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Machine Learning Techniques in Brain Tumor Diagnosis using MRI

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***Abstract*-- Brain tumors require early and precise diagnosis to prevent severe clinical consequences. The complexity of tumor characteristics necessitates expert analysis through MRI, a process that is traditionally labor-intensive. To address this, automated systems leveraging Machine Learning (ML) architectures have emerged. This study evaluates the potential of high-precision computational frameworks for the automated detection and classification of brain tumors in MRI scans. A review of 18 recent studies highlights the effectiveness of ML methods, particularly Convolutional Neural Networks (CNNs), achieving up to 99.85% accuracy. Our research confirms that various ML methods can reliably identify pathological tissues, allowing for the assessment of tumor histology (type) and malignancy grade. Furthermore, the use of multimodal data, such as incorporating PET scans alongside MRI, is recommended to enhance diagnostic outcomes. While CNN-based models show promising results, they require extensive training data; therefore, transfer learning and hybrid models are encouraged to mitigate data scarcity and improve detection accuracy.**

***Index* Terms- Brain tumors; Brain abnormalities; Image processing; Machine learning; MRI.**

I. Introduction

The brain is a complex, essential organ comprising nearly 100 billion neurons. Positioned at the center of the nervous system, it orchestrates all bodily functions [1]. Consequently, any brain disorder poses significant health risks. Among these, brain tumors are particularly perilous, characterized by the abnormal and uncontrolled proliferation of brain cells. Brain tumors are categorized into primary and secondary types. A primary tumor originates within the brain tissue itself, whereas secondary tumors develop when cancerous cells migrate from other body parts via the bloodstream to the brain tissue [2, 3].

Symptoms of brain tumors can vary depending on their location and type, but may include seizures, behavioral changes, balance issues, memory difficulties, vision alterations, and confusion [4]. Medical imaging techniques such as Computed Tomography (CT), X-ray, Ultrasound Imaging (UI), and Magnetic Resonance Imaging (MRI) are extensively employed for monitoring, diagnosing, and treating various conditions. MRI, in particular, is favored for detecting, classifying, and diagnosing brain tumors due to its superior resolution [5]. It utilizes non-ionizing radiation to generate images through various parameters [6, 7].

Accurate segmentation and classification of brain tumors enhance treatment outcomes. The primary goal of tumor segmentation is to distinguish tumor tissues, including necrotic core, edema, and active cells, from normal brain tissues like Cerebrospinal Fluid (CSF) and Gray Matter (GM) [8, 9].

Timely diagnosis and treatment are vital for preserving health. Over the last decade, the automated analysis of brain MRIs using Computer-Aided Diagnosis (CAD) systems has become a significant research focus [10, 11]. Recent developments in Machine Learning (ML) have further

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propelled the adoption of these methods in healthcare, requiring sophisticated decision-making capabilities. ML approaches are particularly adept at handling complex, multi-parameter problems. The development and deployment of automated, robust, and efficient CAD systems are essential for alleviating healthcare professionals' workload, streamlining hospital procedures, and enabling swift result generation and reporting.

Ischemic stroke (infarct), hemorrhage, neurodegenerative such as Alzheimer and Parkinson, and demyelinating diseases are several other types of diseases that pose significant clinical challenges [12-15].

The issue of automatic diagnosis is examined through three sub-problems: segmentation, classification, and detection [16, 17]. Detection encompasses both classification and segmentation, offering a broader framework, but it primarily concentrates on identifying the presence or absence of a tumor. Classification pertains to the categorization of tumor types under specific conditions, such as Glioma, Meningioma, or pituitary tumors, as well as the grading of tumors [18, 19], which includes High-Grade Glioma (HGG) and Low-Grade Glioma (LGG) [20].

This manuscript functions as a review article, and its primary objective is to offer a comprehensive and systematic analysis of existing ML techniques applied to brain tumor diagnosis using MRI. It does not aim to introduce a novel clinical or methodological contribution but rather to synthesize and critically evaluate the current landscape of research in this domain.

While numerous studies have explored ML for brain tumor diagnosis, the literature is often fragmented. This review aims to bridge this gap by providing a consolidated, high-level perspective. It consolidates, analyzes, and synthesizes findings from a broad array of prior investigations.

A core aim of this review is to explicitly identify and elaborate on the limitations of existing research (e.g., small sample sizes, need for multimodal data, validation challenges) and to propose concrete avenues for future study.

This paper is structured as follows: Section II describes the materials and methods. Section III introduces the most widely used ML techniques along with related studies. Section IV discusses the experimental results and analysis, while Section V offers conclusions and suggestions for future research.

II. Materials and Methods

A. *Research question and study design*

This systematic review is conducted in accordance with the PRISMA [21, 22]. The systematic review's main objectives are to provide a summary of the recent research on the aspects of brain tumors in MRI as a method, to aid in the diagnosis of brain tumors, and pinpoint areas for future study. Unlike studies that introduce a specific novel algorithm, this review provides a systematic synthesis and comparative analysis of numerous ML methods, datasets, and their reported outcomes. This allows researchers to understand the strengths and weaknesses of different approaches within a unified framework.

The selection of 18 core studies is driven by the need to represent a wide spectrum of computational strategies, ranging from traditional CNNs to state-of-the-art Hybrid models. To ensure the reliability of the synthesis, studies are selected based on their publication in high-impact venues and their use of large-scale benchmark datasets such as BraTS. The PRISMA diagram is shown in Fig. 1.

The novelty of this review lies in its comprehensiveness, critical evaluation, and systematic presentation of the current research landscape, thereby providing a foundational understanding and clear direction for advancing the field of ML-driven brain tumor diagnosis.

B. *Eligibility requirements*

To be eligible for inclusion, studies had to meet the following criteria:

(a) Focus on human brain tumor detection, classification, or segmentation

(b) Utilization of MRI datasets (monomodal or multimodal)

(c) Reporting of standardized performance metrics (Accuracy, Dice Score, or Sensitivity).

Exclusion criteria involved:

(1) studies involving animal subjects

(2) papers based on datasets with fewer than 100 total MRI scans to avoid statistical bias

(3) studies lacking a clear description of the ML architecture.

C. *Sources of information and methods of searching*

We perform a systematic search across seven major academic databases and publishers, including: Science Direct (Elsevier), Springer, IEEE, Wiley, Medical Image Analysis, Neuro Image, and Medical Physics. The search string included combinations of the following keywords: "Brain tumors", "MRI", "Deep Learning", " Diagnosis/ Classification/ Segmentation ", and "Machine Learning".

Using the title and abstract, each paper is assessed separately based on the criteria for inclusion and exclusion. The selection process prioritized recent publications that demonstrate superior accuracy and incorporate a wide array of ML methodologies. An author (KP) developed a data extraction table to gather information from each publication, including the first author, the nation, the applied ML method, the number of participants, the publication year, the journal, and the number of related references. Another author (RA) verified and approved the data extraction table.

D. *Synthesis of findings*

The findings from each article are summarized by KP and confirmed by every author involved. With respect to the data that exists at the moment, each author has used narrative synthesis to investigate and combine the findings and gaps.

