

Artificial Intelligence for Brain Tumor Classification Using MRI Imaging

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Abstract

One of the most crucial disorders is that of brain tumor. In brain tumors, it is of utmost important to provide diagnosis early and accurately for an effective treatment and to increase the chances of survival. Magnetic Resonance Imaging (MRI) is very often used in brain tumor diagnosis, since it clearly depicts soft tissues in an elevated resolution image. Though manual interpretation is very tedious and is subjective leading to different diagnoses based on the human interpretation of image. This paper review study about the use of Artificial Intelligence (AI), primarily focused on machine learning and deep learning algorithms for classification of brain tumor using MRI imaging. This paper has analyzed most frequently used AI models namely Convolutional Neural Networks (CNNs), Support Vector Machines (SVM), Random Forests, and hybrid deep learning architectures for automated brain tumor detection and classification. Pre-processing techniques such as image normalization,

segmentation, noise reduction and feature extraction that affect the performance of models are also considered. Review has looked upon publicly available datasets, evaluation metrics used and a comparative study which confirms that AI based algorithms are superior to traditional diagnosis methods. Although much advancement has been made, some limitations are still existing such as, lack of annotated data set, model generalization, interpretability problem, clinical integration issues etc. This review has summarized recent work in AI-based classification of brain tumors, so as to

enable radiologists in getting fastest, most efficient and dependable diagnosis.

Introduction

1. Clinical and Epidemiological Imperatives of Brain Tumor Classification

Amongst the vast landscape of neurological diseases currently in modern medicine, intracranial neoplasms are considered one of the most destructive. Intracranial neoplasms are defined as an uncontrolled growth of abnormal cells inside the brain or skull. The epidemiological statistics show that they pose a great public health problem: Intracranial neoplasms are classified as the most frequent cancer found in children and adolescents (Shah, 2024) and approximately 88,000 adults and 5,500 children are diagnosed in the US alone each year. These tumors have one of the highest rates of fatality, the 5-year relative survival rate of a malignant brain or central nervous system tumor is 35.6% in adults (Aleid et al., 2023).

Early and high-accuracy diagnosis of brain tumors is paramount in clinical oncology as it dictates treatment planning and selection, as well as surgical approaches. Until the present, the diagnosis and characterization of brain tumors have primarily relied on histopathological examination of tissue collected from stereotactic biopsies or resections, which is considered the gold standard. Surgical biopsies are minimally invasive and risk hemorrhage, neural deficits, or infection (Afridi et al., 2022, April), and because they take a sample from only one location of the tumor they do not take into account the intratumoral spatial heterogeneity that exists in the high-grade areas, therefore can lead to undergrading or underdiagnosis. Similarly, the manual segmentation and qualitative analysis of brain tumors performed by doctors is time-consuming and it requires many years of experience; it is also associated with significant inter-rater variability and cognitive fatigue (Gull & Akbar, 2021).

Adhesin ALS4112 can mediate strong adhesion to keratinocytes and extracellular matrix components which gives it skin tropism. It can "hide" the beta-glucans from recognition by Dectin-1 because of the thick cell wall of mannans, thus preventing recognition by host's innate defenses (Khazaee et al., 2022). T1-weighted (T1), T2-weighted (T2), Fluid-Attenuated Inversion Recovery (FLAIR) and gadolinium-contrast-enhanced T1-weighted (T1Gd) sequences comprise the standard neuroimaging protocol. T1-weighted sequences serve to visualize anatomy. Their contrast relies on the T1 relaxation times of the hydrogen protons, which can be adjusted by using short repetition times (TR= 400-700ms) and echo times (TE<30ms). In these parameter ranges fat tissues have a short T1 relaxation time, so the contrast in the T1-weighted image is hyperintense, whilst CSF appears dark and gray matter slightly darker than white matter Tandel et al., 2020). T2-weighted images measure the T2 relaxation times and so they are produced using long repetition times (TR>2000ms) and echo times (TE long). In this sequence it is the prolonged transverse relaxation times, characteristic of free water and pathologic fluids that appear hyperintense. CSF and vasogenic edema are hyperintense while white matter is darker than gray matter in the T2-weighted images (Rasheed et al., 2023). In FLAIR sequences an inversion recovery pulse is applied to nullify the signal from CSF, an inversion recovery pulse effectively adds the effect of nullifying the bright CSF signal and the use of a specific delay period followed by a T2-weighted sequence. Peritumoral vasogenic edema, infiltrative tumor margins and subcortical lesions are thus visualized clearly against a dark background Saleh et al., 2020, August). T1Gd images involve the administration of gadolinium based contrast which shortens the T1 relaxation time of nearby protons; and so the highly vascularised tumor margins and the actively enhancing tumor borders are hyperintense while the necrotic, non-enhancing tumors cores remain hypointense Vankdothu & Hameed, 2022).

