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Brain Tumor Detection from MRI Images Using an Ensemble-Based Machine Learning Framework

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Abstract **The early detection of brain tumors from MRI images is critical for effective treatment planning. Still, manual analysis of these images is time-consuming and prone to inter-observer variability. This paper suggests a machine learning framework for automated brain tumor detection that uses an ensemble of classifiers to make it more accurate and reliable. The suggested framework combines Support Vector Machine (SVM), Random Forest (RF), and k-Nearest Neighbor (k-NN) classifiers. It uses a majority voting method at the decision level to make final predictions. The model uses both handcrafted texture features from the Gray-Level Co-occurrence Matrix (GLCM) and deep features from a pre-trained ResNet50 model to make it more effective at distinguishing between things. The framework was tested using three publicly available MRI datasets: Figshare, SARTAJ, and BR35H. These datasets had a total of 9,826 images. The ensemble model got 95.2% correct, with 94.6%, 94.1%, and 94.3% for precision, recall, and F1-score, respectively. This was better than any of the individual classifiers. The area under the curve (AUC) was also 0.97, which means it was very good at telling the difference between things. The experimental results demonstrate that the ensemble approach not only delivers a robust solution but also ensures computational efficiency, rendering it appropriate for clinical applications. This framework shows that it could be used in computer-aided diagnosis systems to detect brain tumors in real time and perform better across different datasets. The suggested ensemble-based framework is a scalable, efficient, and reliable way to use MRI to find brain tumors. It gets around the problems that single classifiers have in medical imaging.**

Keywords **Brain tumor detection; MRI; Ensemble learning; Machine learning; Medical informatics**

I. Introduction

Brain tumors are a significant problem and rank as the second most common cause of cancer deaths in humans. Due to the complicated structure of the brain, the type of some tumors and the aggressive growth of some tumor types, precise diagnostics and classification are crucial. MRI is the preferred imaging technique for brain tumors owing to its superior soft tissue contrast, resolution, and non-invasive nature. Human interpretation of MRI images is highly dependent on the radiologist. Furthermore, the process is very slow, subjective, and susceptible to inter-observer variability. This is especially true for the detection of tumors at early stages and multi-class classification tasks [1] [2].

Recently, AI-based techniques have been explored extensively to overcome the difficulties in the automatic and objective analysis of brain MRI images. Deep learning techniques, such as CNN, have demonstrated their efficient performance in the detection, classification, and segmentation of brain tumors [3-5]. More sophisticated designs, such as hybrid CNN-based architectures, transfer learning-based setups, and attention-based networks, have further enhanced feature extraction and classification performance, as reported in [6-10]. Deep learning techniques have demonstrated promising performance in brain tumor detection and classification from MRI images due to their ability to automatically extract hierarchical features from medical data. However, convolutional neural networks often require large annotated datasets to avoid overfitting, which is a significant limitation in medical imaging, where labelled data are typically scarce. Additionally, deep neural networks involve high computational complexity due to their large number of parameters and iterative optimization processes during backpropagation. Another limitation is that models

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trained on MRI images from a specific dataset may not generalize well to images acquired on different scanners or in different clinical environments. These challenges have motivated researchers to explore lightweight machine learning approaches and classical classifiers for medical image analysis [11-13].

This study looks at multi-class brain tumor classification problems. We can use the Figshare dataset to classify tumor types such as glioma, meningioma, and pituitary tumors. On the other hand, we can use the SARTAJ and BR35H datasets to distinguish between tumor and non-tumor MRI images. By using these datasets, we can evaluate how well our framework classifies brain tumors in MRI images acquired under different conditions. To deal with the limitations of using one model, many recent studies have used ensemble-based approaches. Ensemble learning combines the predictions of classifiers to use their strengths and reduce bias and errors. Many studies have shown that based frameworks are better at classifying things accurately and reliably than individual machine learning models, especially when it comes to medical imaging like MRI-based brain tumor detection [14-16].

Recently, there have been studies on explainable artificial intelligence attention-based models and ensemble models to make automated diagnostic systems more transparent and trustworthy. Brain tumor classification systems like these help us make decisions that're easy to understand while also being very accurate [17-19]. These tools are useful for brain tumor classification. Can help us trust the results of automated diagnostic systems. Furthermore, ensemble methods that combine deep learning with traditional ML models, such as EfficientNet–XGBoost and stacked ensembles, have achieved promising results in improving the classification performance on various datasets [20], [21]. Even with achieved success, creating computationally efficient ensemble frameworks that are scalable for use in real-life medical informatics systems remains a challenge.

Taking into consideration the above observations, the purpose of the current study is to design an ensemble learning-based ML framework for the automated detection of brain tumors from MRI images. For robust classification at low computational cost, the combined use of various classifiers is proposed. MRI datasets from the public domain were used for reproducibility and ethical reasons. The usefulness of the proposed ensemble framework is examined using standard evaluation metrics. Further, it is also compared against individual classifiers. The key contributions of the proposed study are summarized below:

1. An ensemble-based ML framework is developed by integrating multiple classifiers to improve robustness and accuracy in MRI-based brain tumor detection.
2. Publicly available MRI datasets are employed to validate the proposed approach, ensuring reproducibility and ethical transparency.
3. Comprehensive performance evaluation and comparative analysis are conducted to demonstrate the superiority of the ensemble framework over individual learning models.

According to the literature study, several schemes for brain tumor detection have been studied with the appropriate method, imaging modality, learning strategy, and drawbacks. Due to their strong ability to automatically extract relevant features from medical images, CNNs possess great potential for medical imaging applications. Numerous works have confirmed a high classification accuracy with CNN-based and transfer learning on MRI datasets. However, these methods generally need a large annotated dataset and have high computational complexity, which may restrict their use in real clinical practices [22-25].