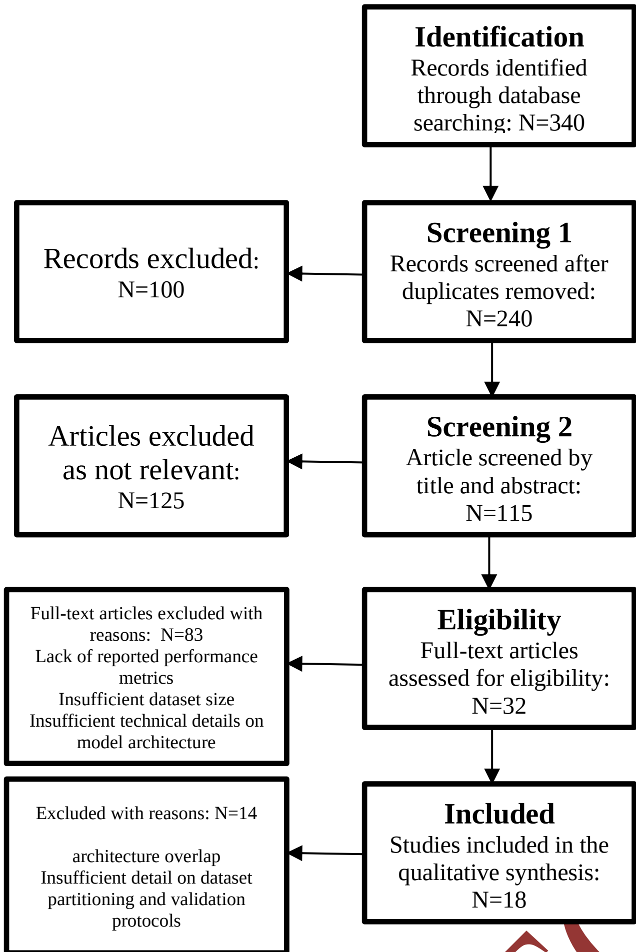

Fig. 1. Scope review flowchart in PRSIMA.

E. Process of choosing evidence sources and data visualization

III. RESULTS

A. Selection of evidence

The review contained 18 related investigations.

B. Specifications of the evidence

The research studies had at least 37500 images in total, including tumor and non-tumor images (benign, malignant, Meningioma, Pituitary, metastatic, Glioma, G-II, G-III, G-IV)

Table I summarizes the features of the research papers.

C. Narrative Synthesis of Relevant Findings from Evidence

In this section, we look at a few of the most widely used ML techniques. It is followed by some recent research that uses the models previously discussed to diagnose brain tumors using MRI images.

D. Machine learning methods

ML is the process of applying a variety of mathematical models and algorithms to constantly improve a task's performance [23]. The preparation of the data sets is necessary to use information sets as a direct source for estimation without the need for extra modification. Assignments in this field come in two varieties: supervised learning and unsupervised learning. Supervised learning is mainly utilized in classification and regression applications, whilst unsupervised learning is well-suited for data analysis and clustering tasks [24].

This study will explore some of the most widely used ML approaches, such as the Convolutional Neural Network (CNN), Support Vector Machine (SVM), Random Forest (RF), Decision Tree (DT), Naive Bayes (NB), and k Nearest Neighbors (kNN), and categorize them based on the type of learning [25, 26].

1) CNN

CNN classifiers are extensively employed to address various image classification challenges, including brain tumor grading. The primary benefits of CNNs lie in their ability to automatically extract and select features, optimize activations, and adjust weights. Consequently, there is no requirement for a complex approach involving separate feature extraction, feature selection, and subsequent application of a classification algorithm. Their intricate and layered architecture allows them to tackle complex classification tasks, albeit with a trade-off in computational complexity when compared to traditional ML techniques like k-means and SVM [20]. Notable CNN models comprise Alex-Net, VGG, EfficientNet, Inception, ResNet, LeNet, and DenseNet.

a) AlexNet

In 2012, Alex Krizhevsky, Ilya Sutskever, and Geoffrey Hinton introduced a CNN model known as AlexNet [27]. This model was trained using the ImageNet dataset, which includes 1000 categories. The architecture of AlexNet comprises five convolutional layers, three pooling layers, and three fully connected layers. Notably, they were pioneers in employing the ReLU activation function and dropout regularization techniques to enhance performance [28].

b) VGG

The Visual Geometric Group (VGG) is a significant advancement in CNN models, building upon the AlexNet architecture. This innovation, proposed by Simonian and Zisserman [29], involves replacing the initial large kernels with a series of smaller 3x3 kernels in the first two convolutional layers. The VGG model, with its impressive performance, requires around 528 MB of storage and has achieved a remarkable 90.1% accuracy on the vast ImageNet dataset, which comprises approximately 138.4 million parameters and 14 million images categorized into 1000 classes [30].

VGG offers two primary variants: VGG16 and VGG19. These models are designed for object classification and detection tasks, capable of categorizing 1000 images into distinct classes. While VGG16 has 16 layers, VGG19 expands on this by adding more layers as the filter size decreases, resulting in 19 layers. Despite this difference, both models function similarly in terms of layer detection [31].

VGG16 has gained widespread recognition in research due to its simple approach and the availability of pretrained weights, enabling easy fine-tuning for new tasks. The architecture consists of 5 max-pooling layers, 2 fully connected layers, and 1 softmax layer, in addition to the convolutional layers. In a modified VGG16 for classification, the fully connected and softmax layers are replaced with a flatten layer, 2 batch normalization layers, a 25% dropout layer, and 2 dense layers, accepting inputs of size 160x160 [32].

c) EfficientNET

EfficientNet, a powerful collection of CNN models, offers exceptional performance with minimal parameters. The name, a blend of efficiency and network, reflects its core purpose. Primarily employed in visual tasks like image classification, EfficientNet delivers remarkable results, balancing computational efficiency and accuracy. This model series provides a range of options, catering to various complexities and scales [29].

Through a multi-objective neural network search, researchers optimized for accuracy and calculations, introducing EfficientNet B0. Building upon this foundation, EfficientNet B7 emerged, setting new standards for accuracy on ImageNet while maintaining efficiency. EfficientNet B0's architecture, with 237 layers, includes flattening, batch normalization, dense layers, and a dropout layer for MRI classification [32].

EfficientNet B7, a sophisticated CNN, employs compound coefficients for uniform scaling. Its 813 layers, along with batch normalization, dense layers, and dropout mechanisms, contribute to its performance. This model ensures consistent and systematic scaling, enhancing its capabilities, and accepts an input size of 160 x 160 for image processing [32].

d) Inception

The Inception model is a CNN framework that revolutionized feature extraction and classification. This innovative design, introduced in the research paper, going deeper with convolutions, aims to enhance performance when handling intricate visual data. By employing a unique structure, it utilizes multiple convolutional layers working in parallel, allowing simultaneous processing and recording of features at various scales. This parallel processing approach is key to the Inception architecture's efficiency in handling complex tasks [33].

e) ResNet

ResNet [34] efficiently and considerably trains deep neural networks; for this reason, it has become a game-changer. ResNet determines the optimal number of layers and operates on building deeper networks than conventional simple networks. These residual networks may be much more accurate from a much deeper level and are easier to tune. Before ResNet152V2, training a deep neural network for the zero gradient problem was challenging. The Resnet152V2 has 564 layers [32].

ResNet50 is a very deep CNN model and consists of 50 layers, which is able to train neural networks by using the skip connection approach and batch normalization. It won the ImageNet large-scale visual recognition challenge in 2015, which is best known for image classification, semantic segmentation, and object detection [31].

f) LeNet

The CNN model, pioneered in the 1990s by the Yann LeCun team at Pierre and Marie Curie University, was initially designed for character recognition tasks and became the first widely adopted CNN for recognizing handwritten digits. This model comprises multiple layers, employing a 5x5 filter with a stride of 1 in the convolutional layer, while a 2x2 filter with a stride of 2 is utilized in the pooling layer [31].

g) DenseNet

DenseNet121 and DenseNet169 are variations of Dense convolutional Networks (DenseNet) designed to improve architectural efficiency and performance. DenseNet121 minimizes redundant feature extraction and mitigates vanishing gradients through direct layer connectivity, while DenseNet169 extends this framework with additional layers for handling complex datasets [35].