Table 1. Structural MRI Sequences: Technical Acquisition Parameters, Tissue Signal Intensities, Pathological Representation in Gliomas, and Clinical

Diagnostic Roles.

MR I Sequence	Technical Acquisition Parameters	Healthy Tissue Signal Intensity	Pathological Representation (Glioblastoma / Glioma)	Diagnostic Clinical Role
T1-Weighted (T1)	TR: 400–700 ms TE: less than 30 ms	CSF: Dark Fat: Bright White Matter: Bright-intermediate	Mass effect, displacement of healthy brain structures, ventriculomegaly	Anatomical baseline, localization, assessment of ventricles
T2-Weighted (T2)	TR: greater than 2000 ms TE: Long	CSF: Bright White Matter: Darker than gray matter	Hyperintense edema, infiltrative tumor regions, heterogeneous necrotic core, hypointense flow voids	Delineating internal tumor heterogeneity and peritumoral edema boundaries
Fluid-Attenuated Inversion Recovery (FLAIR)	Inversion pulse with a specific delay followed by T2-weighted readout	CSF: Suppressed (dark) Brain parenchyma: Intermediate	Highly hyperintense infiltrative borders, hypointense necrotic or cystic areas	Delineating non-enhancing infiltrative margins and vasogenic edema

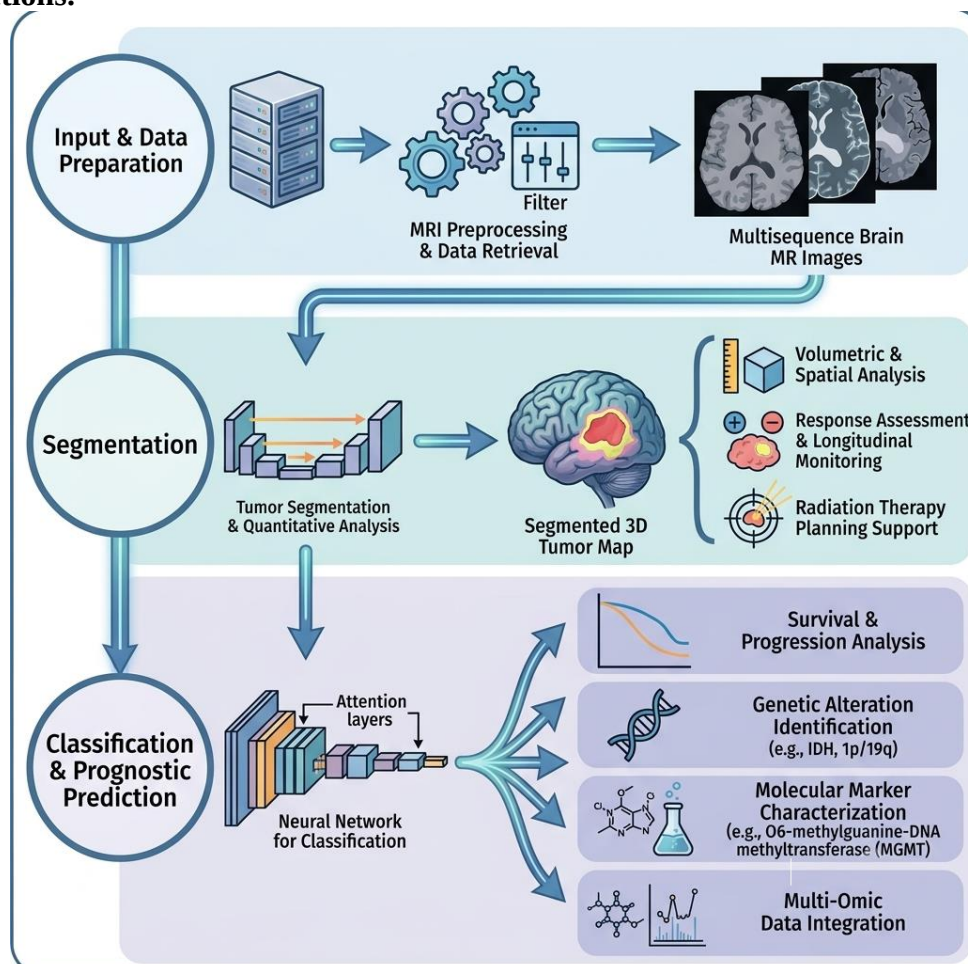
A major shift in the diagnostic landscape has occurred with the release of the fifth edition of the World Health Organization (WHO) Classification of Tumors of the Central Nervous System, which integrates molecular, genetic and pathogenetic markers within the classification schema in addition to histological characteristics (C et al., 2023). Specific mutations and genetic features such as Isocitrate Dehydrogenase (IDH) mutation, MGMT promoter methylation, EGFR amplification and 1p/19q co-deletion now represent a suite of defining markers that guide classification, grade, prognosis and therapeutic sensitivity (Srinivas et al., 2022).

