ Haubold et al.'s multiparametric 18F-Positron Emission Tomography (PET)-MRI model attained an 85.2% AUC for distinguishing low-grade and high-grade gliomas.²⁰

Current challenges and future opportunities

Multi-sequence MR data contains untapped information on glioma genetics and invasiveness that radiomics and DL can leverage to refine grading models. However, inconsistent data quality, small sample sizes, and subjective annotation hinder research reproducibility. Future work requires standardised imaging/annotation protocols and model integration into clinical workflows.²¹

Prediction of molecular typing

Preoperative non-invasive molecular typing guides personalise glioma treatment, with radiomics and DL enabling variable performance in non-invasive detection of key molecular markers, and notable disparities in predictive reliability across molecular subtypes. Radiogenomics shows potential for non-invasive glioma molecular subtype prediction, but most radiogenomic models lack robust external validation and cross-centre generalisability, limiting their clinical translation.²²⁻²⁴

Isocitrate Dehydrogenase Mutation

Isocitrate dehydrogenase (IDH) mutation status correlates with improved survival and temozolomide (TMZ) sensitivity in gliomas.²⁵ Park et al.'s Random Forest model, trained on 168 low-grade glioma patients, achieved an AUC

of 0.90 for IDH prediction by combining MR and histology features (vs. 0.83 for conventional imaging alone).²² Choi et al.'s fully automated model yielded accuracies of 0.94 (internal test) and 0.79 (external validation) for IDH status, with corresponding AUCs of 0.96 and 0.86.²³ Lu et al.'s multicentre radiomics nomogram reached 86.96% accuracy and 0.891 AUC for IDH prediction in test cohorts.²⁵ while Pasquini et al.'s CNN model achieved 83% accuracy for IDH typing via relative cerebral blood volume mapping.²⁶ Representative studies in glioma radiomics and deep learning are summarised in Table-1.

O6-methylguanine-deoxyribonucleic acid (DNA) Methyltransferase (MGMT) Promoter Methylation

O6-methylguanine-deoxyribonucleic acid (DNA) methyltransferase (MGMT), which primarily localises to the cell nucleus (with only minor cytoplasmic expression), has its promoter methylation status closely associated with enhanced glioma chemosensitivity to TMZ, but reliable non-invasive prediction of MGMT promoter methylation via radiomics or DL remains a clinical challenge, as most models lack robust external validation and cross-centre generalisability. Jiang et al's Least Absolute Shrinkage and Selection Operator (LASSO)-selected fusion radiomics model (1,702 features from 122 low-grade

Table-1: Summary of core studies in glioma radiomics and deep learning (DL) research.

Study (Year)	Design	Cohort Size	Validation Status	Main Findings	Limitations
Choi et al. (2021) ²³	Retrospective	1,166	Internal + 2 external	DL predicts IDH mutation (AUC = 0.96, 0.86)	No multi centre imaging standardisation
Lin et al. (2022) ¹⁹	Retrospective	320	Internal	Radiomics predicts grading (AUC = 0.97)	Lack of external validation
Jiang et al. (2019) ²⁷	Retrospective	122	Internal + Validation	Fusion radiomics predicts MGMT methylation (AUC=0.97, 0.90)	Small cohort size
Huo et al. (2023) ²⁹	Retrospective	109	Internal + Validation	Multimodal MRI predicts TERT mutation (AUC=0.897, 0.882)	Focus on IDH wildtype LGG only
Zhang et al. (2023) ³⁰	Retrospective	Unknown	Internal	Multimodal MR radiomics differentiates RN from progression (AUC=0.96)	No external validation
Luo et al. (2021) ¹⁶	Retrospective	655	Cross validation	Image signature based radiomics predicts grading (accuracy = 89.8%)	No external validation
Park et al. (2020) ²²	Retrospective	168	Internal	DTI radiomics improves IDH subtyping (AUC=0.90)	Limited to lower grade gliomas
Wu et al. (2024) ³	Retrospective	Unknown	Internal	Multimodal fusion radiomics guides radiochemotherapy (AUC = 0.950)	Lack of external validation

glioma patients) attained AUCs of 0.97 (training) and 0.90 (validation) for MGMT prediction.²⁷ Saxena's ResNet model achieved an AUC of 0.753 for MGMT typing,²⁶ and Pease et al.'s radiomics model reached an AUC of 0.83 for this task.²⁸