2) Transfer learning

Transfer learning involves using the knowledge gained from training a model on a specific task and subsequently applying that knowledge to another related task, and is a fundamental concept in ML. In the field of neural networks, transfer learning shows considerable power. Taking a pre-trained model, which is usually trained on a large and diverse dataset, and fine-tuning it on a new dataset or task is called transfer learning [36, 37].

3) SVM

The fundamental concept of this ML method involves employing hyperplanes to create decision boundaries within SVM that differentiate various categories of data points. SVMs are capable of addressing both simple, linear classification tasks and more complex, nonlinear classification challenges. To facilitate the resolution of classification problems, SVMs transform the original data points from the input space into a high or infinite-dimensional feature space. This transformation is achieved by selecting a suitable kernel function [38].

4) Attention with channel attention

Channel attention mechanisms play a crucial role in enhancing the performance of ML models for brain tumor classification by accurately pinpointing the most critical features in MRI images. The main role of channel attention blocks is to amplify the representational capacity of CNNs by allowing the model to concentrate on essential channels within the feature maps. This approach enhances the extraction of pertinent information while minimizing the influence of less informative data. The success of channel attention blocks lies in their capability to emphasize vital features based on their relevance for tumor classification. By dynamically adjusting the weights of different channels according to their significance, channel attention blocks refine the model's focus on crucial areas for accurate diagnoses. This selective attention mechanism is particularly beneficial in medical imaging, where distinguishing tumors from surrounding tissues can be subtle and challenging without sufficient emphasis on relevant features. Moreover, integrating channel attention blocks into sophisticated CNN architectures has demonstrated substantial improvements in performance metrics for tumor detection tasks [39].

5) Soft attention

The soft attention mechanism helps the model emphasize important tumor features by focusing on relevant areas in the MRI image, while downplaying less important areas. This ensures that the model makes decisions based on the most critical parts of the image [40].

6) CJHBA-based DRN

The Chronological Jaya Honey Badger Algorithm (CJHBA) integrates the Jaya and Honey Badger (HBA) algorithms with a temporal concept to optimize the training of a Deep Residual Network (DRN), which processes the extracted features for classification. The periodic details of things that change over time are identified using the temporal concept. HBA is useful in solving optimization challenges. It also has a good balance between exploration-exploitation and converges very quickly. In the Jaya algorithm, simple general parameters are used for optimization, and no algorithm-specific parameters are required. Owing to this benefit, the algorithm proves beneficial in addressing a range of real-world optimization challenges, including mechanical design issues, automatic clustering, and optimal power flow. Nonetheless, its application to intricate multidimensional problems is challenging, resulting in slow convergence. Consequently, integrating the temporal concept, HBA, with the Jaya algorithm is advantageous for the efficient classification of brain tumors [41].

7) Bi-LSTM

Bidirectional Long Short-Term Memory (Bi-LSTM) is employed to extract features for brain tumor classification. This model is an advanced version of LSTM, capable of processing information in both forward and reverse directions. It is instrumental in modeling spatial dependencies and capturing significant sequential relationships among features across various MRI slices. Bi-LSTM utilizes a sequential processing method that comprises two LSTMs: one processes the feature Fe in a forward direction, while the other processes it in reverse. By doing so, Bi-LSTM effectively increases the amount of data available to the network, thereby improving classification accuracy [42].

8) modified LinkNet

LinkNet, an ML framework commonly employed in image processing tasks such as image classification, holds potential as a structure for brain tumor classification. In this domain, LinkNet introduces skip connections that facilitate smooth data flow across network layers while maintaining crucial details necessary for precise brain tumor diagnosis. However, the current version of LinkNet exhibits slower convergence and a higher risk of information loss. To address the computational cost of training, a newly modified LinkNet model is proposed for brain tumor classification. This modified version incorporates additional layers, such as max pooling and transposed convolution layers. Furthermore, the four encoder blocks in LinkNet are enhanced by integrating convolutional layers, batch normalization, and the tanh function. The inclusion of the batch normalization layer in the encoder block enhances network stability and speed. The existing ReLU activation is prone to outliers and lacks robustness, making it inadequate for handling uncertainties. Consequently, a novel activation function, based on hybrid activation functions, has been developed. This hybrid activation function combines elish and swish activations, improving the network's computational efficiency. Therefore, for brain tumor classification, the enhanced LinkNet is the optimal choice for achieving computational efficiency [42].

9) Deep Hierarchy-Aware Segmentation (DHAS)

To address the limitations of conventional segmentation models that often overlook the intrinsic biological correlations between tumor sub-regions, Cheng et al. [43] proposed the DHAS framework. The core innovation of DHAS lies in its departure from standard multi-class classification, which typically treats segmentation labels as independent entities. Instead, the authors introduced a tree-structured hierarchical label system that explicitly models the nested anatomical relationships inherent in brain tumors, specifically the inclusion of the Tumor Core (TC) and Enhancing Tumor (ET) within the Whole Tumor (WT). Furthermore, the DHAS framework integrates metric learning within its architecture to refine the feature space. This ensures that the learned representations maintain a clear semantic hierarchy, thereby enhancing the model's ability to delineate complex and ambiguous boundaries. By enforcing semantic consistency through this hierarchical prior, the DHAS approach not only achieves superior segmentation accuracy but also provides greater interpretability, ensuring that the generated masks are more consistent with clinical and pathological expectations [43].

10) Conv-MLP-Permutation (CMP) framework

The CMP framework is proposed as a hybrid hierarchical architecture that synergizes the local representation power of CNNs with the global context-capturing capabilities of MLPs. At the heart of this framework is the Efficient MLP-Permutation (EMP) module. Unlike standard transformers that rely on computationally expensive self-attention mechanisms, the EMP module utilizes axis-based permutations to perform spatial mixing. Specifically, the framework permutes the feature map dimensions along the Height (H), Width (W), and Depth (D) axes, allowing simple MLPs to learn long-range spatial dependencies across each dimension independently. This permutation strategy enables the model to achieve a global receptive field with linear complexity, making it highly efficient for volumetric (3D) medical image segmentation. By embedding these EMP modules within a convolutional encoder-decoder structure, the CMP framework effectively boosts the network's ability to model complex anatomical structures in multimodal MRI datasets [44].

11) Dynamic Reinforcement Ensemble Learning (DREL)

The DREL approach is introduced as an adaptive framework for multi-class brain tumor diagnosis, designed to optimize the synergy between multiple base learners. The core innovation lies in integrating Reinforcement Learning (RL) to dynamically manage the ensemble process. Unlike static ensemble methods that assign fixed weights to individual models, DREL employs an intelligent agent that learns to adjust the contribution of each base classifier based on the specific characteristics of the input MRI features. The framework operates by formulating the ensemble selection as a Markov Decision Process (MDP). In this setup, the agent observes the performance of various deep learning architectures (the 'state') and takes 'actions' by re-weighting or selecting the most competent models for a given diagnostic task. This dynamic adjustment is guided by a reward function tied to classification accuracy and robustness. Consequently, DREL effectively mitigates the weaknesses of individual models and achieves a more reliable and generalized performance across diverse tumor types in multimodal MRI datasets [45].