A major shift in the diagnostic landscape has occurred with the release of the fifth edition of the World Health Organization (WHO) Classification of Tumors of the Central Nervous System, which integrates molecular, genetic and pathogenetic markers within the classification schema in addition to histological characteristics (Mehrotra et al., 2020). Specific mutations and genetic features such as IDH mutation, MGMT promoter methylation, EGFR amplification and 1p/19q co-deletion now represent a suite of defining markers that guide classification, grade, prognosis and therapeutic sensitivity (Ismael et al., 2020).

To overcome the diagnostic challenges presented, AI and DL are rapidly advancing to provide sophisticated solutions in the domain of medical image computing. It is now possible to conduct automated tumor segmentation, quantify tumor volumes, and achieve multi-class pathological classification based on non-invasive neuroimaging using modern machine learning algorithms (Kaifi, 2023). AI systems are also improving workflow efficiency through reduced scanning time,

enhanced image reconstruction, noise reduction and super-resolution, automated triage, and automated case prioritization (Wong et al., 2025).

Figure 1. Comprehensive workflow of an AI-driven neuro-oncology computer-aided system, detailing multi-sequence MRI input preparation, U-Net-based tumor segmentation with spatial/radiotherapy planning analysis, and deep neural network classification integrated with prognostic multi-omic biomarker predictions.



2. Multi-Sequence MRI Physics and Pathological Representation

Magnetic Resonance Imaging (MRI) is the preferred non-invasive imaging modality for neuro-oncology due to its soft-tissue contrast and ability to acquire multi-planar views. In clinical practice, evaluating intracranial tumors requires combining multiple complementary MRI sequences to capture different anatomical, physiological, and metabolic characteristics of the tissue (Khan et al., 2020).

2.1 Structural MRI Sequences and Contrast Mechanisms

Standard neuroimaging sequence for structure: T1-weighted (T1), T2-weighted (T2), Fluid Attenuation Inversion Recovery (FLAIR), and Gadolinium-enhanced T1-weighted sequence (T1Gd). The T1-weighted sequence shows structural outline of tissues. The image contrast is related to longitudinal relaxation time (T1) of protons of hydrogen, achieved by using short repetition time (TR of 400-700 ms) and short echo time (TE of less than 30 ms). In such parameters, short T1 relaxation time (fat) would show intense hyperintensity signal, cerebrospinal fluid (CSF) show dark, and gray matter is dark than white matter (Bada & Barjaktarovi, 2020).

The T2-weighted image depends on the transverse relaxation time (T2) of proton and usually achieved by long TR (above 2000 ms) and long TE to minimize T1 effects. Water (as in free water and pathological fluid), due to its long T2, would show high hyperintensity, and white matter appears dark than gray matter (Jiang et al., 2023).

FLAIR is special type of inversion recovery sequence that nullifies the

hyperintensity of the free water. It used inversion recovery pulse to suppress the signal of CSF, which follows a particular delay time before the acquisition of the T2 sequence. As a result, the peritumoral vasogenic edema, infiltrative margin of tumor, and the abnormality at subcortex are clearly visualized on the dark background (Aamir et al., 2022).