Telomerase Reverse Transcriptase (TERT) Promoter Mutation

Telomerase reverse transcriptase (TERT) mutations are common in adult diffuse gliomas, and inform treatment stratification. Huo et al.'s combined radiomics-clinical model (age, tumour border, midline crossing) achieved AUCs of 0.897 (training) and 0.882 (validation) for TERT prediction in IDH-wildtype low-grade gliomas.²⁹

Radiomics and DL possess the capacity to extract more refined and highly representative imaging features. Multimodal data fusion (imaging, clinical, genetic) is a key research focus for molecular typing, as it enhances model capacity to capture tumour biological properties. Future work shall prioritise lightweight architectures for real-time, bedside molecular diagnosis.

Prediction of OS

Radiomics nomogram (multiparametric MR+clinical factors) achieved a consistency index of 0.97 in both training and validation cohorts for survival assessment. Radiomics and DL reveal intratumour heterogeneity to preoperatively predict glioma survival and stratify risk.

Radiomics and DL can forecast the survival of glioma patients prior to surgical intervention and to evaluate risk factors in a stratified manner. Small sample sizes and inconsistent treatment plans limit study reliability. Integrating metabolomics and standardised treatment data into prospective studies will improve the robustness of survival prediction models.

Discrimination between radiation necrosis and true tumour progression after radiotherapy

Radiation necrosis (RN) requires no intervention, while true tumour progression demands urgent treatment adjustment, and conventional MR imaging cannot reliably distinguish these outcomes. Zhang et al.'s multimodal MR radiomics model achieved an AUC of 0.99 for classifying RN and recurrence.³⁰ Differentiating pseudo progression from true tumour progression is widely regarded by neuroradiologists as a top challenge in post-radiotherapy glioma management: the two entities have overlapping imaging phenotypes and require integration of dynamic clinical follow-up, molecular typing and treatment history for definitive diagnosis. While AI models show promise, they still depend on high-quality, annotated multicentre datasets to translate experimental performance into real-

world clinical utility.

Aligned with the Response Assessment in Neuro-Oncology (RANO) Working Group's updated response assessment criteria for high-grade gliomas, the core clinical goal of distinguishing radiation necrosis from true tumour progression is to standardise treatment response evaluation and avoid unnecessary interventions.³¹ The utilisation of radiomics and DL enables a more precise evaluation of the effects of radiotherapy. However, inconsistent imaging equipment/parameters and limited annotated post-radiotherapy data reduce model generalisability. Multicentre cohort studies are needed to validate and refine these diagnostic tools.

Sensitivity to immunotherapy and chemotherapy

Radiomics and DL can provide a relatively accurate assessment of glioma patients' sensitivity to specific chemotherapeutic and targeted drugs, enabling physicians to administer personalised, precise treatments and to optimise clinical management. Li et al.'s radiomics model (3,668 MR features) identified recurrent glioma patients responsive to anlotinib+TMZ, with responders demonstrating superior survival.³² Wei et al.'s multi-sequence radiomics model stratified 105 astrocytoma patients into TMZ high/low-risk groups, guiding personalised chemotherapy.³³

Current Challenges in LMICs and Future Opportunities

Radiomics and DL have transformative potential for glioma precision medicine in LMICs but face core LMIC-adapted challenges:

1. **Standardisation gaps:** LMICs have heterogeneous MRI hardware (1.5T/3T mix) and limited annotation expertise, with ill-defined lesions prone to greater subjective bias. LMIC-tailored standardised imaging/annotation protocols are urgently needed.
2. **Retrospective study limitations:** Most LMIC research uses small, single-centre cohorts with non-uniform treatment plans. Multicentre, prospective LMIC studies with harmonised therapies and integrated genomics data are needed to improve model reliability.
3. **Tumour heterogeneity:** LMIC glioma patients exhibit distinct inter/intra-patient variability due to delayed diagnosis, and dynamic treatment-related changes are under-monitored. Future DL models must adapt to LMIC-specific disease trajectories to reflect real-time tumour status.
4. **Model interpretability:** Poorly interpretable radiomics/DL models hinder adoption by LMIC clinicians with limited AI literacy. Integrating tools into

basic clinical workflows and enhancing localised transparency will boost trust.