12) Cooperative Multi-task Learning (CoMTL)

The CoMTL is an advanced ML paradigm designed to optimize performance by simultaneously addressing multiple related objectives within a unified computational framework. Unlike traditional single-task learning, which processes isolated functions independently, CoMTL leverages the inherent correlations between tasks to facilitate a synergistic exchange of information. At the architectural level, CoMTL utilizes shared layers to extract common underlying features from the input data. This joint feature space captures fundamental patterns that are universally relevant across all sub-tasks, thereby reducing the risk of learning task-specific noise. The "cooperative" aspect distinguishes this approach from standard multi-task learning. In a CoMTL setting, the intermediate representations or outputs of one task serve as inductive cues or auxiliary constraints for others. This bidirectional feedback loop enables the model to resolve ambiguities in one task by utilizing the high-confidence predictions or structured knowledge derived from another. The CoMTL introduces a robust inductive bias by treating each task as a form of regularization for the others. By enforcing the model to satisfy multiple objective functions concurrently, the optimization process is guided toward a more generalized region of the hypothesis space, significantly enhancing the model's generalization capabilities and preventing overfitting. The learning process is governed by a composite loss function that aggregates the empirical risk of all tasks. This joint optimization ensures that the gradient updates reflect a global equilibrium, allowing the model to achieve superior performance compared to independent models, particularly in scenarios where labeled data for specific tasks is scarce [46].

E. Related works

Brain tumor classification in the domain of medical imaging is a challenging task [47]. The main goal of this section is to review existing work in the field of brain tumor diagnosis and the models that have been used by experts in this field to solve this problem.

Özkaya and Sağiroğlu [20] presented innovative methods for brain tumor analysis, encompassing segmentation and grading. Their initial approach involved employing CNN models to distinguish between HGG and LGG tumors, achieving remarkable accuracy levels of 99.85%. Additionally, they suggested a novel pipeline for HGG-LGG classification, integrating merging techniques, normalization, and CNN models. In the context of segmentation, the authors proposed an algorithm that utilizes histograms, thresholding, and morphological filtering with feature fusion. This algorithm demonstrated an average Dice similarity of 70.58% for full tumor segmentation, outperforming a fixed threshold of 15%. The results indicated its potential as a feature extraction tool for brain MR images of varying sizes. Furthermore, the extracted centroid features hold promises for enhancing segmentation techniques in ML algorithms, particularly in T1 and T1CE methods.

To build an accurate and efficient model for tumor detection and classification from MR images, Akter et al. [32] proposed a deep CNN-based architecture for automatic classification of brain images into four classes and a U-Net-based segmentation model. They tested the classification model and trained the segmentation model using six benchmark datasets, allowing for a side-by-side comparison of the impact of segmentation on tumor classification in brain MRI. They also evaluated two classification methods based on precision, recall, accuracy, and AUC. The results show that this classification model achieves 98.7% accuracy when using a merged dataset and 98.8% accuracy when using a segmentation approach, while the highest classification accuracy among the four individual datasets used is 97.7%.

Sharif et al. [47] proposed an end-to-end optimized ML system for multimodal brain tumor classification. For evaluation, the BRATS dataset is used, but in the very first step, the contrast is enhanced using the combined split histogram equalization along the ant colony optimization approach, and a newly designed nine-layer CNN model is trained. The features are extracted from the second fully connected layer and optimized via mouth flame optimization and differential evolution. The outputs of both methods are merged before entering the multiclass SVM (MC-SVM), using the matrix length approach. In the testing process, the proposed method achieved accuracies of 99.06%, 98.76%, 98.18%, and 94.6% on BRATS 2013, BRATS 2015, BRATS 2017, and BRATS 2018, respectively.

Khushi et al. [31] analyzed and compared the performance of many different CNN models, including LeNet, AlexNet, VGG16, VGG19, and ResNet50, trained on the publicly available Br35H dataset for brain tumor detection. In this research, a variety of optimizers, such as Adam, Stochastic Gradient Descent (SGD), and Root Mean Square propagation (RMSprop), were employed to enhance the performance of the CNN model. To assess the efficacy of five distinct CNN architectures trained with these three optimizers, metrics such as accuracy, misclassification rate, sensitivity, specificity, Negative Predictive Value (NPV), Positive Predictive Value (PPV), F1-score, and False Rejection Rate (FOR) were utilized.

The findings indicate that the AlexNet architecture, when optimized with SGD, surpasses other CNN architectures paired with different optimizers. The achieved metrics for accuracy, sensitivity, specificity, NPV, PPV, F1-score, and FOR are 98.79%, 98.98%, 98.58%, 98.93%, 98.65%, 98.82%, and 1.06%, respectively.

Mohanty et al. [40] developed a meticulously structured CNN featuring four convolutional layers to present a novel ML model that utilizes the soft attention mechanism. A significant innovation in their methodology is the feature extraction technique. Unlike traditional models that extract features solely from the final layer, their strategy involves aggregating and integrating features from all layers, ensuring that the essential characteristics of each layer are preserved and amalgamated into a comprehensive and robust feature vector. The incorporation of the soft attention mechanism in the concluding stages highlights the most critical and pertinent features, thereby enhancing classification accuracy. To assess the model's efficacy as proposed in [40], standard datasets were employed for both training and testing. The model achieved an accuracy of 95.1%, with precision, recall, F1-score, and specificity recorded at 95.57%, 96.88%, 95.98%, and 87.41%, respectively.

Deepa et al. [9] have introduced a proficient hybrid optimization method for the segmentation and classification of brain tumors. This classification process utilizes extracted features as inputs into a DRN, which is trained using a combination of the Jaya algorithm, the HBA, and a temporal concept known as the CJHBA. The effectiveness of this approach was assessed using the Figshare and BRATS 2018 datasets, achieving maximum accuracy, sensitivity, and specificity of 92.10%, 93.13%, and 92.84%, respectively, with the BRATS dataset.

Srinivasan et al. [41] introduced three unique CNN models aimed at improving early detection across various classification tasks. The initial CNN model demonstrates an outstanding detection accuracy of 99.53% for identifying the presence or absence of tumors. The second model, achieving an accuracy of 93.81%, effectively categorizes brain tumors into five types: glioma, meningioma, pituitary, normal, and metastatic. Additionally, the third model attains an accuracy of 98.56% in distinguishing the grades of glioma tumors. To optimize performance, a network search optimization method is employed to automatically adjust all parameters associated with the CNN models. The utilization of extensive, publicly accessible clinical datasets contributes to the robustness and reliability of the classification outcomes.

Ali and Agrawal [26] introduced a hybrid approach for the automated segmentation of MRI brain tumor images, utilizing the VGG19 architecture in conjunction with ResNet101. The classifier's optimization is conducted through Bayesian methods, followed by cross-validation to select the optimal parameters for the refined classifiers. Throughout the research, various transfer learning models are assessed to determine the most efficient model for detecting brain malignancies using neural networks. The results indicate an accuracy of 97.0%, with precision, recall, and F1-score values of 97.0%, 98.0%, and 96.0%, respectively.

Ranjbarzadeh et al. [48] proposed a brain tumor segmentation framework utilizing a CNN optimized by the Improved Chimp Optimization Algorithm (IChOA). The process begins with normalizing four MRI sequences (Flair, T1, T1c, and T2) to highlight potential tumorous regions. Subsequently, the IChOA is employed for feature selection via an SVM-based pixel-wise classification approach. These optimal features are then fed into the CNN, where the IChOA further optimizes the network's hyperparameters to perform the final segmentation. By treating segmentation as a fine-grained classification of pixels, this method achieved a Dice score of 97.04% on the BraTS 2018 dataset. This method, tested on the BRATS 2018 dataset, achieved impressive results: precision of 97.41%, recall of 95.78%, and a Dice score of 97.04%.

