

Received 21 September 2024, accepted 12 October 2024, date of publication 24 October 2024,
date of current version 11 November 2024.

Digital Object Identifier 10.1109/ACCESS.2024.3485895

RESEARCH ARTICLE

Brain Tumor Classification Using an Ensemble of Deep Learning Techniques

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This work was supported by the Deanship of Research and Graduate Studies at King Khalid University through the Large Research Project under Grant RGP 2/291/45.

ABSTRACT The article reflects on the classification of brain tumors where several deep learning (DL) approaches are used. Both primary and secondary brain tumors reduce the patient's quality of life, and therefore, any sign of the tumor should be treated immediately for adequate response and survival rates. DL, especially in the diagnosis of brain tumors using MRI and CT scans, has applied its abilities to identify excellent patterns. The proposed ensemble framework begins with the image preprocessing of the brain MRI to enhance the quality of images. These images are then utilized to train seven DL models and all of these models recognize the features related to the tumor. There are four models which are General, Glioma, Meningioma, and Pituitary tumors or No Tumor model, which helps in reaching a joint profitable prediction and concentrating solely on the strength of the estimation and outcome. This is a significant improvement over all the individual models, attaining a 99.43% accuracy. The data used in this research was gotten from Kaggle website and comprised of 7023 images belonging to four classes. Future work will focus on increasing the dataset size, investigating additional DL architectures, and enhancing real-time detection to improve the accuracy of diagnostic scans and their overall relevance to clinical practice.

INDEX TERMS Brain tumor, deep learning, ensemble, glioma, meningioma, MRI, pituitary.

I. INTRODUCTION

Brain tumors are swellings that result from the uncontrolled growth of tissue within the brain and could either be non-cancerous or cancerous. It can impact diverse areas of the brain and substantially alter one's living standards. In order to be treated and to survive it is crucial to be diagnosed and have the ailment detected early [1]. This is the stage where DL becomes useful in increasing the chances of diagnosing brain tumors. DL algorithms are effective in the identification

of patterns and is efficient in detecting tumors by analysing different medical images like the MRI and the CT scans. These models can also help the division of tumors from the encircling brain tissue, its content as benign or malignant, and the immediate positioning of the tumor during surgery. On its positive effects, there are several being listed as follows; better treatment results, precision, and speed in diagnosing the diseases [2], [3]. Such improvements are being made help of methods like CNNs, transferring learning, and segmentation structures like U-Net and SegNet. DL is almost at the precipice of revolutionizing the detection of brain tumors and thereby assist medical practitioners in the delivery of better

The associate editor coordinating the review of this manuscript and approving it for publication was Sun-Yuan Hsieh.

health care as well as improvement on the quality of life of patients with this disease [4], [5], [6].

Tumor in the context of this paper refers to an uncontrollable growth of cells within the central spinal canal or the brain. There are two types of tumors, namely, intracranial tumors which develops in the brain, and extracranial ones which spread or arise from other parts of the body. The normal functioning of the brain might be affected by the presence of tumor and these include headache, seizures, changes in cognition or personality, and neurological signs depending on the size and location of the tumor [7].

DL is a branch of AI and has emerged as a powerful technology to solve intricate problems in the medical context, especially when it comes to the identification of brain tumors. There are several Algorithms that can be used in DL models to analyze large amounts of medical imaging data such as MRI, CT scans to look for patterns and irregularities that may point towards the presence of a tumor. These models are trained on large data set to learn the minor differences between healthy and tumor tissue [8]. DL not only improves the specificity of the identification process but also brings more efficiency by replacing human operations with computers, which lowers the chance of mistakes. This has proved useful, especially in the early diagnose of brain tumors as this may greatly affect the results of the disease. Also worth pointing out is that there is a high potential of the appearance of more efficient diagnostic aids and individual treatment algorithms in the future because DL models are capable of learning from new data inspired [9], [51].

It is also now apparent, the ensemble learning's effectiveness in the detection of brain tumor. Whereas prior works have recently introduced a range of frameworks that utilize individual transfer learning models, these models often encounter false-positive prediction problems [10]. The term 'False Positive' in context with brain tumor detection means that the opportunity of a brain tumor is predicted by the model when in reality, there is no tumor present in the individual. They come with lots of stress and even may lead to additional, baseless operations. Our study incorporates a large database of brain tumor-positive and brain tumor-negative cases to formulate a more accurate model and minimize false-positive predictions, thus filling this research need.

In this study, an ensemble learning approach is used which combines the outcome of seven different transfer learning models. This ensemble model not only has high generalization and high prediction accuracy but also there is no chance of having false positive predictions. The ensemble system minimises the bias-variance trade-off and improves the model when applied to new datasets through incorporating a number of learners, and making the model more reliable. This robustness is especially advantageous for the deployment in the backend of IoT and smart devices, as it enhances current diagnostic methodologies.

The primary contributions of this research are as follows:

- A low false-positive rate is achieved by proposing an ensemble of transfer learning algorithms for the reliable detection of brain tumors.
- The performance of the proposed ensemble model is evaluated in comparison to the currently available state-of-the-art transfer learning models.
- The ensemble framework that has been proposed is capable of achieving high prediction accuracy and can be integrated into smart devices to facilitate the early detection of brain tumors.

The article is divided into sections: Section II includes literature review, Section III describes the technique, Section IV presents the findings, and Section V includes conclusion and future work.

II. LITERATURE STUDY

The application of DL models in the detection of brain tumors has seen considerable advancements in recent years. Researchers have employed a variety of techniques to enhance the accuracy and efficiency of these models.