T1Gd introduces gadolinium-based contrast medium that highlights regions with enhanced vascularity and blood-brain barrier (BBB) breakdown. Gadolinium reduces the T1 relaxation time of the protons around, thereby demonstrating highly vascularized and active margin of the tumor as hyperintense signal while those are necrotic tumor core is hypointense (Kuraparthi et al., 2021).

2.2 Findings of Glioblastoma (GBM) on pathological scan

The utility of multiple sequence MRI in the context of high-grade aggressive tumor like GBM is well-established. On T2 sequences, hyperintense area represents vasogenic edema, infiltration of tumor cells and necrotic tumor components while heterogeneously hyperintense area is seen as central necrotic core with mixed fluid contents (Sharma et al., 2023). Another feature of T2 sequences are the flow voids, represented by dark, hypointense tubular or serpiginous structure which indicates the highly active blood flow within patent abnormal tumor vessel where moving proton will flow outside of the slice during excitation and thus losing signal (Kumar et al., 2023).

On FLAIR sequence, suppressing CSF signal helps to differentiate edema and infiltrative pattern much more clearly than on T2 image. Necrotic or cystic area of tumor usually show hypointensity on FLAIR, and are often characterized by irregularity hyperintense border that represents active infiltration (Solanki et al., 2023).

2.3 Advanced physiological neuroimaging

Advanced sequences in MRI provided the physiological and functional information that would complement structural scan. Diffusion-Weighted Imaging (DWI) and Apparent Diffusion Coefficient (ADC) map reflect the restriction to the Brownian motion of water, which reflects the cell density. Tumor with high cell density restricts water diffusion, demonstrating increased hyperintensity on DWI and hypointensity on ADC map (Huang et al., 2022).

Perfusion-Weighted Imaging (PWI), especially Dynamic Susceptibility Contrast Perfusion-Weighted Imaging (DSC-PWI) which reflect the microvascular hemodynamics and regional cerebral blood volume (rCBV), is able to distinguish high grade from low grade tumor and differentiate tumor progression from treatment induced radiation necrosis (Mehnatkesh et al., 2023). Magnetic Resonance Spectroscopy (MRS) measure tissue metabolism, by measuring concentration of Choline (reflecting cell membrane turnover) and N-acetylaspartate (reflecting neuronal integrity). Magnetic Resonance Imaging (MRI) White Matter tracts (using Diffusion Tensor Imaging DTI) and functional area (fMRI) helps in the planning of pre-surgery procedure, mapping motor area, language area etc relative to tumor border (Arunkumar et al., 2020).

Table 2: Multi-Sequence MRI Contrast Mechanisms, Pathological Representation, and Clinical Applications

MRI Sequence	Technical Acquisition Parameters	Healthy Tissue Signal Intensity	Pathological Representation (Glioblastoma / Glioma)	Diagnostic Clinical Role
T1-Weighted (T1)	TR: 400–700 ms TE:	CSF : Dark Fat:	Mass effect, displacement of healthy brain structures,	Anatomic baseline, localization, assessing ventricles

	<30 ms	Bright White Matter: Bright-Intermediate	ventriculomegaly	
T2-Weighted (T2)	TR: >2000 ms TE: Long	CSF : Bright White Matter: Darker than gray matter	Hyperintense edema, infiltrative tumor, heterogeneous necrotic core, hypointense flow voids	Delineating internal tumor heterogeneity and peritumoral edema boundaries
Fluid-Attenuated Inversion Recovery (FLAIR)	Inversion pulse with specific delay followed by T2 readout	CSF : Suppressed (Dark) Brain Parenchyma: Intermediate	Highly hyperintense infiltrative borders, hypointense necrotic/cystic areas	Delineating non-enhancing infiltrative margins and vasogenic edema
Gadolinium-Enhanced T1 (T1Gd)	Post-contrast administration of Gadolinium agent	Blood Vessels: Bright Healthy Parenchyma: Dark	Hyperintense enhancing margins, hypointense central necrosis	Visualizing blood-brain barrier disruption and active neoangiogenesis
Diffusion-Weighted Imaging (DWI / ADC)	Motion-sensitizing gradient pulses (b-values)	Normal CSF: Free diffusion (Dark on DWI, Bright on ADC)	Hypercellular tumor regions: Restricted diffusion (Bright on DWI, Dark on ADC)	Grading tumors, differentiating cellular tumors from abscesses/cystic lesions
Perfusion-Weighted Imaging (PWI)	Dynamic susceptibility contrast tracking	Normal Perfused Brain: Stable cerebral blood volume	Neovascularization zones: Elevated relative cerebral blood volume (rCBV)	Identifying high-grade tumor focus, guiding biopsies, post-treatment tracking