The study by Khaliki and Başarslan [30] explores brain tumor classification using various CNN and CNN-based techniques. They employed five distinct models, namely InceptionV3, EfficientNetB4, VGG16, VGG19, and a multilayer CNN, to categorize brain tumors and benchmarked their performance on a specific dataset. The dataset was divided into 10% for testing, 15% for validation, and 75% for training purposes. The evaluation metrics included F-score, recall, imprinting, and accuracy, which were used to assess the effectiveness of these models. The best accuracy, F1-score, AUC, recall, and precision when using VGG16 are 98%, 97%, 99%, 98%, and 98%, respectively.

The primary objective of the study by Kanchanamala et al. [49] was to develop an effective method for brain tumor classification utilizing a hybrid Quantum Dilated Convolutional Neural Network-Deep Maxout Network (QDCNN-DMN). In this approach, MRI serves as the input for the image enhancement process, where it undergoes sharpening through logarithmic transformations. The skull-stripping phase employs Deep Embedded Clustering (DEC). Following this, tumor segmentation is executed using the Structure Correcting Adversarial Network (SCAN), after which statistical and other significant features are extracted. The subsequent detection and classification of brain tumors are carried out using the proposed hybrid QDCNN-DMN. This network is constructed by integrating the QDCNN with the DMN. The study demonstrates that the QDCNN-DMN, when applied to the Figshare dataset for brain tumor classification, achieves specificity, sensitivity, and accuracy, recorded at 93.7%, 94.5%, and 94.0%, respectively.

Hekmat et al. [35] introduced an innovative technique that integrates Contrast Limited Adaptive Histogram Equalization (CLAHE) with Discrete Wavelet Transform (DWT) to enhance image fusion, thereby improving the contrast and detail in MR images. The resulting fused images are processed through a feature fusion framework utilizing DenseNet121 and DenseNet169 models, which are adept at learning hierarchical features. An attention mechanism is integrated to effectively manage the transmission of fused features for classification, ensuring the prioritization of essential information. Furthermore, the Chirplet transform is employed post-feature fusion to capture nuanced tumor characteristics and optimize feature sequence extraction. The effectiveness of the proposed model was assessed using two publicly accessible brain tumor datasets: Kaggle (7,023 MRI) and Figshare (3,064 MRI). Data augmentation techniques were applied to satisfy the input size requirements for the CNN. The findings indicate that the proposed model surpassed individual base models and existing approaches, achieving classification accuracies of 99.16% on the Kaggle dataset and 94.28% on the Figshare dataset.

Kusuma and Reddy [42] introduced a method for classifying brain tumors using MRI scans. Initially, the T1, TIC, T2, and T2 flair input images are combined using an enhanced fusion technique. Following this, Median Filtering (MF) is utilized to preprocess the combined image. The authors propose a modified SegNet model with a novel pooling operation for the segmentation task. From the segmented image, features such as the Improved Local Gabor Binary Pattern Histogram Sequence (ILGBPHS), Weber Local Descriptor (WLD), and Tetrolet waveform are extracted. The classification process employs HDLA, which integrates Bi-LSTM and modified LinkNet models. With 90% of the data used for training, the proposed approach achieves an accuracy rate of 98%.

Batool and Byun [50] presented a lightweight Multipath Convolutional Neural Network (M-CNN) designed to extract features through diverse convolutional filters at each layer. Additionally, an optimal features module was incorporated to identify the most effective features, thereby enhancing the performance and computational efficiency of the proposed multipath framework. The authors assessed the performance of the M-CNN against the CNN, deep convolutional neural network, and other advanced deep learning models using both complete and selected feature sets for brain tumor detection. The M-CNN demonstrated superior performance over conventional CNN models, achieving an accuracy of 92.25% with all features and 96.03% with selected features. This model successfully facilitated precise brain tumor classification while minimizing overfitting risks and optimizing computational efficiency.

Cheng et al. [43] proposed a DHAS framework to address the challenges of multi-scale feature representation in brain tumor MRI segmentation. The authors introduced a novel approach that incorporates hierarchical label structures and metric learning to enhance the model's understanding of the semantic relationships between different tumor regions. By utilizing a hierarchy-aware architecture, the framework effectively captures both global contextual information and fine-grained local details, leading to improved boundary delineation and overall segmentation accuracy. Furthermore, the integration of hierarchical priors enhances the interpretability of the deep learning model, providing more biologically consistent results.

Lin et al. [44] introduced the CMP framework, a hybrid architecture designed to enhance volumetric medical image segmentation. To overcome the limitations of local receptive fields in standard CNNs, the authors developed an efficient MLP-Permutation strategy that captures long-range dependencies without the heavy computational overhead typically associated with transformers. By applying this method to the BraTS 2021 dataset, they utilized multimodal MRI sequences (T1, T1ce, T2, and FLAIR) to achieve high-precision delineation of tumor sub-regions. The authors reported superior performance metrics, including Dice scores of 92.4% for Whole Tumor (WT), 89.7% for Tumor Core (TC), and 86.1% for Enhancing Tumor (ET), alongside a remarkable specificity of 99.6%. Their work demonstrates that integrating permutation-based MLPs with convolutional layers provides a robust and efficient solution for multi-class segmentation in complex clinical datasets.

Yang et al. [45] introduced a DREL framework to address the complexities of multi-class brain tumor diagnosis. In this study, the authors moved beyond static ensemble models by implementing a reinforcement learning agent that adaptively optimizes the weights of various base classifiers based on real-time performance feedback. Using the Figshare dataset for primary evaluation and BraTS 2021 for cross-validation, the proposed method achieved a remarkable overall accuracy of 98.42%, with a sensitivity of 97.8% and a specificity of 98.9%. Their findings suggest that the DREL approach significantly enhances the reliability of distinguishing between meningioma, glioma, and pituitary tumors, offering a robust computational strategy for automated clinical diagnosis.

Chen et al. [46] proposed a novel CoMTL framework designed to simultaneously perform glioma grading and molecular subtyping. They developed a bidirectional interaction mechanism that allows the model to exploit the inherent correlations between histopathological features and genetic mutations. To enhance clinical transparency, they integrated interpretable image biomarkers, effectively linking deep learning representations with established radiologic characteristics. Through their experiments, the authors demonstrated that this cooperative approach significantly improves diagnostic performance and robustness compared to independent task models, providing a more reliable computational tool for precision oncology and surgical planning.

IV. Discussion

The synthesis of the reviewed literature indicates that brain MRI analysis can provide useful information in the field of brain tumor diagnosis. There are various goals of analyzing MRI images from a patient, such as tumor detection, tumor segmentation, tumor type detection, and the grade of glioma tumors. In fact, ML techniques are used to classify the MR images. Table I summarizes the results of related works using MR images for tumor diagnosis.

Limitations:

One of the critical challenges identified in the reviewed studies is the lack of transparency in reporting key parameters, alongside the potential risk of data leakage resulting from slice-level rather than patient-level data partitioning.

A notable observation in this review is the over-reliance on accuracy as a primary metric in many studies. In medical imaging, where class imbalance is prevalent, metrics such as sensitivity, specificity, and the Dice score are more clinically significant. The absence of these metrics in several reviewed papers limits the ability to perform a robust meta-analysis and underscores the need for more standardized evaluation protocols in future research.