Rajinikanth et al. [11] detected glioma and glioblastoma on MRI images using pre-trained VGG16 and VGG19 CNNs and various pooling methods. The study tested SoftMax, Decision Tree, KNN, and SVM classifiers with the ADAM optimizer on 2000 pictures. With VGG16 and average pooling, the DT classifier had the best classification accuracy (>99%), showing that DL can accurately identify and classify brain tumors. Deep neural networks and ML were used to identify brain cancer early in MRI data by Wani et al. [12]. They used CNNs like GoogleNet, AlexNet, VGG-19 DL models. Emphasizing data collection, preprocessing, and classification to address class imbalance and data uniformity, the study achieved a best accuracy of 90.625%. This work demonstrated the promising future of combining deep and conventional ML for improving brain tumor diagnosis. Li et al. [13] introduced the TransBTS network for brain tumor segmentation, employing a unique encoder-decoder architecture. During the encoding phase, a 3D CNN extracted spatial features to capture local 3D context information. These features were transformed into tokens and processed by a feature extractor. The decoder utilized Transformer-embedded information to enhance segmentation accuracy. Bashkandi et al. [14] employed eight EfficientNet models (B0-B7) to automate brain cancer MRI image categorization using DL. Among these, EfficientNet-B7 stood out with exceptional performance, achieving a training accuracy of 99.71% and a validation accuracy of 99.67%. This model not only surpassed traditional CNN models but also offered faster image processing. The study showed that optimizing layer combinations, picture quality, and channel integration in EfficientNet improves MRI image classification accuracy. More et al. [15] developed a system for object and image detection using a large dataset and the DL technique

CNN(CNN), achieving an 89% accuracy rate. The system currently provides a binary tumor presence output (yes/no), and future work will include classifying tumor type, size, and location. A web application was created to display results and provide tumor information and treatment details.

To enhance brain tumor categorization, Afshar et al. [16] employed CapsNets. They acknowledged that standard diagnosis methods might be inaccurate, yet brain tumor types are crucial for therapy and patient survival. While CNNs have been used to automate this process, they do not fully utilize spatial relations crucial for tumor classification. Their study considers the tumor's surrounding tissue, improving classification accuracy and outperforming other methods. Nandihal et al. [17] proposed a method that integrates the Region Growth Algorithm with tumor segmentation to extract texture features from Gray-Level-Run-Length-Matrix and Center-Symmetric-Local-Binary-Patterns. This technique is a promising option for the early identification of tumors in MRI. It achieved a high accuracy of 99.80%, with a sensitivity of 0.97% and specificity of 0.85%. Kumar et al. developed an advanced brain tumor detection technique [18]. Image segmentation, feature extraction, and classification by texture, shape, and intensity are done in this procedure. To discover relevant characteristics from MRI scans, they used Particle Swarm Optimization for feature selection and an SVM classifier for cancer classification. MRI scans were retrieved from a tumor database online. A new brain tumor categorization method was suggested by Gumaei et al. [19]. A regularized extreme learning machine algorithm, picture preprocessing, and hybrid feature extraction are used in this method. On a public brain imaging dataset, their technique surpassed others with 94.23% classification accuracy. An automated brain tumor categorization system will help radiologists and clinicians make accurate diagnosis and treatment choices, overcoming current system limitations.

ZainEldin et al. [20] suggested a BCM CNN model for brain tumor classification from MRI data. This model classified images using the BRATS brain tumor dataset. The ADSCFGWO approach optimized hyperparameters. For brain tumor segmentation, a 3D U-Net achieved 99.33% accuracy. The model outperformed SVM, K-NN, LD model, and DT in classification with 99.99% accuracy. Despite their popularity, many DL methods train new networks. Transfer learning using ImageNet-trained networks is underutilized. Only one research has evaluated GoogLeNet in this setting, whereas other prominent networks like ResNet18 [21] have not. In this work, the ResNet18 model is tested for brain tumor detection from MRI scans. Hossain et al. [22] extracted brain tumors from 2D MRI data using classical classifiers, CNNs, and fuzzy C-Means clustering. A CNN created using Keras and TensorFlow was used with logistic regression, SVM, Naive Bayes, KNN, random forest, and MLP. CNN outperforms classical classifiers with 97.87% accuracy. Vaiyapuri et al. [23] created the ELCAD-BTC model to identify brain tumors using MRI. Ensemble learning

using feature extractors like EfficientNet, DenseNet, and MobileNet, denoising autoencoders for tumor identification, and Gabor filtering for noise reduction were used. They also tuned hyperparameters using the Social Spider Optimization Algorithm (SSOA). This strategy was tested using the BRATS 2015 database to improve MRI-based brain tumor classification and aid early diagnosis. The exceptional efficacy of MobileNet-V2 was underscored by Arbane et al. [24], who implemented transfer learning with three CNN architectures: ResNet, Xception, and MobileNet-V2. The latter achieved a 98.24% accuracy and a 98.42% F1-score. Their research emphasizes the practicality of pre-trained models and the superiority of DL, thereby demonstrating a substantial advancement in medical image analysis.

In order to detect brain tumors in magnetic resonance imaging (MRI) images, Raut et al. [25] implemented a CNN model. In order to generate an adequate amount of data, mitigate noise, and improve precision, they implemented image augmentation and preprocessing methodologies. The CNN was trained on preprocessed MRI images to classify new images as either normal or tumorous based on the extracted features. The model achieved a testing accuracy of 95.55% thanks to the assistance of autoencoders and K-means algorithms in segmenting the tumor region, thereby automating and expediting the detection of brain tumors. Medical science is dependent on the accurate diagnosis of brain tumors and the prediction of their survival rates. It has been demonstrated that the identification of tumors is enhanced by DL models such as CNN and VGG-16. The efficacy of these models was demonstrated through an examination of 253 MRI images, with VGG-16 outperforming despite its slower processing speed and increased memory usage [26]. Effective treatment necessitates early detection of brain tumors. With minimal preprocessing and only 35 epochs, a novel convolutional-based system accurately classifies MRI brain images as tumorous or non-tumorous, achieving a 96.08% accuracy and a 97.3 F1-score. Future research will concentrate on neurosophical concepts, as this study underscores the significance of ML in the identification of brain tumors and the planning of therapy [27]. The fused CNN method for the classification of brain tumors based on MRI was first introduced by Kushwaha et al. [28]. This technique used VGGNet 16, AlexNet, Inception Net, and Xception Net for preprocessing, segmentation, feature extraction, and classification to reliably classify tumor types. The FCNN method obtained 97.4% to 98.2% classification accuracy by segmenting images with significant maps. Using a combination of computational imaging and ML techniques, Suresha et al. [29] introduced a method for identifying brain tumors in MR images. Binary thresholding and spot detection are implemented by the system to extract features from images, which are then clustered using the K-Means technique. The SVM is trained to differentiate between normal and tumor brain tissue using the resulting feature set. This method automatically identified brain tumors with high precision and speed.