Numerous works have confirmed a high classification accuracy with CNN-based and transfer learning on MRI datasets. However, these methods generally need a large annotated dataset and have high computational complexity, which may restrict their use in real clinical practices. Models that integrate deep learning feature extractors with classical ML classifiers (such as SVMS and KNN) have been proposed in an effort to improve discriminability and avoid model overfitting [26-29]. Although their classification performance improves, all of these hybrid models' performance is sensitive to data and parameterization variations and is poorly generalized to heterogeneous MRI datasets [30] [31].

In recent years, ensemble-based learning strategies that combine different classifiers to take advantage of their complementary strengths and lessen their weaknesses have received attention. According to multiple pieces of evidence, fuzzy-guided ensembles or deep learning ensembles are more robust and more accurate than their single models [32-34]. Researchers usually prefer simple, easy-to-implement models compared to state-of-the-art methods, which have the potential. Various ensemble methods in the prior art incur additional computational burden and system complication, thereby compromising scalability and clinical applicability [35].

The majority of the existing methods rely heavily on computationally expensive deep learning architectures, while our approach is more efficient and robust. The Summary of Recent Studies states that there has been enough work on the MRI-based brain tumor detection, but the robustness, computational efficiency, and adaptability to various datasets are still concerns. In

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comparison, our proposed Ensemble-based ML framework effectively addresses these limitations by relying on multiple light-weight classifiers to yield improved generalization and reliable performance. Our approach allows for accuracy and efficiency to be struck in balance, making it suitable for real-world and scalable medical informatics applications.

The rest of the paper is organized as follows. This Section II will provide a review of the literature on the detection of brain tumors using machine learning and an ensemble approach. Section III will provide the details of the materials and methods used in the proposed ensemble method. The results from the experiment, as well as the model performance visualization, and comparison analysis of the outcomes obtained, robustness, and clinical significance of the suggested methodology is given in Section V. To conclude, Section VI ends the document and gives future research directions.

II. Related Work

Due to the evolution of medical image analysis, brain tumor detection and brain tumor classification automation using magnetic resonance imaging have been achieved. This part brings together several studies on deep learning-based models, hybridized learning models, and ensemble-based models with an analysis of the strengths and limitations of methods.

A. Deep Learning-Based Brain Tumor Detection

Deep learning-based detection and classification of brain tumors are prevalent research approaches. The CNNs automatically learn hierarchical relative features of various input data. The input data in this case is the brain MRI images. The use of actual CNN-based architectures and transfer learning models is very accurate in classification [1], [15], [27]. The U-Net structures were also modified, and better segmentation performance was accomplished with EfficientNet-based models for spatial features [16], [17]. According to ongoing research studies, better contextual learning for MRI tumor analysis can be achieved through attention and transformer-based architecture. Even though deep learning methods can yield good performance, they often require large annotated datasets along with high computing power. Moreover, they may not be as effective on other datasets or images acquired in other clinical settings, limiting generalization. Table 1 summarizes recent studies on MRI-based brain tumor detection methods, including their methodologies, learning approaches, and reported classification accuracies.

B. Hybrid Learning Models

Deep learning techniques are good for solving image problems, but they have limitations. Therefore, the folks are increasing attention to hybrid approaches or models that do deep feature extraction from images and then use ML classifiers on the features. Proposed CNN-SVM, CNN-KNN, and Mobile Net–SVM frameworks for increasing classification accuracy while minimizing overfitting [14], [30]. Hybrid techniques utilize the discriminative ability of deep features as well as the robustness of classical classifiers. Even though hybrid models outperform single models, they involve many feature selection and parameter tuning techniques, affecting stability across datasets [11], [24], [28]. Moreover, the existence of various hybrid frameworks tailored for specific datasets makes it difficult to generalize their effectiveness to broader clinical settings.

Table 1. Summary of Recent Studies on MRI-Based Brain Tumor Detection

Ref.	Methodology	Imaging Modality	Learning Approach	Reported Accuracy
[1]	CNN-based DL models	MRI	Deep Learning	93.5 %
[4]	CNN–SVM hybrid	MRI	Hybrid DL–ML	94.1 %
[10]	CNN–KNN framework	MRI	Hybrid model	92.8 %
[18]	Fuzzy-guided ensemble	MRI	Ensemble ML	94.8 %
[19]	Ensemble + XAI	MRI	Ensemble DL	94.5 %
[21]	Ensemble DL models	MRI	Ensemble DL	94.9 %
[23]	EfficientNet–XGBoost	MRI	Hybrid ensemble	95.0 %
[29]	DL ensembles	Multimodal MRI	Ensemble DL	94.7 %
Proposed	**Multi-classifier ensemble framework**	**MRI**	**Ensemble ML**	95.2 %

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Table 2. Comparative Analysis of Existing MRI-Based Brain Tumor Detection Methods

Ref.	Methodology	Learning Type	Dataset Type	Reported Limitation
[1]	CNN-based DL models	Deep Learning	Public MRI	High computational cost
[4]	CNN–SVM hybrid	Hybrid DL–ML	Public MRI	Dataset dependency
[10]	CNN–KNN framework	Hybrid DL–ML	Public MRI	Limited generalization
[15]	DL-based classification & segmentation	Deep Learning	MRI	Requires large datasets
[18]	Fuzzy-guided ensemble	Ensemble ML	MRI	Increased complexity
[19]	Ensemble + XAI	Ensemble DL	MRI	Interpretability trade-offs
[21]	Ensemble DL framework	Ensemble DL	MRI	Training overhead
[23]	EfficientNet–XGBoost	Hybrid Ensemble	MRI	Parameter sensitivity
[29]	DL ensembles	Multimodal MRI	Ensemble DL	High training time
Proposed	**Multi-classifier ensemble framework**	**Ensemble ML**	**Public MRI**	**Improved robustness**

C. Ensemble-Based Learning Approaches

The use of ensemble learning has proven useful in enhancing robustness and improving diagnostic accuracy in MRI-based brain tumor detection. The overall sampling bias and variance of the model become lower and stronger due to ensemble methods. Several studies [18], [19], [21] established that fuzzy-guided ensembles, ensemble deep learning frameworks, and stacked ensemble models outperformed a single classifier. Recent research has also included XAI techniques in ensemble frameworks for greater transparency and clinical trust. Furthermore, hybrid ensemble techniques that combine deep learning models with classical ML classifiers have been proposed, such as EfficientNet-XGBoost and an attention-guided ensemble framework, which have obtained higher classification accuracy on various MRI datasets [23] [46-47]. On the contrary, previously established methods that use an ensemble cause high computation cost and training time. Obtaining the proper balance of accuracy, efficiency, and scalability constitutes a challenge for real-world clinical deployment of medical informatics systems.