3. Classical Machine Learning and Convolutional Neural Networks

Clinical implementation of computer aided diagnosis has progressed from classical ML classifiers to modern DL models (Jena et al. 2022).

3.1 Classical ML Classifiers

Prior to DL techniques, automated brain tumor classification was achieved through traditional ML models such as KNN, SVM, BPNN, and RF. The method typically followed a pipeline of image preprocessing, segmentation, extraction of handcrafted features (such as features related to shape, intensity, and texture), and finally classification (Nassar et al. 2024).

Classical classifiers, however, come with limitations. For instance, when evaluating two methods using a multivariate estimation model and a random forest classifier, classification accuracies for non-tumor classification were achieved at 74% and 90% respectively, however neither of them could effectively determine multi-class tumor grade and segmentation due to the high variation in tumor shape, size and locations (Jia & Chen 2020). Manually engineered features rarely capture the highly non-linear interactions of heterogeneous tumor boundaries, which would cause such systems to be sensitive to scanner variations.

3.2 Deep Convolutional Neural Networks and Transfer Learning

Classical classifiers limitations then made CNNs the obvious choice of DL architecture in brain tumor classification as CNNs can automatically learn a hierarchical representation of features directly from raw multi-sequence MR images. To tackle the limitation of data availability, transfer learning using a pre-trained models on large natural image databases (ImageNet) which is later fine-tuned on the medical images dataset.

In a specific work, a custom DL architecture was compared with a pre-trained ResNet18 model to perform four classes (glioma, meningioma, pituitary tumors and healthy brain) on T1-weighted contrast-enhanced MRI. The overall accuracy achieved with the pre-trained ResNet18 was 99.7% with a precision of 99.5% and an F1-score of 99.6%, which outperforms the baseline custom CNN model. The effectiveness of transfer learning in the medical field is thus confirmed (Alshuhail et al. 2024).

Likewise, another system using a pre-trained VGG16 base model had obtained a 99.24% classification accuracy for four classes. After fine-tuning on 17,136 medical images that was largely augmented, this system was put online in an HTML web application using Dash components for medical practitioners to upload slices and receive classification (Asiri et al. 2023). The YOLOv7 object detection algorithm, adapted from original CNN model with modified hyper-parameters can locate tumors with bounding boxes on preprocessed image datasets. By resizing the image size by aspect ratio normalization, this approach effectively helps in locating tumors, and accurately segmenting tumors with consistent boundary (Maqsood et al. 2022).