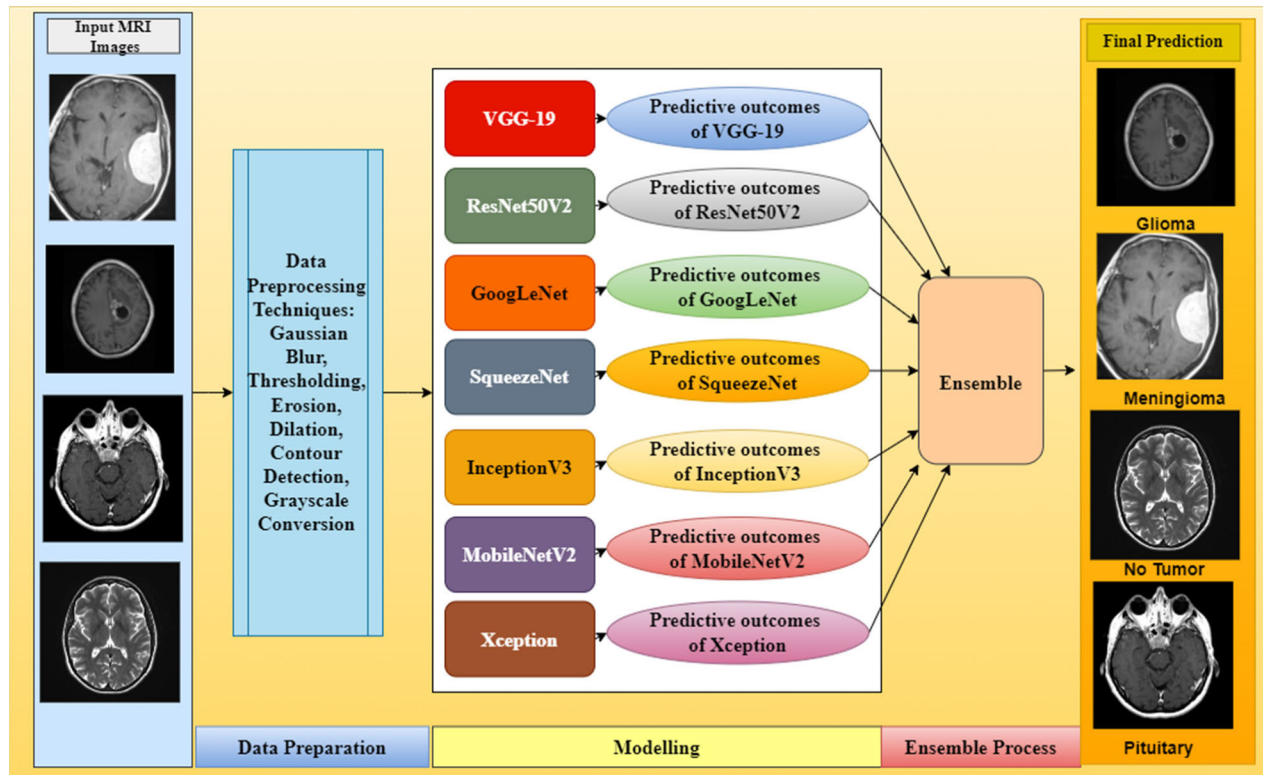


FIGURE 1. Workflow of our proposed approach for brain tumor detection.

The rapid progress in the use of DL models for brain tumor detection is underscored by these advancements, which offer promising tools for enhancing diagnostic accuracy and patient outcomes in clinical applications.

III. MATERIALS AND METHODS

A. PROPOSED FRAMEWORK

The general architecture of the proposed ensemble framework (shown in Fig. 1) for the brain tumor detection using DL starts with inputting the MRI images of the human brain; the images are further preprocessed to eliminate noise, normalized and resized. The preprocessed images mentioned above are then applied to train seven distinct convolutional DL models where each model brings prior knowledge of features to search for when differentiating between the existence of the tumorous portions of the brain and non-existent ones. All the models provide different predictive results of the existence of the tumors like Glioma, Meningioma, No Tumor, and Pituitary Tumor. These individual predictions are then combined employing an ensembling method in which all the models' strengths are harnessed to create a more accurate prediction. The given ensembled output acts as a final verdict of the classification of the brain MRI images into one of the 4 categories, which makes the diagnosis remarkably accurate. Decision fusion in the ensemble framework was much better than the individual models, attaining almost negligible false positive rates.

B. DEEP LEARNING MODELS

1) VGG-19

Medical imaging analysis has effectively detected brain tumors using VGG-19, a VGG neural network variation. This 19-layer DL model has 16 convolutional layers and 3 FCLs with 138 million parameters. The architecture processes 3D MRI images using convolutional and max-pooling techniques followed by ReLU activation functions. The model captures characteristics at several sizes by organising the convolutional layers into five blocks with increasing numbers of filters (64, 128, 256, 512, and 512). The model makes predictions using extracted characteristics and 4096-neuron FCLs. VGG-19's strong design can learn spatial hierarchies of information from MRI images to accurately identify and segment brain tumors. Fine-tuning the pre-trained VGG-19 model on a large dataset of labelled MRI images can improve its performance, helping radiologists and physicians detect brain tumors early [30].