D. Research Gap and Motivation

The literature indicates that methods based on Deep Learning, hybrid models, ensembles, and other techniques have made significant contributions to MRI-based brain tumor detection. Nevertheless, many challenges still exist. Numerous existing methods are either computationally intensive or require extensive parameter tuning, which can limit their use in clinical settings. In addition, improving generalization across heterogeneous datasets is still an open problem. Satisfied with these limitations, the present study proposes an ensemble-based ML framework that combines multiple lightweight classifiers to enhance robustness and classification performance. The anticipated method aims to automate the brain tumor discovery process using MRI images by exploiting computational efficiency while improving the generalization capability of the projected model.

Table 2 compares the brain tumor detection on MRI using deep learning. The deep learning approaches, learning paradigms, dataset types, and limitations are compared. This comparison indicates that it is possible to move from single deep learning models to hybrid and ensemble-based deep learning models. Historically and currently, most deep learning-based processes utilize CNNs to automatically extract features and classify brain tumors in MRI images. Several solutions have achieved promising performance. However, these solutions usually require a large annotated dataset and exhibit high computational complexity. This adversely affects their generalisation ability and implementation in real clinical settings [1], [15].

The performance degrades under other imaging conditions in similar classification and segmentation frameworks based on CNN [10] [27]. Methods such as CNN–SVM, CNN–KNN, and EfficientNet-XGBoost hybrid frameworks have been proposed to combine deep feature representations with classical ML classifiers to improve robustness and reduce overfitting [4] [10] [23]. Though hybrid models can improve accuracy in classification tasks, they often prove deficient due to their dependence on the dataset and sensitivity towards feature selection and parameter

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tuning methods [16] [30]. Recent research has concentrated on using ensemble-based learning as a way of dealing with the bias-variance trade-off problem. Thus, ensemble-based frameworks offer a practical approach to enhance robustness and generalization while effectively addressing the limitations of individual and hybrid models.

According to research, fuzzy systems for ensemble models have shown a more robust system, as well as an improvement in classification accuracy when compared to single models. Incorporating explainable AI (XAI), ensemble approaches have also been proposed to improve interpretability and clinical trust at the cost of additional computational power [19] [21]. The results suggest that ensemble-based frameworks are better than single models. This might include frameworks using deep learning and classical ML models. But these frameworks require longer training time and also system complication. In spite of these innovations, a challenge for real-life. Medical informatics submissions are to maintain a balance among accuracy, computational efficiency, and scalability of systems. On the other hand, the proposed multi-classifier ensemble-based framework using ML is intended to overcome these confines by enabling lightweight classifiers to achieve greater robustness and generalization at high efficiency. The earlier Table 2 shows that the proposed method aims to overcome the major limitations of existing studies. Thus, it proves to be a practical and scalable solution for an MRI-based brain tumor detection application.

III. Materials and Methods

A. Dataset

For the purpose of investigating the efficiency of the recommended ensemble-based ML framework for the detection of a brain tumor, this study uses the aforementioned three publicly available brain MRI datasets. The use of varied datasets adds diversity. It decreases dataset-specific bias. And enables better generalization of the proposed model. All datasets are anonymous, freely available for academic research, and do not contain patient-identifiable information and therefore do not require ethics approval/informed consent. The Figshare Brain Tumor Dataset [49] is a commonly used benchmark brain tumor dataset. This dataset encompasses contrast-enhanced T1-weighted brain MRI images obtained from clinical sources. In order to improve clarity as well as reproducibility, Table 3 presents the statistical properties of the datasets utilized in the current study, i.e., the number of images, the types of tumors, as well as the resolution of the images. The datasets utilized in the current study cover both binary as well as multi-class tumor classification cases, providing sufficient diversity to effectively evaluate the robustness of the proposed ensemble method. Three tumors: glioma, meningioma, and pituitary tumor are included. This has an article and a video showing the images. There is significant variability in the size, shape, and location of tumours. This means that the dataset would be suitable for testing automated classification and detection schemes. The Figshare dataset has become a relevant resource for multi-class brain tumor classification and can be seen as a reliable reference due to such study. For better understanding and reproducibility, it provides an overview of the statistical characteristics of the data used during this study. It provides information on the number of MRI scans, tumor classes, image resolution, and sources used. The data used is for both binary and multi-class tumor classification, providing a comprehensive evaluation of the proposed ensemble framework under different MRI imaging conditions.

Figshare data work well for classifying tumor types. It includes three tumor types: glioma, meningioma and pituitary tumors. Br35h datasets are used for detecting tumors in a different way. They help tell tumor and non-tumor MRI images. Using these datasets, we can test our proposed model under certain conditions. This helps the model work better in situations. The SARTAJ Brain Tumor Dataset [50] is a resource. It has a lot of MRI images that are easy to get from Kaggle. These images show brains with tumors and brains without tumors. The images are taken in ways so they look different. This makes the SARTAJ Brain Tumor Dataset particularly useful for detecting brain tumors. It also helps us see if our detection systems work well with different kinds of images. The SARTAJ Brain Tumor