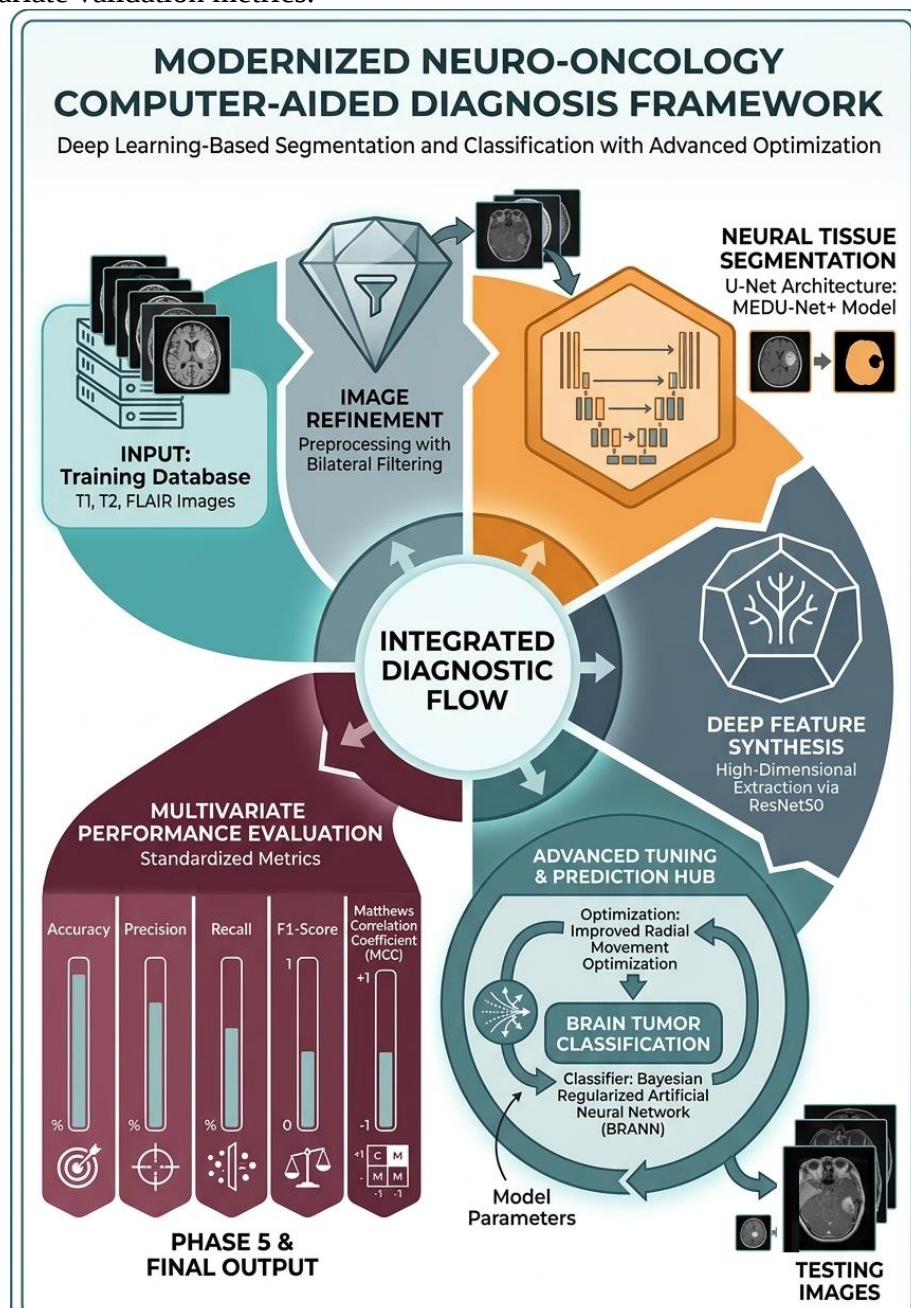
3.3 Specialized Residual and Region-based Architectures

Due to highly heterogeneous and complex characteristics of brain tumors, several specialized CNN models have been developed. One such specialized architecture called Res-BRNet is a deep residual and region-based CNN architecture that classifies brain tumors on MRIs (Asiri et al. 2024).

In this architecture, combined regional and boundary-based operations are designed through modifications of spatial and residual blocks. The spatial blocks extract features based on the information on homogeneity, heterogeneity and boundary. While the residual blocks capture local and global texture variations. Isolate boundary-based operation leads to the highest accuracy 98.22%, sensitivity 98.11% and F1-score 98.41%, outperforming conventional CNN models (Guan et al. 2021).

Figure 2. Architecture of the modernized computer-aided diagnosis (CAD) framework, highlighting bilateral filter preprocessing, MEDU-Net+ semantic segmentation, ResNetSO deep feature synthesis, and Radial Movement Optimization-tuned Bayesian Regularized Artificial Neural Networks (BRANN) alongside standard

multivariate validation metrics.



4. Vision Transformers, Swin Paradigms, and Hybrid Architectures

Localizing detail: CNNs capture local details well, but their local receptive fields hinder them from modeling long-range spatial dependency and global context throughout the volume. This can be a bottleneck in segmentation or classification of large, irregularly shaped, or multi-focal brain lesions (Veeramuthu et al., 2022).

4.1 Vision Transformers and Swin Transformers for medical imaging

To compensate for the deficiencies of CNNs by capturing global context directly, vision Transformers (ViTs) use self-attention mechanisms to directly model long-range spatial dependencies throughout the volume. But with quadratic complexity, ViTs have computationally intensive usage with high-resolution medical image volumes and 3D volumetric data (Islam et al., 2023).