2) ResNet50V2

It is a powerful deep CNN that solves the vanishing gradient problem that hinders deep network training. This 50-layer DL model has 25.6 million parameters. To process 3D MRI images, each layer performs convolutional, batch normalisation, and ReLU activation. The network has 16 residual blocks with 3 convolutional layers and 64, 64, and 256 filters. Residual connections let the model learn residual functions

instead of the target output, improving feature extraction. The model uses spatial attention to focus on relevant input data areas. Each residual block has three layers: a 1×1 convolution to decrease dimensionality, a 3×3 for spatial processing, and another 1×1 to restore dimensionality. Batch normalisation and ReLU activation precede convolutional layers in ResNet50V2. This pre-activation structure boosts training efficiency and accuracy, making ResNet50V2 ideal for image classification, object identification, and semantic segmentation [31].

3) GoogLeNet

Inception Network version called GoogLeNet. There are 22 layers and 6.8 million parameters in this DL model. The layers handle 3D MRI images using convolutional, pooling, and ReLU activation processes. Nine Inception modules with numerous parallel branches, filter sizes (1×1 , 3×3 , 5×5), and pooling layers allow the model to collect information at many scales. The network can collect geographical features while efficiently computing with this configuration. Reduced dimensionality using 1×1 convolutions reduces computational cost and overfitting. Assistive classifiers in intermediary layers help GoogLeNet enhance gradient flow and lessen the vanishing gradient issue during training. This novel, economical structure improves picture classification [32].

4) SQUEEZENET

It is a small deep CNN with AlexNet-like accuracy and fewer parameters. Its 18 layers and 1.2 million parameters make this DL model compact and computationally efficient. For 3D MRI images, each layer performs convolutional, max-pooling, and ReLU activation. The network uses a novel “fire” module with a squeeze layer (1×1 convolutions) and an expand layer (1×1 and 3×3 convolutions) for efficient feature extraction. A global average pooling layer and dropout layer increase generalisation in SqueezeNet. SqueezeNet reduces model size by utilising 1×1 filters instead of bigger ones, reducing input channels to 3×3 , and downsampling late to retain feature information in previous layers. The network has 50x fewer parameters than AlexNet yet achieves equivalent picture classification accuracy. SqueezeNet’s small size and efficiency make it suited for resource-constrained mobile and embedded devices. SqueezeNet can accurately identify and segment brain tumors in real time in clinical situations with minimal processing resources and memory [33].

5) InceptionV3

Deep CNN perform better and more efficiently using InceptionV3, an improved architecture. InceptionV3 uses factorised convolutions and more aggressive regularisation to build on its predecessors. It has 42 layers and 23.6 million parameters. For 3D MRI images, each layer performs convolutional, pooling, and ReLU activation procedures. The model captures characteristics at numerous scales using

multiple Inception modules with parallel branches, filter sizes (1×1 , 3×3 , 5×5 , and 7×7), and pooling layers. InceptionV3 improves generalisation using factorised 7×7 convolutions, spatial attention, and a global average pooling layer. The model regularises training via batch normalisation and dropout layers. It improves training convergence using batch normalisation, auxiliary classifiers, and label smoothing. The architecture’s modules analyse several spatial scales inside the network to collect multi-level characteristics. These design decisions allow InceptionV3 to classify images with high accuracy on demanding datasets like ImageNet while being computationally efficient, making it appropriate for many real-world applications [34].

6) MobileNetV2

MobileNetV2, a cutting-edge CNN architecture for mobile and embedded vision applications, prioritises accuracy and processing economy. It’s 53 layers and 3.5 million parameters make it compact and computationally efficient. Each layer uses convolutional, depthwise separable, and ReLU activation to handle 3D MRI images. A unique “bottleneck” layer of expansion (1×1 convolutions), depthwise separable, and linear layers optimises feature extraction in the network. Additionally, MobileNetV2’s linear bottleneck prevents non-linearities in thin layers, preserving information during feature extraction. The architecture uses inverted residual blocks with shortcut connections to optimise gradient flow and training efficiency. With a depth multiplier to alter network width, MobileNetV2 can balance latency and accuracy for object identification, segmentation, and classification on resource-constrained devices [35].

7) Xception

The depthwise separable convolutions of the DL architecture Xception, short for “Extreme Inception,” improve the Inception model. This method boosts efficiency and effectiveness, making Xception ideal for difficult jobs like brain tumor identification. This 36-layer model has 22.9 million parameters. Each layer uses convolutional, depthwise separable, and ReLU activation to handle 3D MRI images. The network’s “separable convolution” layer divides ordinary convolutions into depthwise and pointwise convolutions, lowering computational cost. It has entry, middle, and exit flow modules with convolutional blocks, residual connections, and ReLU activations. Xception is trained on medical imaging datasets like MRI images to detect brain tumors using complicated patterns and characteristics. Xception also uses residual connections, spatial attention, and a global average pooling layer to boost generalisation. Xception accurately distinguishes tumors from healthy brain tissue, making it a potent medical diagnostic tool. The model’s capacity to handle high-dimensional data and represent complicated spatial hierarchies helps detect brain tumors [35].

Table 1 highlights each model’s benefits and shortcomings, especially for brain tumor identification, which typically

TABLE 1. Advantages and disadvantages of 7 DL models.