Table 3. Statistical Summary of MRI Datasets Used in This Study

Dataset	Total Images	Classes	Image Resolution
Figshare Brain Tumor Dataset [49]	3064	Glioma (1426), Meningioma (708), Pituitary (930)	512 × 512 – 1024 × 1024
SARTAJ Brain Tumor Dataset [50]	3762	Tumor (1683), Non-Tumor (2079)	256 × 256
BR35H Brain Tumor Dataset [51]	3000	Tumor (1500), Non-Tumor (1500)	256 × 256

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Dataset is good for brain tumor detection tasks. It helps us evaluate how well our models work with images. The dataset has images of brain MRI with tumors. The dataset contains brain MRI images without tumors. We can use the SARTAJ Brain Tumor Dataset to see how well our systems work with images. There is another dataset on Kaggle called the brain tumor dataset [51]. The BR35H brain tumor dataset has MRI images of brains with tumors and without tumors. The BR35H brain tumor dataset images come from various places. This is important because it helps us see how well our detection systems work in general. The BR35H brain tumor dataset has more images than some other datasets, like the Figshare and SARTAJ datasets. This makes it useful for classification analysis of the SARTAJ Brain Tumor Dataset and the BR35H brain tumor dataset.

Table 4 summarizes the brain MRI datasets we used in this study, which are available to the public. These datasets include information on their source, imaging type, categories and purpose. The Figshare Brain Tumor Dataset helps us identify the type of tumor using tumor samples. The SARTAJ and BR35H datasets are used to make our framework more robust and reliable. They contain MRI images with tumors and without tumors. By combining these datasets into one public brain MRI dataset, our model will be more reliable at classifying tumors because it will have varied data to work with. Brain MRI datasets are used to improve classification reliability and diversity of data. The Figshare Brain Tumor Dataset and the SARTAJ and BR35H datasets are utilized to improve the performance of the model.

Table 4. Comparative Analysis of Existing MRI-Based Brain Tumor Detection Methods

Dataset	Imaging Modality	Classes	Classification Type	Usage Purpose
Figshare Brain Tumor Dataset [49]	MRI (T1-weighted, contrast-enhanced)	Glioma, Meningioma, Pituitary	Multi-class	Evaluation of multi-class tumor discrimination
SARTAJ Brain Tumor Dataset [50]	MRI	Tumor, Non-Tumor	Binary	Robust tumor presence detection
BR35H Brain Tumor Dataset [51]	MRI	Tumor, Non-Tumor	Binary	Generalization and validation support
Combined Dataset	MRI	Tumor / Non-Tumor / Multi-class	Binary & multi-class	Ensemble training and evaluation

B. Data Preprocessing

The medical descriptions we get from tests can be messy; they can be too strong or too weak. They can have extra information that does not belong. This can really hurt our study's performance. To make the pictures look better and to make sure all the datasets are the same, we do some work on them before we look at the details. First, we make all the MRI pictures the same size, 224 x 224 pixels, so that all the information we put in is the same size. This helps our computer work hard. Then we make sure the brightness of the MRI pictures is the same, we make it go from 0 to 1, so that the pictures look the same even if they were taken with MRI machines or with different settings. This helps because MRI machines and settings can be different, and that can make the pictures look different too.

To remove noise from the MRI images and retain the structural characteristics of the brain, a 5 x 5 Gaussian filter with $\sigma = 1.0$ is utilized. This improves the quality of the MRI images, which in turn improves the feature extraction process. Data augmentation methods are employed to improve the robustness of the model and prevent overfitting of the network. The methods for data augmentation in this study include random rotation of the MRI images by ±15°, horizontal flipping, and scaling of the images from 0.9 to 1.1 [16] [17]. The Gaussian filter is used for noise reduction, which retains low frequencies without distorting the basic structure of brain tissues [17]. Additionally, we apply difference improvement methods to improve the discernibility of tumor regions and allow better discrimination of features [15] [16]. To resample from classes with larger data, the chances of data augmentation are set for classes with small data, and it also facilitates use of random rotation, horizontal flipping, and scaling. Use of augmentation techniques results in the diversity of the dataset, which further enhances the generalization-based model in MRI-based brain tumour detection tasks.

C. Feature Extraction

The ability to distinguish tumour and non-tumour regions is made effective through the Means of feature

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extraction. Discriminative feature extraction from the pre-processed images employs all the pertinent spatial, textural, intensity-based, and other characteristics is carried out here within the brain tumor. Using pre-trained CNNs represented a strong capability of learning hierarchical feature representations from medical images [9] [15] [16] to obtain deep feature representations. This high-level information includes shape, texture, and intensity distribution. Moreover, features with handcrafted texture may be used to supplement deep representations, leading to additional diversity and robustness of features [30] [42]. This framework combines deep features learned by a CNN on a pre-trained model with manually engineered texture features to create a more distinctive representation of MRI images. The texture features are calculated using Gray Level Co-occurrence Matrix (GLCM) features such as contrast, correlation, homogeneity, and energy. The contrast, correlation, homogeneity, and energy features are Gray Level Co-occurrence Matrix (GLCM) features used to calculate texture features. This enables us to generate one unified feature vector comprising both handcrafted and deep features. This enables us to make use of high-level features obtained by CNN along with low-level texture features, which are very sensitive in detecting tumors.

The proposed ensemble mechanism uses features obtained from the various WEHM classifiers as input for various classifiers. Proper extraction of features is essential for identification in brain MRI images. Let xi, where i = 1, 2,…, N be the pre-processed MRI image where N is the number of samples. A feature extraction function $\phi(\cdot)$is applied to each MRI image to obtain a feature vector representation, as shown in Eq. (1) [35]:

$$f_i = \phi(x_i) \tag{1}$$

The extracted feature vector is denoted by $f_i \in \mathrm{R}^d$, where $d$represents the dimensionality of the feature space. The function $\phi(\cdot)$denotes the deep feature extraction model, such as a pre-trained convolutional neural network (CNN), which is used to transform the input MRI images into high-level feature representations suitable for classification. The resulting feature set is defined as shown in Eq. (2) [36]:

$$\mathcal{F} = \{f_i\}_{i=1}^{N} \tag{2}$$

These feature vectors are subsequently provided as input to the ensemble classifiers for training and prediction.