A major limitation identified in the reviewed studies is the lack of cross-institutional validation. Most models are trained and tested on datasets from a single source, increasing the risk of overfitting and making them susceptible to performance degradation due to domain shift (variations in scanner types or acquisition parameters). For these tools to be integrated into real-world clinical workflows, future research must prioritize evaluation on diverse, multi-center datasets to ensure robust generalizability.

It is imperative to acknowledge the inherent limitations in performing a direct cross-study comparison within this domain. The reviewed literature exhibits significant heterogeneity regarding MRI acquisition protocols, pre-processing techniques, and validation strategies. Furthermore, variations in the number of target classes and the imbalance of datasets across different studies further complicate the standardization of performance results. Consequently, the reported accuracy values originate from diverse experimental contexts, and a direct ranking of machine learning algorithms based solely on these figures may be misleading. Future research should prioritize benchmarking on standardized, multi-institutional datasets to facilitate more objective and scientifically rigorous comparisons.

TABLE I
Related Studies Using brain Tumor MRI

Ref	year	dataset	ML method	Accuracy	Sensitivity	Specificity	MRI modality	Training and test data	outcome	Indicators
[30]	2024	G 926 M 937 P 901 No 440 Total3204	EfficientNetB4 InceptionV3 VGG19 VGG16 CNN	97 95 96 98 91	98	ND	ND	Train 75% Test 10 % Validation 15%	No-tumor Glioma Meningioma Pituitary	Extracting features and classification to 4 classes
[20]	2023	Brats2020 Total 369	mobilenet V2 morphological operations	99.85 70.58 Dice	99.85	ND	T1CE, T2, and FLAIR T2 and FLAIR	10-fold cross-validation	HGG LGG Segmented images	modality fusion and classification to 2 classes Segmentation
[32]	2024	G 1426 M 708 P930 Total3064 G 926 M 937 P 901 No 500 Total3264 G 2500 M 2500 P 2500 No 2500 Total10000 (Pradeep2021) G 1038 M 1318 P 1255 No 681 Total 4292 (sheriff2020)	Deep CNN	96.7 Merged dataset S 98.8 NS 98.7	ND	ND	T1CE T1, T2, and FLAIR ND ND	Train 80% Test 20 %	No-tumor Glioma Meningioma Pituitary	Classification when tumor MRIs are segmented using the proposed segmentation model, and when they are not segmented

[47]	2024	Brats 2013 Brats 2015 Brats 2017 Brats 2018	MC-SVM	99.06 98.76 98.18 94.60	ND	ND	T1CE, T2, T1 FLAIR	10-fold cross-validation	ND	Contrast is enhanced, The newly designed nine-layered CNN model is trained, Features are optimized by DE and MF algorithms, and combined in one vector for classification
[31]	2024	Br35h	Alex-Net architecture with SGD optimizer	98.79	ND	ND	ND	Train 80% validation.20 %	Benign Malignant	Data and labels converted to a NumPy array, Normalization, feature extraction, parameter tuning, Soft Max classifier.
[40]	2024	G 4278 M 3540 P 3720 Total11538 Figshare	Soft attention CNN	95.1 (per-class > 97.1%)	ND	ND	T1CE	Train 80% Test 10 % Validation 10%	Glioma Meningioma Pituitary	image augmentation, soft attention, Features from each layer, Soft Attention
[9]	2023	Brats 2018 + Figshare	Implemented CJHBA-based DRN	92.1	93.13	92.84	T1CE, T2, T1 FLAIR T1CE	Train 90% Test 10 %	Tumor liom	Normalization, Segmentation, features extracted, data augmentation, classification
[41]	2024	Figshare+ REMBRANDT+ TCGA-LGG+ 3067	hybrid deep CNN	99.53 93.89 98.56	ND	ND	T1CE ND T1CE+ FLAIR T1CE	Train 60% Test 20 % Validation 20%	Tumor Healthy tissue benign, malignant, Meningioma, Pituitary, metastatic G-II, G-III, G-IV	
[26]	2024	2620	Hybrid Model (CNN -ResNet101)	97	ND	ND	ND	ND	Tumor Healthy tissue	Preprocessing Decoloring extracting feature maps segmentation
[48]	2024	Brats 2018	multipath CNN framework	97.04 DICE	95.78	ND	T1CE, T2, T1 FLAIR	ND	Tumor Healthy tissue	Normalization feature extraction feature selection optimization segmentation

[49]	2025	Brats 2018 + Figshare + MRI dataset	Hybrid CNN Model (QDCNN-DMN)	94	94.5	93.7	T1CE, T2, T1 FLAIR T1CE	Variable	Tumor Healthy tissue	1. Image preprocessing 2. Feature extraction 3. Tumor detection using hybrid deep learning 4. Classification of brain tumors utilizing hybrid deep learning
[35]	2025	Kaggle + Figshare	CLAHE & DWT (attention mechanisms DenseNet121 and DenseNet169 pre-trained CNN)	99.16 94.28	ND	ND	T1CE, T2, T1 FLAIR	Variable	Healthy tissue Glioma Meningioma pituitary	1. Image preprocessing 2. Feature extraction
[42]	2025	Brats 2015 + Brats 2021	Hybrid Deep Learning Architecture HDLA (Bi-LSTM + modified Linknet)	96.22 96.52	94.11 89.54	94.48 96.57	T1CE, T2, T1 FLAIR	Train 90%		Fusion images median filtering the segmentation classification
[50]	2025	Kaggle	Multipath CNN	92.25 96.03	ND	ND	T2, T1 FLAIR	ND	Healthy tissue Glioma Meningioma Pituitary	
[43]	2026	BraTS 2018, BraTS 2019, BraTS 2020	Hybrid CNN Model (DHAS)	(Dice Score) 91.2% 86.8% 82.5%	92.1% for WT	99.4% for WT	T1CE, T2, T1 FLAIR	5-fold cross	Whole Tumor (WT) Tumor Core (TC) Enhancing Tumor (ET):	
[44]	2025	BraTS 2021	Hybrid CNN Model (CMP) framework	Average Dice: 91.8% 92.4% 89.7% 86.1%	93.1%	99.6%	T1CE, T2, T1 FLAIR	training (1,000 cases) validation (251 cases)	WT TC ET	
[45]	2025	Figshare BraTS 2021	Dynamic Reinforcement Ensemble Learning (DREL)	98.42%	97.8%	98.9%	T1ce T2	5-fold cross-validation	Glioma Meningioma pituitary	
[46]	2025	TCGA-LGG GPPH	Cooperative Multi-task Learning (CoMTL)	93.84% 91.13%	94.12%	93.55%	T1CE, T2, T1 FLAIR	652 patients from TCGA for training 124 patients from GPPH for test	Glioma Grades	

Based on this table, there are more than 18 ML methods that have been used to analyze MR images. Each of them has advantages and disadvantages that should be considered before using them. Recent studies are different in the datasets, ML strategies, MRI modality, the applied protocols, and the aim of their investigation, but all of them are utilizing the MR images for tumor diagnosis.

Consequently, future work should focus on developing more suitable protocols to increase the accuracy percentage of the results.

The comparison between tumor detection with different results and their performance is shown in Fig. 2.

Based on the results shown in Fig. 2, the different objectives of tumor detection, tumor segmentation, tumor type detection, and glioma tumor grade all achieve acceptable results.

Distribution of reported accuracies across various ML architectures and datasets is shown in Fig. 3.

Evolutionary trends of ML methodology usage are shown in Fig. 4.