Model	Advantages	Disadvantages
VGG-19	- Simple architecture - Deep layers capture intricate features - High performance on small datasets	- Large number of parameters - High computational cost - Slow training
ResNet50V2	- Residual connections mitigate vanishing gradient problem - Deeper network without degradation	- High computational cost - Complex architecture - May require large datasets
GoogLeNet	- Inception modules reduce computational cost - Efficient parameter usage	- Complex architecture - Harder to fine-tune - May not perform well on very small datasets
SqueezeNet	- Good accuracy - Small model size - Low computational cost - Suitable for deployment on devices with limited resources	- Lower accuracy compared to larger models - May struggle with very complex patterns
InceptionV3	- Improved efficiency with Inception modules - Good accuracy - Lower computational cost than traditional CNNs	- Complex architecture - Requires significant fine-tuning - Higher memory usage
MobileNetV2	- Lightweight - Efficient on mobile and embedded devices - Good balance of accuracy and performance	- Lower accuracy on high-complexity tasks - Limited capacity compared to larger models
Xception	- Depthwise separable convolutions improve efficiency - High accuracy - Good at capturing spatial hierarchies	- High computational cost - Complex architecture - Requires large datasets for optimal performance

requires sophisticated and high-dimensional medical imaging data.

C. LOSS FUNCTION

The loss function in DL models measures performance and aims to minimise loss for improved performance. It assesses model predictions and adjusts layer weights to enhance accuracy. Probabilistic loss and regression loss are the major loss functions. This research employs categorical cross-entropy, a probabilistic loss function, for multiclass classification issues like brain tumor diagnosis. The categorical cross-entropy loss function calculates output layer losses using probability values of distinct classes. Input photos are classified into tumor varieties by the model for brain tumor identification. The model reaches saturation faster with the cross-entropy-based loss function for inputs with larger boundaries.

Mathematically, for inputs $(x_1, x_2, x_3, \dots, x_n)$, the outputs are $(y_1, y_2, y_3, \dots, y_n)$ respectively. This means x_1 has the actual output y_1 , and the output predicted by the model is \hat{y} ,

where \hat{y} for the i^{th} input is calculated as:

$$\hat{y}_i = f(w_i^T * x_i + b_i)$$

Here, \hat{y}_i is the predicted output for the i th input, w_i^T represents the corresponding weights, b_i is the bias value, and f is a non-linear activation function called Rectified Linear Unit (ReLU), which converts negative values to zero while keeping positive values unchanged. The ReLU activation function is defined as:

$$RELU(f) = \max(0, x)$$

For a multiclass classification problem, the loss function φ for C classes are defined as:

$$\varphi(\hat{y}_i, y_i) = - \sum_{i=1}^C y_i \log \hat{y}_i$$

The cost function for k training samples is then formulated as:

$$\lambda(w, b) = -\frac{1}{k} \sum_{i=1}^k \varphi(\hat{y}_i, y_i)$$

The cost function updates network weights and biases, increasing brain tumor detection and classification.

D. ENSEMBLE LEARNING APPROACH

It improves system performance and resilience by integrating model predictive power [36]. Bias, variation, and irreducible errors affect a model's predictive power. The model error is the sum of several errors:

$$\text{Model Error} = \text{Bias Error} + \text{Variance Error} + \text{Irreducible Error}$$

Bias error quantifies the average difference between expected and actual values. High bias causes underfitting, where the model misses significant training patterns. Variance assesses model sensitivity to training data. High variance leads to overfitting, where the model performs well on the training data but poorly on validation data. The goal is to minimize both bias and variance errors. The reducible error (bias and variance) can be minimized through learning, while irreducible error, caused by noise and outliers in the data, cannot be eliminated.

Probability averaging, Max-voting, and weighted probability averaging are popular ensemble methods. This study detects brain tumors using probability averaging. The ensemble process described as follows: Suppose we use T different models $(T_1, T_2, T_3, \dots, T_m)$ to classify n classes. For i^{th} input x_i , the probability values for each class from model T_1 are:

$$Z_{T_1}^i = (P_{1T_1}^i, P_{2T_1}^i, P_{3T_1}^i, \dots, P_{nT_1}^i)$$

This process is repeated for all T models $(Z_{T_1}^i, Z_{T_2}^i, \dots, Z_{T_m}^i)$. The final prediction score for the i^{th} input

using probability averaging is:

$Z_{ensemble}$

$$= \left\{ \frac{\sum_{k=1}^m P_{1T_k}^i}{m}, \frac{\sum_{k=1}^m P_{2T_k}^i}{m}, \frac{\sum_{k=1}^m P_{3T_k}^i}{m}, \dots, \frac{\sum_{k=1}^m P_{nT_k}^i}{m} \right\}$$

$$= \{T_1, T_2, T_3, \dots, T_m\}$$

The final prediction is the class with the highest average probability value:

$$\text{Predicted Class} = \max(T_1, T_2, T_3, \dots, T_m)$$

The predicted class is then compared with the actual label to determine the error and accuracy. This approach ensures a robust and accurate classification of brain tumor types by leveraging the strengths of multiple models.

IV. EXPERIMENTAL RESULTS AND EVALUATIONS

A. DESCRIPTION OF THE DATASET

For the simulation of the proposed methodology, the dataset was sourced from Kaggle [37], which includes images from four classes: Pituitary (1757), Glioma (1621), Meningioma (1645), and No tumor (2000). The dataset contains a total of 7,023 images, which are divided into training and testing data as reflected in Table 2. Although the dataset is imbalanced, the authors conducted experiments with a balanced dataset as well. The results were consistent, indicating that the class imbalance does not affect the outcomes. At this stage, the data is partitioned into training (70%) and validation (30%) sets.

TABLE 2. Split of training and testing data.

Name of Class	Glioma	Meningioma	No tumor	Pituitary
Training	1135	1152	1400	1230
Testing	486	493	600	527

B. DATA COLLECTION AND PREPROCESSING

The first step in our process is to pull a diverse dataset of MRI images from Kaggle which will help us build our models. After that, the data is subject to rigorous preprocessing to eliminate noise and obtain uniformities in the inputs. First, the images are pre-processed by applying Gaussian blur to eliminate unnecessary noise and fine details. The next step is called thresholding where the image is divided into foreground and background to make the features such as tumor, more visible. We then use erosion to eliminate small noise points and dilation to undo the effects of erosion we had done on the objects. Following thresholding function, contours are detected to determine the appearance and configuration of the major objects in the images. Because the size of images may be different in the given dataset, all images are normalized to the same size of 256×256 pixels. In order to home in on regions of interest we find the vertices of the

TABLE 3. Performance evaluation metrics on 4-class brain MRI datasets for each DL and ensemble approach.