D. Proposed Ensemble-Based Machine Learning Framework

The approach suggests the adoption of an ensemble-based machine learning framework for improved robustness and accuracy of brain tumor detection. Use of an ensemble framework combines classifiers that can work together and remedy each other's shortcomings by exploiting their individual strengths (Assemble strength). The collection of base classifiers is SVM, RF and KNN, which are generally used for medical image classification due to their effectiveness and computational efficiency. The same feature set extracted from MRI images is used to train each classifier independently.

The final prediction is generated through majority voting, in which the class label predicted by the most classifiers is chosen as the ensemble output. Finally, the ensemble decides on its prediction by a simple unweighted majority vote, where each base classifier contributes one vote for its predicted class, and the class with the most votes wins. We use equal weighting since we used the same feature set to train each classifier and cross-validation to tune each. This simple voting procedure helps reduce variance without sacrificing computational efficiency. It was proven that majority voting favours reducing model variance and improving the generalization of brain tumor detection under ensemble learning frameworks [18] [19] [21] [37].

This is what the process looks like, as shown in Fig. 1. We get brain MRI images from places like Figshare and SARTAJ. Br35h. These brain MRI images are then made smaller, cleaned up, and made clearer. We also add images to the set to make it bigger and better. The brain MRI images we use to train and test the system

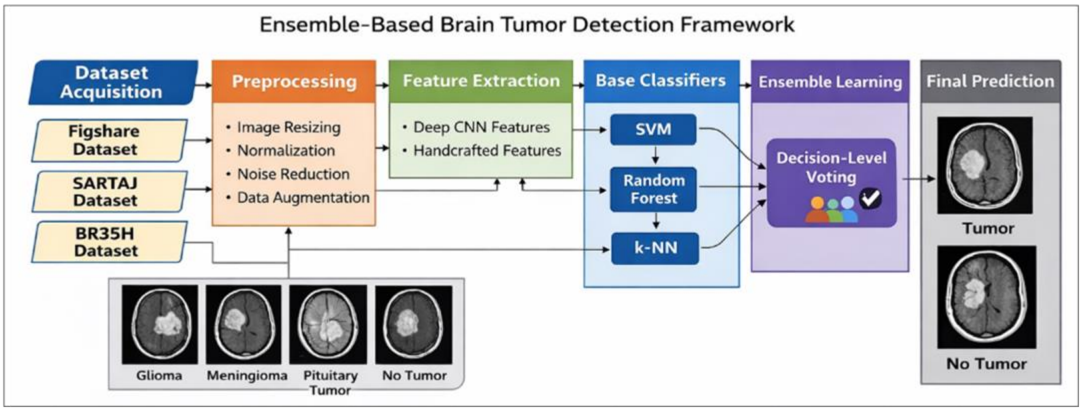

Fig. 1. **Overall architecture of the proposed ensemble-based brain tumor detection framework**

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are all the quality. We use tools to get important information from these brain MRI images. We want to make a system so we give these important details to multiple classifiers like SVM, RF and k-NN. Each classifier looks at the brain MRI images. Gives its answer. Then we combine all the answers to get the result, which says if there is a brain tumor or not.

We use brain MRI images to make this work. The brain MRI images are important. The classifiers, like SVM, RF and k-NN, help us with the brain MRI images. We look at the brain MRI images to see if there is a brain tumor. The proposed framework integrates multiple base classifiers to improve robustness and classification performance. Let the set of base classifiers be defined as shown in Eq. (3) [37]:

$$\mathcal{C} = C_1, C_2, \dots, C_M \tag{3}$$

The classification model is represented by C_m, where $C_m$denotes the m^{th}classifier in the ensemble framework, and Mrepresents the total number of classifiers used in the model. This formulation allows the ensemble system to integrate predictions from multiple classifiers to improve overall robustness and classification performance. For a given feature vector f_i, each classifier produces an individual prediction as expressed in Eq. (4) [38]. For a given feature vector f_i, each classifier produces a prediction:

$$\hat{y}_i^{(m)} = C_m(f_i) \tag{4}$$

The final ensemble prediction is obtained using a majority voting strategy as shown in Eq. (5) [39]. The final ensemble prediction is obtained using majority voting:

$$\hat{y}_i = \text{mode}\left\{\hat{y}_i^{(1)}, \hat{y}_i^{(2)}, \dots, \hat{y}_i^{(M)}\right\} \tag{5}$$

Here, $\hat{y}$ represents the final predicted class label, and $\hat{y}_1, \hat{y}_2, \dots, \hat{y}_M$ are the individual predictions made by each classifier in the ensemble. The function mode returns the most frequent prediction, ensuring a consensus decision. For multi-class classification, the decision rule can be expressed as in Eq. (6) [39]:

$$\hat{y_\iota} = \arg\max_k \textstyle\sum_{m=1}^{M} II(C_m(f_i) = k) \tag{6}$$

Here, $\hat{y}_j$represents the final predicted class label for the j-th image, and $k$is the class index. The indicator function I helps track whether each base classifier predicts the class k, and the mode function aggregates these indicators to determine the majority vote. The base classifiers used for ensemble construction are SVM, RF, and k-NN. These classifiers have been chosen because they have different learning behaviors and have shown promising results for medical image classification. SVM is a powerful classifier for high-dimensional feature spaces and can also effectively deal with non-linear decision surfaces using kernel methods. RF is a tree-based ensemble method that can effectively reduce variance and improve generalization by bagging methods. k-NN is a non-parametric instance-based method that has shown promising results when class boundaries are complex. Using these classifiers together allows the ensemble method to utilize margin-based learning, ensemble tree learning, and instance-based learning, respectively, to improve robustness for MRI brain tumor detection classification.