With linear complexity, Swin Transformer overcomes the issue by modeling self-attention within a local non-overlapping window. It uses shifted window partitioning (W-MSA and SW-MSA) to achieve cross-window connections and model global context (Nanmaran et al., 2022).

These are some relevant Swin Transformer architectures for different tasks:

SwinMR for accelerated MRI reconstruction, which minimizes long scan times

and helps patients avoid long discomforts or motion artifacts. SwinMR has an Input Module (IM), Feature Extraction Module (FEM) consisting of cascade Residual Swin Transformer Blocks (RSTBs) and an Output Module (OM)(Khalighi et al., 2024).

Swin UNETR for denoising diffusion MRI scans, it models high precision by combining a Swin Transformer encoder and a fully convolutional decoder via skip connection (Ahmed et al., 2024).

HRSTNet(High Resolution Swin Transformer Network) for tumor sub-segmentation uses a high-resolution network instead of a U-Net structure and keeps the full resolution for all features in segmentation pipelines, benefiting the preservation of fine structures (Khaliki & Baarslan, 2024).

4.2 Two-Stage Cascaded 3D Segmentation pipelines

The difficulties in the precise delineation of subregions such as necrotic core, active enhancing tumor and peritumoral edema from multi-modal 3D MRI scans motivates researchers to introduce two-stage cascaded 3D segmentation pipeline (Vankdothu & Hameed, 2022). The first stage performs a course, multi-scale segmentation based on a Swin Transformer encoder with ASPP and SE blocks, whereas the second stage performs accurate segmentation based on the result from the first stage using a class-wise attention decoder that mask the original input with the coarse prediction to focus on the regions related to the tumor subregions (Irmak, 2021). Due to significant class imbalances that often occur with tumor segmentation, weighted Tversky loss is used to train the model:

The Tversky loss for input of two volumes, prediction P and ground truth G, is defined as 1- a ratio where the numerator is the intersection of the two volumes, plus a small epsilon value to improve numerical stability, and the denominator is a weighted sum of the overlap, the number of false positives and the number of false negatives, all plus an epsilon value(Senan et al., 2022).

P and G refer to the predicted and ground truth volumes, respectively, while alpha and beta weight the penalty terms given to false positive and false negative, respectively. With Dice score of 0.99 for healthy tissue and >0.5 for tumor subregions on BraTS 2020, the framework proves to perform significantly well (Shamshad et al., 2024).

4.3 Hybrid CNN-Transformer Networks

Brain tumor classification has recently moved towards hybrid architectures, which use CNNs for local detail extraction and Transformers for global modeling (Senan et al., 2022). The MultiAttenNet uses multi-scale CNNs coupled with Transformer-based attention mechanisms for capturing local detail information as well as context. It has shown impressive results for classification on multi-class dataset for glioma, meningioma and pituitary tumors (overall accuracy of 98.4%, sensitivity of 96.8%, specificity of 99.2%, false positive rate of 1.3%) (Shamshad et al., 2024). SwT+ResNet50V2 is another hybrid system that uses a Swin Transformer to first learn the high-level, global features of the multi-modal MRI volumes. Pre-trained ResNet50V2 network is then used for subsequent feature refinement using its residual blocks and final classification using its fully connected layers. This hybrid approach has obtained 99.9% accuracy on binary Br35H and 96.8% accuracy on a 4 class Kaggle dataset, performing significantly better than single models like VGG16, MobileNetV2 and conventional CNN models (Alanazi et al., 2022).

Table 3: Comparison of Advanced Machine Learning and Deep Learning Architectures for Brain Tumor Tasks

Model Framework	Primary Architecture & Key Component	Target Pathologies & Tasks	Computational Advantages	Performance Metrics