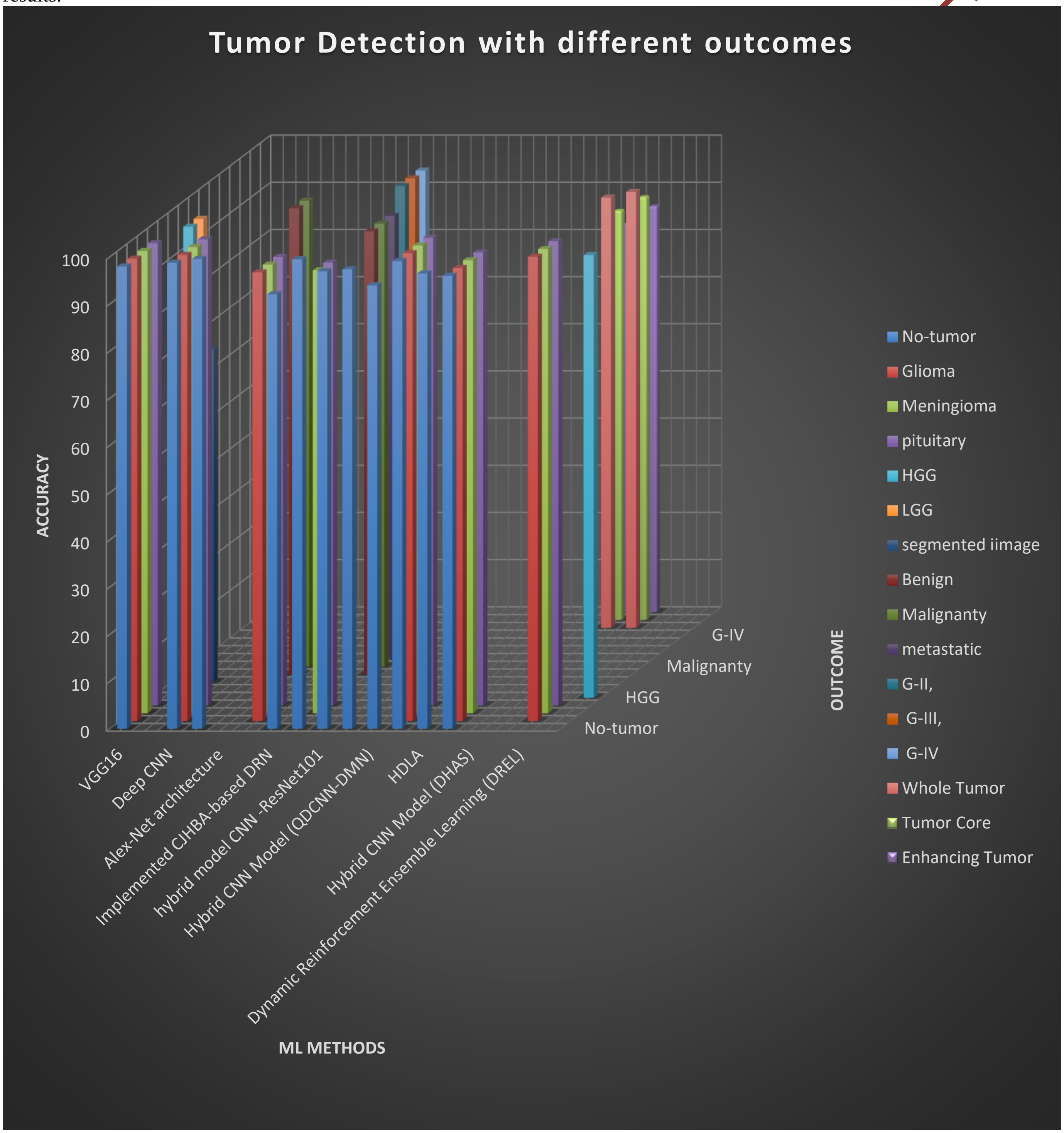

Fig. 2. Tumor Detection with different outcomes.

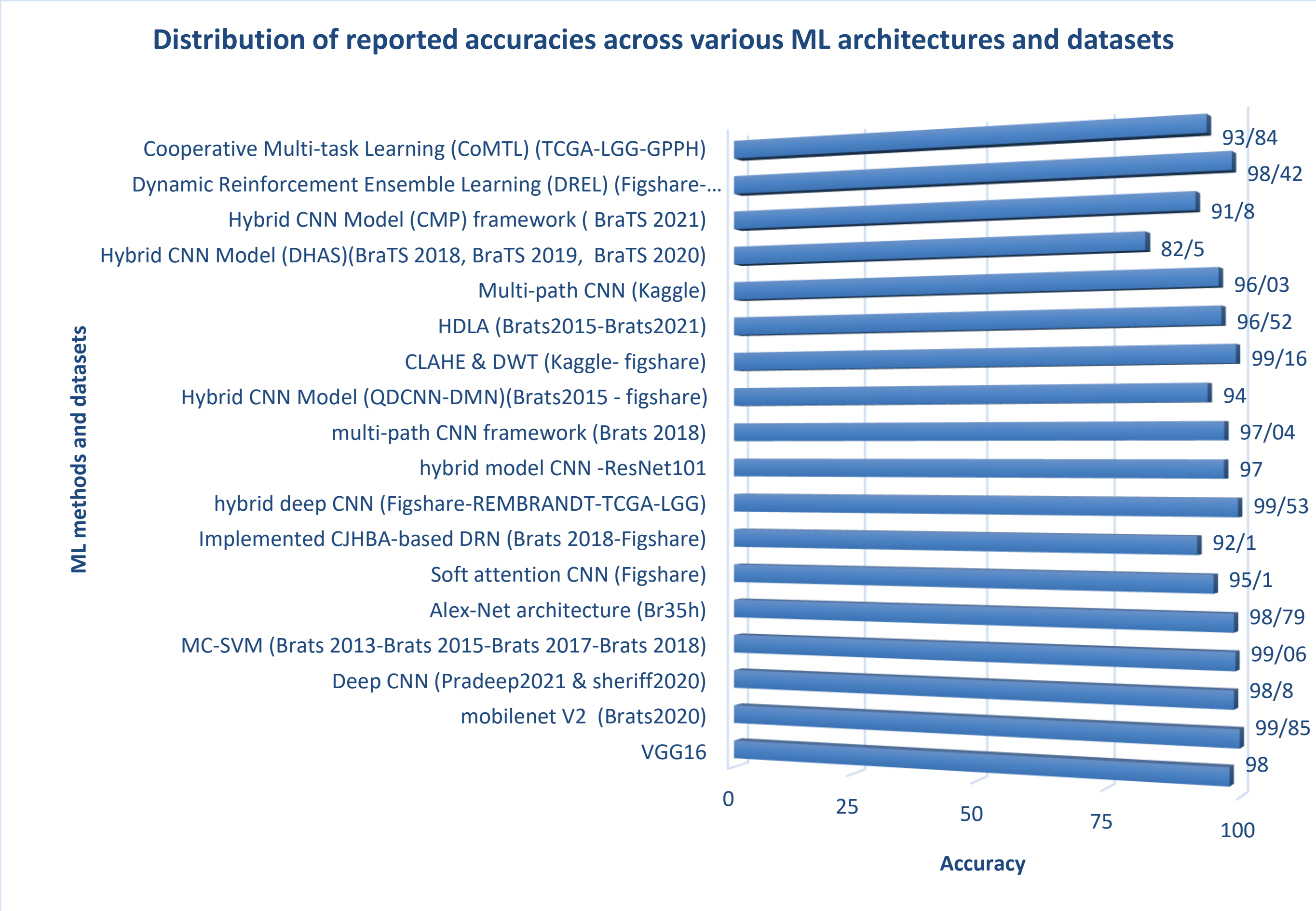

Fig. 3. Distribution of reported accuracies across ML architectures and Datasets.