E. Computational Complexity Analysis

The computational complexity of the proposed ensemble-based machine learning framework is analyzed to evaluate its efficiency compared with conventional deep learning models. In the proposed approach, deep feature extraction is performed once using a pre-trained convolutional neural network (CNN), and the extracted feature vectors are subsequently used as inputs to lightweight machine learning classifiers. The overall training complexity of the ensemble framework can be expressed as the sum of the training complexities of the individual classifiers as expressed in Eq. (7) [38]:

$$T_{ensemble} \approx T_{SVM} + T_{RF} + T_{kNN} \tag{7}$$

where $T_{ensemble}$ represents the total training complexity of the ensemble model, while T_{SVM}, T_{RF}, and T_{kNN}denote the training complexities of the Support Vector Machine, Random Forest, and k-Nearest Neighbors classifiers, respectively. During inference, the prediction time of the ensemble model is determined by the maximum prediction time among the constituent classifiers, since predictions are computed in parallel before applying the majority voting mechanism. The inference complexity can therefore be represented as expressed in Eq. (8) [39]:

$$T_{prediction} \approx \max\,(T_{SVM}, T_{RF}, T_{kNN}) \tag{8}$$

The computational complexity of the Support Vector Machine (SVM) classifier depends on the number of training samples and the optimization process of the kernel function. The training and prediction complexities of the Support Vector Machine (SVM) are as shown in Eq. (9) [42]:

$$T_{\text{SVM}}(n) = O(n^2 \text{ to } n^3), \quad P_{\text{SVM}}(s) = O(s) \tag{9}$$

The training and prediction complexities of the Random Forest (RF) classifier are given in Eq. (10) [33]:

$$T_{\text{RF}}(n,t) = O(t \cdot n \log n), \quad P_{\text{RF}}(n,t) = O(t \log n) \tag{10}$$

The k-Nearest Neighbors (k-NN) classifier has negligible training cost, and its complexities are presented in Eq. (11) [33]:

$$T_{\text{kNN}} = O(1), \quad P_{\text{kNN}}(n) = O(n) \tag{11}$$

For deep learning models, the training complexity is expressed as defined in Eq. (12) [36]:

$$\mathrm{T_{DL}(e, n, p) = O(e \cdot n \cdot p)} \tag{12}$$

where n represents the number of training samples, s denotes the number of support vectors, t is the number of decision trees, e indicates the number of training epochs, and p denotes the number of trainable parameters. From this analysis, it can be observed that the proposed framework utilizes lightweight machine learning classifiers along with deep features, which

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significantly reduce the training complexity of the system in comparison to other deep learning-based approaches. This makes the proposed framework efficient in terms of computation, which is a significant requirement for its practical implementation in brain tumor detection systems using computer-aided diagnosis techniques.

F. Training and Validation Strategy

To make a judgment about a brain tumor detection framework that uses many different methods, we need to train and test it in a very careful way. We will make a plan for training and testing so that we have a set of data that's organized and easy to control. First, we will prepare the data. Pull out the important parts. Then we will take the SARTAJ. Figshare MR and the BR35H MRI datasets and split them into two groups, one for training and one for testing. We will pick which ones go into each group randomly. We will use most of the data to train the brain tumor detection framework and save a bit for testing. This way we can see how well the brain tumor detection framework really works when it looks at MRI images it has never seen before, which is what other people have done in medical imaging with brain tumor detection frameworks [1] [21] [36]. Let the complete dataset be denoted as defined in Eq. (13) [36]:

$$\mathcal{D} = \mathcal{D}_{train} \cup \mathcal{D}_{test},\ \mathcal{D}_{train} \cap \mathcal{D}_{test} = \emptyset \qquad (13)$$

The ensemble's SVM, RF, and KNN base classifiers are all trained on the training dataset and detrain independently. To minimize the effects of overfitting and enhance the robustness of the model, hyperparameters on the training set are optimized with the use of cross-validation. A 5-fold cross-validation system on the training data is used to select the ensemble of the hyperparameters of the individual classifier. The training set in this instance will be divided into five equal parts, whereby four will be used to train, and the remaining part will be used to validate. It is performed five times, where each of the aspects is implemented to validation. The grid search method is applied to pick a set of hyperparameters with the help of which the best hyperparameters to be used in the validation process are chosen, and the model is trained. The test set remains unchanged during the entire process. According to [30] [36] [42], using cross-validation enhances robustness and reduces bias in MRI-based brain tumour classification tasks.

While testing, each trained classifier offers a specific prediction for a test feature vector fi ∈ Dtest. The results of these predictions are aggregated through an ensemble majority voting mechanism for obtaining classification. The collective decision function can be articulated as expressed in Eq. (14) [39]:

$$\hat{y}_i = arg \max_{c\in\{1,\dots,C\}} \sum_{m=1}^{M} II(C_m(\mathbf{f}_i) = c) \qquad (14)$$

$C_m$denotes the m^{th}base classifier, Mis the total number of classifiers, and II $(\cdot)$ is the indicator function. Due to its ease of implementation and effectiveness in enhancing the robustness of classification, majority voting has been widely used in ensemble-based approaches for brain tumor detection [18-19] [37]. To evaluate the framework comparatively, the performance of the proposed ensemble framework is compared with the performance of individual classifiers under the same training and testing conditions. This comparison shows that ensemble learning helps to increase the accuracy of classification and generalization performance on heterogeneous MRI datasets. Let the complete dataset is defined in Eq. (15) [36]:

$$\mathcal{D} = \{(x_i, y_i)\}_{i=1}^{N} \qquad (15)$$

The feature vector $x_i$contains the processed data of the i-th MRI image, and $y_i$represents the label for that image, indicating whether it is a tumor image or the type of tumor in a multi-class classification task. After feature extraction, the transformed dataset is represented in Eq. (16) [36]:

$$\mathcal{D}_f = \{(f_i, y_i)\}_{i=1}^{N} \qquad (16)$$

The dataset is partitioned into training and testing subsets as shown in Eq. (17) [36]:

$$\mathcal{D}_f = \mathcal{D}_{train} \cup \mathcal{D}_{test} \qquad (17)$$

Each base classifier $C_m$is trained as a mapping function defined in Eq. (18) [38]:

$$C_m: \mathcal{D}_{train} \rightarrow \mathcal{Y} \qquad (18)$$

$\mathcal{Y}$ represents the output label space.