Model	Class Name	Precision	Recall	f1-score	Specificity	Accuracy (%)	AUC
VGG-19	G	0.9797	0.9938	0.9867	0.9938	98.43	0.9938
	M	0.9819	0.9899	0.9859	0.9944		0.9921
	No	0.9882	0.9733	0.9807	0.9954		0.9843
	P	0.9867	0.9829	0.9848	0.9956		0.9892
ResNet50V2	G	0.9777	0.9918	0.9847	0.9932	98.34	0.9925
	M	0.9779	0.9878	0.9828	0.9932		0.9905
	No	0.9915	0.9733	0.9823	0.9967		0.9850
	P	0.9848	0.9829	0.9839	0.9949		0.9889
GoogLeNet	G	0.9857	0.9959	0.9908	0.9957	98.81	0.9958
	M	0.9839	0.9919	0.9879	0.995		0.9935
	No	0.9949	0.9800	0.9874	0.998		0.9890
	P	0.9867	0.9867	0.9867	0.9956		0.9911
SqueezeNet	G	0.9797	0.9938	0.9867	0.9938	98.58	0.9938
	M	0.9839	0.9899	0.9869	0.9950		0.9924
	No	0.9932	0.9767	0.9849	0.9973		0.9870
	P	0.9848	0.9848	0.9848	0.9949		0.9899
Inceptionv3	G	0.9878	0.9959	0.9918	0.9963	98.96	0.9961
	M	0.9879	0.9899	0.9889	0.9963		0.9931
	No	0.9933	0.9833	0.9883	0.9973		0.9903
	P	0.9886	0.9905	0.9896	0.9962		0.9934
MobileNetV2	G	0.9898	0.9979	0.9939	0.9969	99.19	0.9974
	M	0.9899	0.9919	0.9909	0.9969		0.9944
	No	0.9950	0.9867	0.9908	0.9980		0.9923
	P	0.9924	0.9924	0.9924	0.9975		0.9949
Xception	G	0.9898	0.9979	0.9939	0.9969	99.24	0.9974
	M	0.9899	0.9939	0.9919	0.9969		0.9954
	No	0.9966	0.9867	0.9916	0.9987		0.9927
	P	0.9924	0.9924	0.9924	0.9975		0.9949
Ensemble		0.9941	0.9945	0.9943	0.9981	99.43	0.9963

* Glioma (G), Meningioma (M), No Tumor (No) and Pituitary (P)

contours for accurate zooming. In brain MRI analysis, intensity normalization involves the process of scaling the pixel