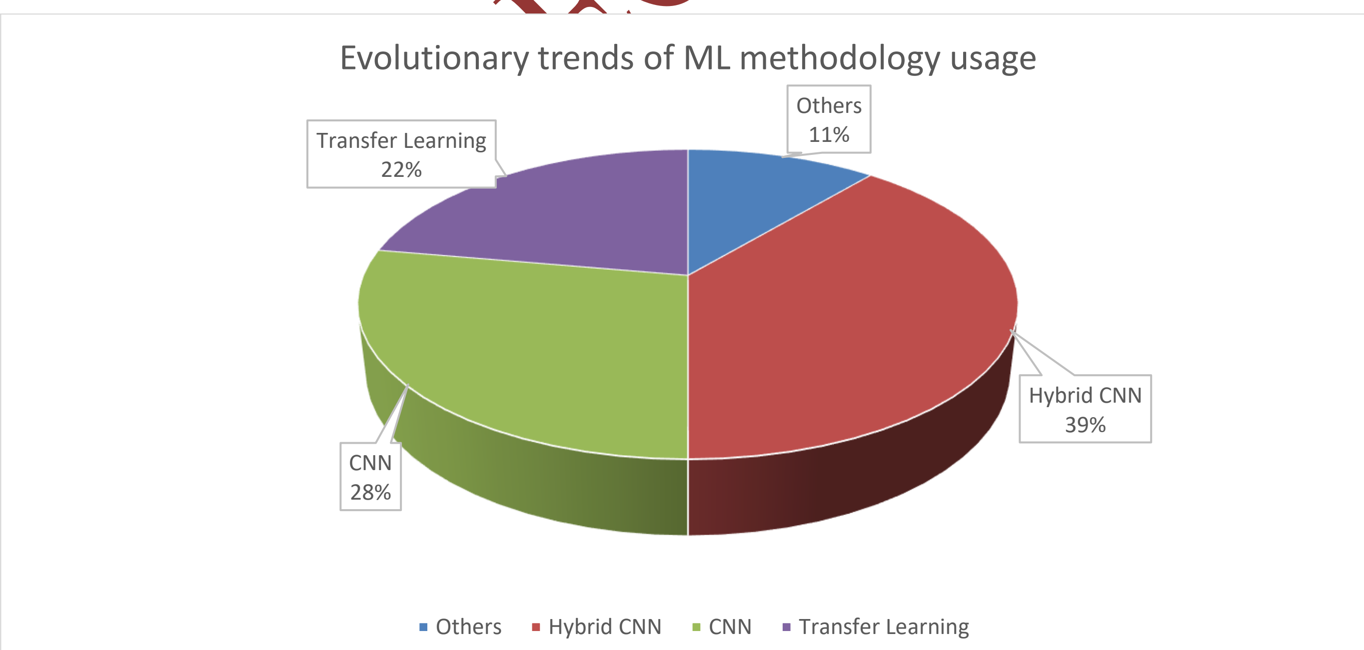

Fig. 4. Evolutionary trends of ML methodology usage.

The comparative analysis of the reviewed studies indicates that performance metrics are intrinsically linked to the complexity of the diagnostic task and the specificities of the datasets employed. For instance, the high accuracy of 99.85% reported for modality fusion and transfer learning using Mobile-Net-V2 [20] for glioma grade detection often pertains to binary classification tasks or highly curated datasets. Conversely, lower accuracy values observed in other frameworks, such as the hybrid CNN model (82.5%) [43], may reflect the challenges of multi-class classification, tumor grading, or the use of more heterogeneous real-world clinical data. Therefore, these metrics should be interpreted as an indication of the overall potential of ML techniques rather than a definitive ranking of algorithmic superiority across disparate experimental settings.

In addition to the different ML methods, according to the applied techniques, the datasets in different MRI experimental studies were different. Among the 18 reviewed articles, 5 articles used CNN, 4 articles utilized transfer learning, and 6 articles utilized a hybrid CNN.

The comparative analysis presented in Fig. 3 and Fig. 4 should be interpreted with caution, considering the inherent heterogeneity of the reviewed studies. As illustrated, the high accuracy rates are predominantly observed in studies utilizing the Figshare or Br35H datasets, which often involve simplified binary or four-class classification tasks. In contrast, frameworks evaluated on the BraTS challenges (e.g., DHAS and CMP) report lower numerical values (expressed as Dice scores) due to the high complexity of 3D volumetric segmentation and the inclusion of nested tumor sub-regions.

Furthermore, Fig. 4 reflects a significant architectural shift in the literature. The dominance of CNN-based models indicates their status as the baseline in the field, while the emergence of hybrid and attention-based models (though fewer in number) represents the state-of-the-art trend toward addressing clinical interpretability and data scarcity. Thus, these figures serve as a meta-trend analysis rather than a direct ranking of algorithmic performance, highlighting the field's progression toward more complex, multi-task learning paradigms.

To ensure the reliability of the comparative analysis, a comprehensive evaluation of the performance metrics reported across the reviewed studies was conducted. The results consistently indicate that high-performing models, particularly those utilizing deep CNN architectures and hybrid frameworks, achieve superior accuracy and sensitivity compared to traditional machine learning methods. This trend reflects a robust enhancement in feature extraction and classification capabilities, as evidenced by the reported metrics in the selected state-of-the-art publications. The consistency of these outcomes across different MRI datasets further supports the effectiveness of these advanced architectures in improving diagnostic precision.

V. Conclusions

This review systematically analyzed the role of key ML techniques in MRI-based brain tumor classification. Our study highlights that anatomical images play a crucial role in tumor diagnosis. Current research indicates that ML strategies can achieve high diagnostic performance, with reported accuracies ranging from 82.5% to 99.85% across various studies. However, it is crucial to note that these metrics are highly dependent on factors such as dataset size, number of classification categories, and validation protocols. While architectures like VGG16 and MobileNetV2 show promise, the scientific value of these results lies in their potential to assist clinical decision-making rather than their raw accuracy values. Future advancements should focus on evaluating these models using standardized, multi-center datasets to ensure their generalizability in real-world clinical environments.

To further develop this approach, it is essential to provide more MRI datasets and additional tumor characteristic data, such as PET scans. Creating a large dataset of anatomical images, including MRI and PET scans of patients with tumors, will be central to achieving high accuracy, reliability, and generalizability in diagnosis. This can be accomplished by utilizing large sample sizes and advanced statistical methods, including ML analysis.

By analyzing the results of multiple studies, the paper identifies and emphasizes significant trends, such as the dominance of CNN architectures, the crucial role of attention mechanisms, and the benefits of multimodal data integration (MRI alongside PET scans). This analysis offers valuable insights that can inform and direct future research.

Future research should focus on gathering and analyzing more MRI and PET scan data from patients with tumors, as there is currently a scarcity of these anatomical images compared with other diseases. The goal is to automate tumor detection based on MRI data by applying various classification techniques. To improve accuracy and other critical metrics in tumor detection, further research is required to develop more suitable imaging modalities.

In-depth studies will help identify which imaging modalities are most effective, and the application of robust ML techniques will facilitate dynamic, real-time analysis of findings and tumor detection.

The reviewed models are best positioned as clinical decision support tools rather than autonomous diagnostic systems, emphasizing their role in triaging or providing second opinions to radiologists.

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