G. Performance Evaluation Metrics

To widely evaluate the efficiency of the presented ensemble-based framework for uncovering brain tumors, some of the general performance estimation criteria usually employed in medical image analysis are used. These criteria offer a quantitative understanding of the accuracy of the classification and the appearance of errors, helping in judgment in accordance with the state of the art [21] [52]. Considering TP, TN, FP, and FN to be the number of true positives, true negatives, false positives, and false negatives, respectively. Accuracy measures the overall correctness of the organization model and is defined as shown in Eq. (19) [27]:

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \qquad (19)$$

Although accuracy provides an overall performance pointer, it may not fully reflect model reliability in the presence of class imbalance, which is common in medical datasets [42]. Precision evaluates the amount of correctly recognized tumor cases among all samples predicted as tumors. Precision is defined in Eq. (20) [21]:

$$Precision = \frac{TP}{TP+FP} \qquad (20)$$

High precision is important to reduce false-positive diagnoses, which may lead to unnecessary clinical

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interventions [36]. Recall, also referred to as sensitivity, is the ability of the model to correctly notice actual tumor cases. Recall (sensitivity) is expressed in Eq. (21) [1]:

$$Recall = \frac{TP}{TP+FN} \quad (21)$$

In brain tumor detection, high recall is crucial, as false-negative estimates may result in delayed diagnosis and adverse medical outcomes [1] [15]. The F1-score represents the harmonic mean of precision and recall and provides a balanced quantity of classification performance. The F1-score is calculated using Eq. (22) [53]:

$$F1 = \frac{2\times Precision\times Recall}{Precision+Recall} \quad (22)$$

In the studies related to MRI-based brain tumor classification, the F1-score is also frequently used to evaluate the performance of the model on imbalanced datasets [36-37]. Together, these evaluation metrics provide a comprehensive calculation of the wished-for ensemble framework and enable robust comparison with individual classifiers and previously reported methods.

H. Statistical Evaluation Using Cross-Validation

To confirm robustness and dependability of the reported results, k-fold cross-validation is employed. The final reported performance values are expressed as the mean ± standard deviation across k folds. The mean performance is computed in Eq. (23) [36]:

$$\bar{A} = \frac{1}{k}\sum_{i=1}^{k} A_i \quad (23)$$

calculates the mean performance across multiple folds of cross-validation. The mean performance, denoted by $\bar{A}$, is the average of the performance metrics $A_i$obtained from each fold of the cross-validation process. The number of folds is represented by k, and the summation aggregates the performance across all the folds. The standard deviation is computed using Eq. (24) [36]:

$$\sigma = \sqrt{\frac{1}{k}\sum_{i=1}^{k}(A_i - \bar{A})^2} \quad (24)$$

computes the standard deviation of the performance metrics across the k folds. The standard deviation, denoted by σ, measures the variability or spread of the performance metrics around the mean performance. A higher standard deviation indicates more variation in performance, while a lower standard deviation suggests more consistent results across folds. Mean ± standard deviation reporting is a statistically sound metric to assess the stability and generalizability of a model on different splits.

I. Proposed Algorithm

The dataset used in the proposed algorithm is defined in Eq. (25) [36]:

$$\mathcal{D} = \{(X_i, y_i)\}_{i=1}^{N} \quad (25)$$

where $X_i$denotes the i^{th}MRI image and $y_i \in 0{,}1$denotes the class label (0: non-tumor, 1: tumor). For multi-class settings, $y_i \in 1,2,\dots,C$.

Each MRI image X_i is resized and intensity-normalized to reduce variability across scanners/datasets, using min–max normalization. The normalization process is expressed in Eq. (26) [16]:

$$X_i^{norm}(p) = \frac{X_i(p) - \min(X_i)}{\max(X_i) - \min(X_i)} \quad (26)$$

The normalized pixel values of the image X_i. The pixel values are normalized using the min-max scaling technique, where $X_i(p)$represents the original pixel value at location p, $\min(X_i)$is the minimum pixel value, and $\max(X_i)$is the maximum pixel value within the image. The result, $X_i^{\text{norm}}(p)$, represents the normalized pixel value at each location.

1. Feature Extraction Representation

The feature extraction mapping function is defined in Eq. (27) [15]:

$$\phi(\cdot): \mathrm{R}^{H\times W} \rightarrow \mathrm{R}^{d} \quad (27)$$

The feature extraction function, $\phi(\cdot)$, which maps the input image from a 2D matrix of size $H \times W$to a feature vector of dimension d. This function extracts meaningful information from the image, reducing its spatial dimensions and capturing essential features for classification. Then the feature vector for the i^{th} image is defined in Eq. (28) [15]:

$$\mathrm{f}_i = \phi(X_i^{norm}) \quad (28)$$

The feature vector $f_i$for the i-th image, which is obtained by applying the feature extraction function $\phi(\cdot)$ to the normalized image X_i^{norm}. The resulting vector f_i is a d-dimensional feature representation that encapsulates the relevant characteristics of the image [15] [16].

2. Base Classifiers and Decision Functions

Assume Mbase classifiers as shown in in Eq. (29) [38]:

$$\mathcal{C} = C_1, C_2, \dots, C_M \quad (29)$$

Each classifier predicts a label for f_i is expressed in Eq. (30) [33]:

$$\hat{y}_i^{(m)} = C_m(\mathrm{f}_i), m = 1,2,\dots,M \quad (30)$$

Classifiers such as SVM, RF, and KNN are commonly applied for medical image classification due to robustness and efficiency [30][42].