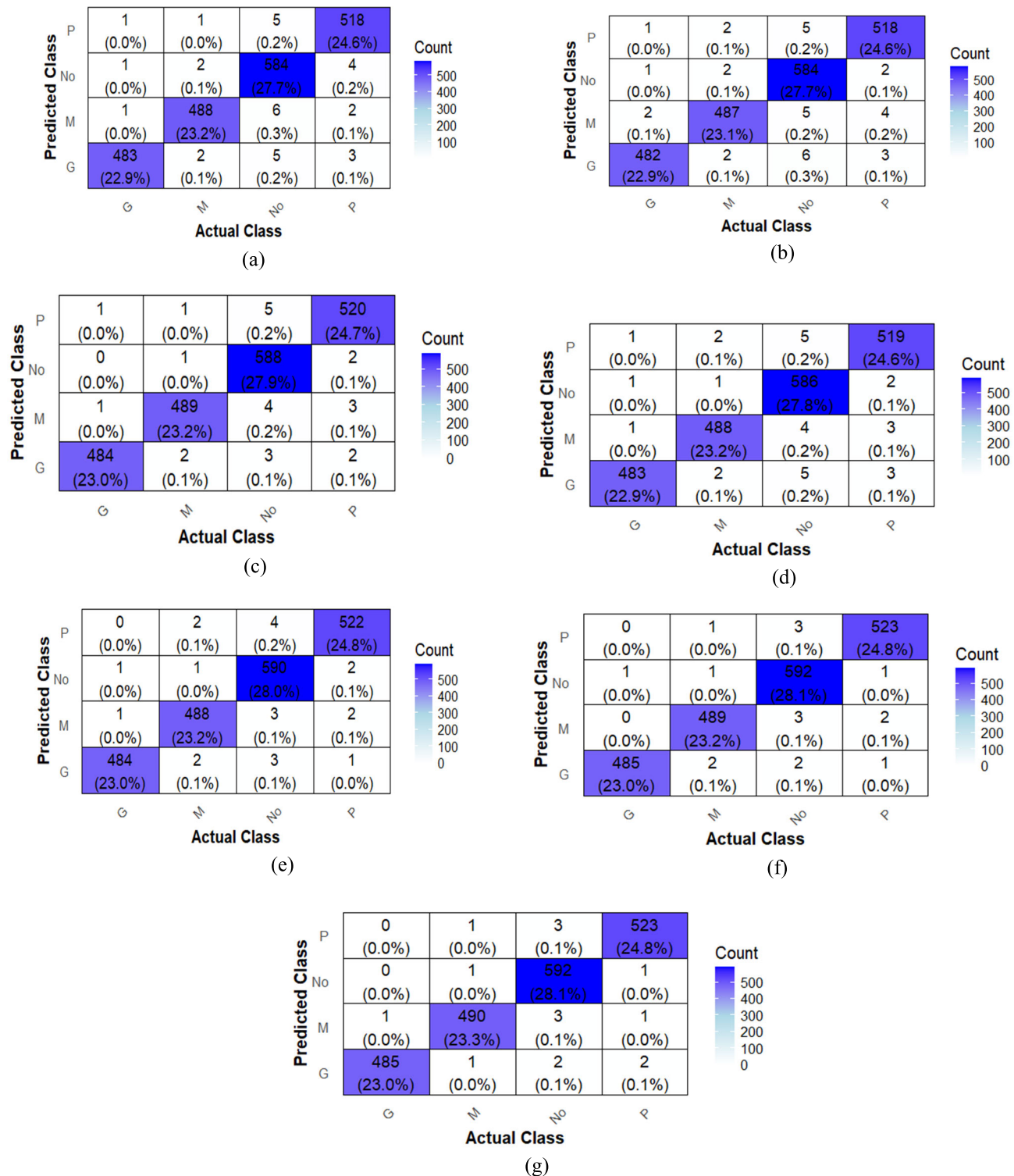


FIGURE 2. Confusion Matrix for (a) VGG-19, (b) ResNet50V2, (c) GoogLeNet, (d) SqueezeNet, (e) InceptionV3, (f) MobileNetV2 and (g) Xception.

intensity values in the images coming from different scanners and collected during different time periods. This step helps to minimize such issues as poor resolution, distortion,

inhomogeneity, misinterpretation, and motion heterogeneity. Lastly, each image is converted to grayscale to reduce its dimensionality and focus on relevant characteristics. All these

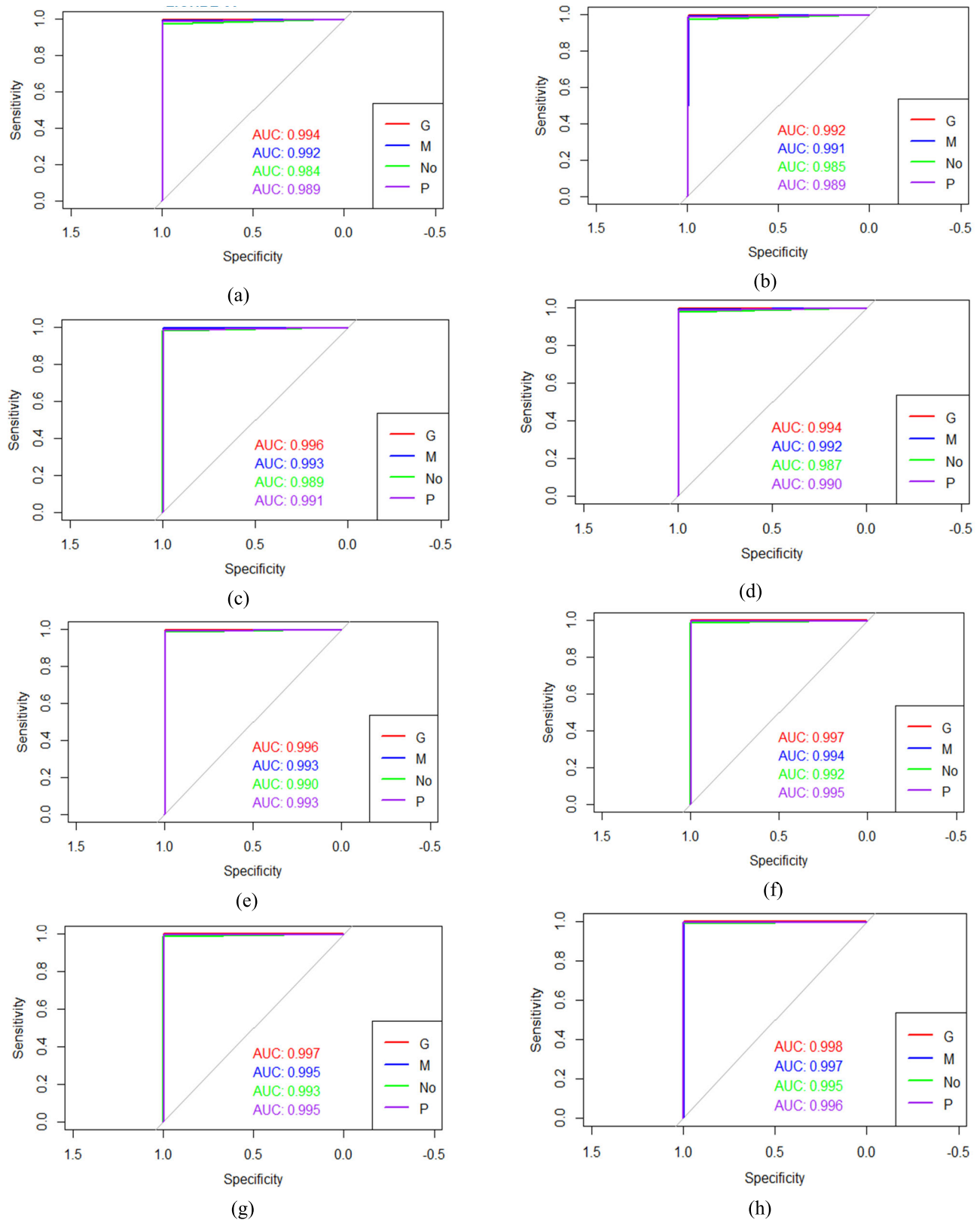


FIGURE 3. AUC ROC curve for (a) VGG-19, (b) ResNet50V2, (c) GoogLeNet, (d) SqueezeNet, (e) InceptionV3, (f) MobileNetV2 and (g) Xception (h) Ensemble approach.

preprocessing steps ensure that the final dataset is as clean as possible in order to allow for highly reliable and accurate diagnostic outcomes.

C. PERFORMANCE EVALUATION

The following performance metrics are used for evaluation.