	s			
Res-BRNet	Modified spatial and residual blocks for regional and boundary feature extraction	Multi-class tumor classification (Glioma, Meningioma, Pituitary, Normal)	Reduced computational depth; optimized for edge and boundary identification	Accuracy: 98.22% Sensitivity: 98.11% Precision: 98.22%
MultiAttentionNet	Multi-scale CNNs integrated with Transformer-based attention mechanisms	Glioma segmentation (BraTS 2023) and multi-class classification	Dual local-global modeling; reduced false positive rates	Accuracy: 98.4% Sensitivity: 96.8% Specificity: 99.2%
SwT + ResNet50V2	Sequential Swin Transformer feature extractor with ResNet50V2 classifier	Binary (Br35H) and 4-Class (Kaggle) diagnostic classification	Combines linear attention complexity with stable residual classification	Binary Accuracy: 99.9% 4-Class Accuracy: 96.8%
Cascaded 3D Swin	3D Swin backbone + ASPP + SE blocks with class-wise attention decoder	3D segmentation of tumor subregions (BraTS 2020)	Handles large class imbalances; multi-scale context capturing	Healthy Tissue Dice: 0.99 Subregion Dice: >0.5
Pre-trained VGG16	VGG 16 base model with transfer learning and fine-tuned weights	Multi-class classification with HTML/Dash web interface	Easily deployed in web services; rapid diagnostic inference	Accuracy: 99.24% (after intensive data augmentation)

5. Preprocessing, Normalization, and Optimization Pipelines

The performance and generalizability of deep learning models depend heavily on the quality and consistency of the input data. MRI scans often exhibit significant intensity variations, noise, and artifacts due to differences in scanner manufacturers, magnetic field strengths, and acquisition protocols. Consequently, robust preprocessing and optimization pipelines are essential (Alanazi et al., 2022).

5.1 Mathematical Preprocessing and Feature Enhancement

To reduce noise and extract informative features before network training,

researchers often apply mathematical transforms. One such method is the Db4 (Daubechies-4) wavelet transform, which decomposes MRI images into spatial-frequency sub-bands. The Db4 wavelet transform helps denoise the image, reduce dimensionality, and highlight high-frequency texture variations, such as tumor boundaries. When integrated into Swin Transformer pipelines, wavelet preprocessing has been shown to improve overall pattern recognition and classification stability (Celik & Inik, 2024).

5.2 Standardization, Normalization, and Histogram Equalization

Before being fed into deep learning networks, MRI slices must undergo standard preprocessing:

1. **Resizing:** Images are resized to standard dimensions such as 224x224 pixels for ResNet18 and SwT+ResNet50V2, or 256x256 pixels for Swin Transformers to balance image detail with computational efficiency (Mahmud et al., 2023).
2. **Normalization:** Voxel intensities are scaled to a range of 0 to 1 (typically by dividing each pixel value by 255) to stabilize gradient descent and accelerate model convergence (Shanthi et al., 2022).
3. **Contrast Enhancement:** Histogram equalization is applied to normalize contrast variations, ensuring that subtle differences in soft-tissue density are visible across different imaging protocols (Yamuna et al., 2024, October).

5.3 Data Augmentation and Leakage Prevention

In order to prevent the problem of overfitting and improve the model's generalizability to small datasets, various data augmentation strategies are employed (Sadam et al., 2021), such as spatial transformation which involves random horizontal and vertical flips (probability=0.5), random rotation of +/-15 degrees, random translation and zoom scaling (range 0.9-1.1), color-space transformation including random change of brightness and random adjustments of color channels. For an unbiased validation of the model, patient-wise division is important (commonly used: 70% for training, 20% for validation and 10% for testing). Libraries such as scikit-learn should be used for this patient-wise splitting of the data, otherwise slices from the same patient would end up in both the training set and testing set. This would mean data leakage and we wouldn't know how the model will really perform on the clinical patients. (Nawaz et al., 2022).

Conclusion

In summary, the development of Artificial Intelligence has revolutionized the domain of brain tumor classification using MRI scans and has led to automated, efficient and accurate diagnostic systems. Deep learning architectures, and in particular CNNs, have exhibited an excellent capacity to discover subtle and complicated patterns within medical images; outperforming traditional machine learning methods for many tasks. The use of AI in the field promises faster and more reliable diagnoses and aids radiologists in making sound clinical judgments. Nevertheless, limitations such as a lack of large and well-annotated datasets, lack of interpretability and poor integration with current clinical workflow inhibit widespread clinical applications. Developing an AI model that performs reliably on different imaging conditions and patient demographics is another important aspect. Future research efforts should focus on explainable AI and the creation of diversified and expanded datasets and they're in-vivo validation. AI has the capability to be an indispensable tool in neuro-oncology, significantly increasing early diagnosis rates and patient prognoses.

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