5. **Medico-legal risks:** Black-box model gaps in LMIC settings cause untraceable decisions, with scarce legal frameworks for liability disputes in misdiagnosis or inappropriate treatment cases.
6. **Clinical safety risks:** Unstandardised low-field MRI protocols in LMICs yield erroneous results, leading to mismatched therapies that threaten already vulnerable patient outcomes and care safety.

In addition to the above technical hurdles, the clinical translation of radiomics and DL for glioma precision medicine in LMICs is further hampered by critical practical barriers:

1. **Workflow and Information Technology (IT) Integration Barriers:** Most LMIC clinical Picture Archiving and Communication System (PACS)/ Radiology Information Systems (RIS) are outdated and lack native compatibility with radiomics/DL platforms, requiring manual data migration that disrupts overburdened radiologists' time-sensitive workflows and increases data security risks.
2. **Reimbursement And Cost Barriers:** LMICs lack universal healthcare reimbursement codes for AI-aided glioma imaging analysis, and the high cost of High-Performance Computing (HPC) infrastructure and model maintenance makes adoption unfeasible for resource-strapped public institutions.
3. **Clinician Capacity And Trust Barriers:** Limited AI/radiomics training for LMIC practicing neuroradiologists and oncologists, coupled with black box model gaps, reduces willingness to rely on these tools for high-stakes treatment decisions in resource-limited settings.
4. **Data Governance Barriers:** LMICs have fragmented

privacy regulations that restrict cross-centre data sharing for multi-institutional validation, while inconsistent low-field MRI protocols lead to irreproducible model outputs in real-world LMIC care settings. Figure 1 illustrates the short term, mid term, and long term development phases for implementing radiomics and deep learning in low and middle income countries, highlighting key tasks and principal stakeholders for achieving clinical translation. The proposed implementation roadmap is shown in (Figure-1).

Conclusion

Radiomics and DL enable non-invasive visualisation of glioma cellular and molecular features, with robust performance in MR segmentation, preoperative grading, molecular typing, survival prediction and treatment response evaluation — capabilities that are particularly valuable for LMICs with limited access to advanced molecular diagnostics. As LMIC-tailored technical limitations are addressed and tools are integrated into basic clinical workflows, these technologies will drive advances in glioma precision diagnosis and treatment in resource-constrained regions, narrowing the global disparity in glioma patient outcomes.

Abbreviations: APT – Amide Proton Transfer, ADS – Automated Diagnostic System, BTS – Brain Tumor Segmentation, CNKI – China National Knowledge Infrastructure, CNS – Central Nervous System, DSC – Dynamic Susceptibility Contrast, DWI – Diffusion-Weighted Imaging, FET – Fluoroethyl-Tyrosine, HPC – High-Performance Computing, LASSO – Least Absolute Shrinkage and Selection Operator, MRS – Magnetic Resonance Spectroscopy, PACS – Picture Archiving and Communication System, PET – Positron Emission Tomography, RANO – Response Assessment in Neuro-Oncology, RIS – Radiology Information System, WHO – World Health Organization.

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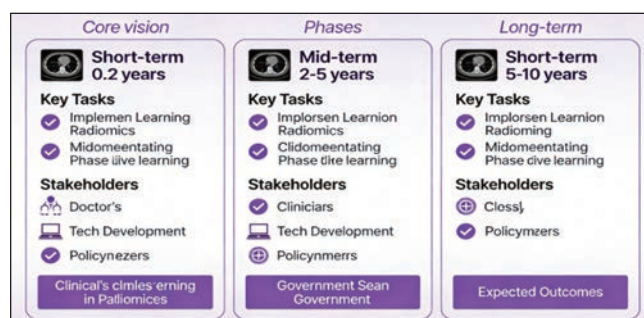


Figure-1: Short-term (0–2 years), mid-term (2–5 years), and long-term (5–10 years) development phases for integrating radiomics and deep learning into clinical workflows in low- and middle-income countries, highlighting key tasks and stakeholder participation across each stage.

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