1. $Precision = \frac{True\ Positive(TP)}{TruePositive + FalsePositive(FP)}$
2. $Sensitivity\ or\ Recall = \frac{True\ Positive}{True\ Positive + False\ Negative(FN)}$
3. $F1 - Score = \frac{2x(Precision\ x\ Recall)}{(Precision + Recall)}$
4. $Specificity = \frac{True\ Negative\ (TN)}{True\ Negative + False\ Positive}$
5. $Accuracy = \frac{TP + TN}{TP + TN + FP + FN}$

The confusion matrix and performance indicators show good accuracy and efficacy in classifying brain tumors using the Xception DL model. The confusion matrix compares the model's predictions to the real classes as rows indicate actual tumor types and columns represent anticipated tumor types. Each class's performance metrics are listed below:

Glioma: In this model, accuracy was 0.9898, recall 0.9979, F1-score 0.9939, specificity 0.9969, and AUC 0.9974. This suggests that the model accurately predicts Glioma tumors with few false positives and negatives.

Meningioma: The model had 0.9899 accuracy, 0.9939 recall, 0.9919 F1-score, 0.9969 specificity, and 0.9954 AUC for meningioma. With good precision and recall, the model detects Meningioma tumors well.

No tumor: The model had 0.9966 precision, 0.9867 recall, 0.9916 F1-score, 0.9987 specificity, and 0.9927 AUC. This shows the model's great specificity and precision in tumor absence detection.

Pituitary: the model had 0.9924 accuracy, 0.9924 recall, 0.9924 F1-score, 0.9975 specificity, and 0.9949 AUC. A balanced precision and recall show that the model detects Pituitary tumors reliably.

The model's accuracy was 99.24% and AUC 0.9951. These measures show the model's effective brain tumor classification. We also analyzed the confusion matrices and performance measures for the other six DL models in our study. Precision measured each DL model's ability to prevent false positives by showing the fraction of real positive predictions among all positive predictions. Recall assessed the model's ability to detect true cases by comparing true positive predictions to all positives. The harmonic mean of precision and recall, the F1-score, balanced the model's performance. The model avoided false negatives by identifying negative cases with specificity. The model's accuracy measured its predictions' accuracy, while AUC scored its ability to distinguish between classes, summarizing its performance across threshold settings. Figures 2 and 3 show confusion matrix and

AUC ROC curve for seven DL models and ensemble technique. Performance metrics on 4-class brain MRI datasets for each ensemble DL model are shown in Table 3. The performance of various DL models on the same dataset is summarized in Table 4.

The brain tumor detection ensemble architecture uses advanced transfer learning for high accuracy and reliability. Seven DL models were used. An ensemble technique combines the predictions of each model for these tumors. This method uses each model's strengths to make a more accurate prediction. Evaluation measures show that the ensemble strategy outperforms individual models. Most positive predictions are accurate with the framework's 0.9941 precision. The model detects virtually all tumor cases with a recall of 0.9945, reducing missed diagnoses. F1, which balances precision and recall, is 0.9943, proving the model's efficacy. With 0.9981 specificity, non-tumor patients are properly diagnosed, decreasing false positives. With 99.43% accuracy, the ensemble framework is confident in its diagnostic powers. AUC 0.9963 shows the model's high performance across all classification criteria. Multiple transfer learning models work together to improve brain tumor detection with high accuracy, specificity, and low false positive rates. The accuracy and comprehensiveness of this diagnostic tool advances medical imaging and cancer diagnosis.

TABLE 4. Various DL model performance against the suggested model on the same dataset [38].

Authors	Models	Optimizer	Accuracy (%)
Benkrama et al. [40]	Apache Spark, CNN, EfficientNetB1	RMSprop	97.00
Gómez et al. [41]	InceptionV3	SGD	97.12
Wankhede et al. [42]	ResNet50-152	RMSprop	98.00
Albalawi et al. [43]	Federated learning-based CNN	SGD	98.00
Hencya et al. [44]	Xception	Adam	98.07
Ali et al. [45]	ShuffleNet with SVM	SGD	98.40
Krishnan et al. [46]	Rotation Invariant Vision Transformer	Adam	98.60
Rahman et al. [47]	Dilated PDCNN structure with ML classifiers	Adam	98.67
Wang et al. [48]	Randomized vision transformer with token merging (RanMerFormer)	SGD	98.86
Bansal et al. [49]	CNN-SVM	RMSprop	99.00
Haque et al. [50]	NeuroNet19- Explainable DNN	Adam	99.30
Stephe et al. [51]	Osprey Optimization Algorithm with DL (BTDC-OOADL)	SGD	99.39
Proposed Model	Ensemble of 7 DL Models	Adam	99.43

V. CONCLUSION

The proposed ensemble framework for brain tumor classification using DL techniques demonstrates a significant

advancement in the field of medical image analysis. By leveraging the strengths of seven individual transfer learning models, the ensemble approach achieves a high accuracy of 99.43% with minimal false positive rates, thereby providing a reliable and comprehensive diagnostic tool. The use of a robust dataset from Kaggle ensures a diverse and representative sample of brain tumor types, enhancing the model's generalizability and performance. The success of this framework underscores the potential of DL in transforming brain tumor detection and diagnosis, making early intervention more feasible and effective. Future work will aim to further refine this approach by incorporating larger datasets, experimenting with cutting-edge DL architectures, and developing real-time detection capabilities to improve clinical applicability and patient outcomes.

AUTHORSHIP CONTRIBUTIONS

All authors contributed equally to this work.

DATA AVAILABILITY

Brain Tumor MRI Dataset are online available from Kaggle: <https://www.kaggle.com/datasets/masoudnickparvar/brain-tumor-mri-dataset>

ACKNOWLEDGMENT

The authors extend their appreciation to the Deanship of Research and Graduate Studies at King Khalid University for funding this work through Large Research Project under grant number RGP2/291/45.

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