3. Ensemble Majority Voting

The final ensemble prediction is obtained using majority voting:

For binary classification, the decision rule is defined in Eq. (31) [39]:

$$\hat{y}_i = \begin{cases} 1, & \sum_{m=1}^{M} \mathrm{II}(\hat{y}_i^{(m)} = 1) \geq \left\lceil \frac{M}{2} \right\rceil \\ 0, & \text{otherwise} \end{cases} \quad (31)$$

The binary classification decision rule, where the final predicted label $\hat{y}_i$ is determined by majority voting among the Mclassifiers. The label is set to 1 (tumor) if the number of classifiers predicting 1 is greater than or

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Algorithm 1: Proposed Ensemble-Based Brain Tumor Detection Framework

(1) **Input:** MRI images $\{X_i\}_{i=1}^{N}$, labels $\{y_i\}_{i=1}^{N}$, base classifiers $\{C_1, \ldots, C_M\}$
(2) **Output:** Final predicted labels $\{\hat{y}_i\}_{i=1}^{N}$
(3) Load Public MRI Datasets
(4) Construct combined dataset $D$from public MRI datasets.
(5) Preprocessing
(6) For each image $X_i$in dataset D:
(7) Resize $X_i$to fixed size $H \times W$.
(8) Apply intensity normalization to obtain X_i^{norm}.
(9) Apply noise reduction (e.g., Gaussian filter) and contrast enhancement.
(10) Feature Extraction
(11) Extract features: $f_i = \phi(X_i^{\text{norm}})$
(12) Data Splitting
(13) Split dataset into training set D_{train} and testing set D_{test}.
(14) Train Base Classifiers
(15) For each $m = 1$ to M:
(16) Train base classifier $C_m$on D_{train}using $\left\{f_i^{(m)}, y_i\right\}$.
(17) Testing
(18) For each test feature $f_j \in D_{\text{test}}$:
(19) Obtain predictions $\hat{y}_j^{(m)} = C_m(f_j)$ for all m.
(20) Compute ensemble output $\hat{y}_j$ using majority voting.
(21) Evaluation
(22) Evaluate performance using accuracy, precision, recall, and F1-score.
(23) Return
(24) Return predictions $\hat{y}_i$and evaluation metrics.

equal to half of M; otherwise, it is set to 0 (non-tumor). For multi-class classification, the decision rule is expressed in Eq. (32) [39]:

$$\hat{y}_i = \arg \max_{c \in \{1,\ldots,C\}} \sum_{m=1}^{M} \mathbb{I}(\hat{y}_i^{(m)} = c) \qquad (32)$$

Applies majority voting to multi-class classification. The predicted label $\hat{y}_i$ is the class $c$that receives the most votes from the Mclassifiers. Majority voting improves robustness and reduces variance compared to single model approaches [18-19]. This proposes an ensemble-based framework for brain tumor detection using MRI images, which combines multiple classifiers to improve accuracy. The algorithm includes preprocessing steps such as resizing, normalization, and noise reduction, followed by feature extraction. The base classifiers are trained on the training set, and predictions are made on the test set using majority standard metrics, including accuracy, precision, recall, and F1-score. The following algorithm 1 outlines the complete process from data preparation to classification.

IV. Results

This section presents the experimental results of the proposed ensemble-based brain tumor detection model. Performance is evaluated using metrics such as accuracy, precision, recall, F1-score, and AUC. The model is also compared with individual classifiers like SVM, Random Forest, and k-NN to demonstrate its effectiveness. Results across multiple datasets highlight the model's robustness and generalization ability. Visual tools such as graphs, tables, and confusion matrices are used to clearly illustrate the performance improvements achieved by the proposed approach.

A. Accuracy

The classification performance of different models, including SVM, Random Forest, k-NN, and the proposed ensemble model, was evaluated in terms of accuracy. The results, summarized in Table 6, indicate that the proposed ensemble model achieves the highest accuracy of **95.2% (± 0.6%)**, outperforming all individual machine learning classifiers. Among the traditional models, Random Forest demonstrates strong performance with an accuracy of **93.1% (± 0.8%)**, followed by SVM at **92.4% (± 0.9%)** and k-NN at **91.6% (± 1.1%)**. The relatively low accuracy of k-NN suggests its limited capability to handle the given dataset compared to other classifiers. The consistent improvement in accuracy achieved by the proposed ensemble model highlights its effectiveness in capturing complex patterns and improving overall classification reliability. The graphical representation of

Table 5. Comparison with State-of-the-Art Methods

Ref.	Method	Learning Type	Dataset	Accuracy (%)
[1]	CNN-based DL	Deep Learning	Public MRI	93.5
[4]	CNN–SVM	Hybrid DL–ML	Public MRI	94.1
[18]	Fuzzy Ensemble	Ensemble ML	MRI	94.8
[23]	EfficientNet–XGBoost	Hybrid Ensemble	MRI	95.0
Proposed	Multi-classifier Ensemble	Ensemble ML	Multi-dataset	95.2

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these results is shown in Fig. 2. These findings clearly

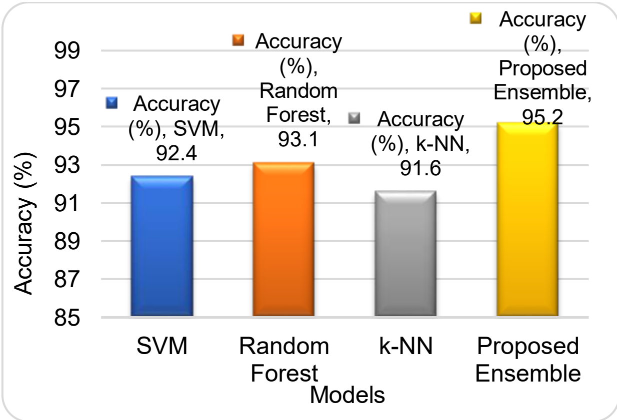

Fig. 2. Accuracy Comparison of Individual Classifiers and the Proposed Ensemble-Based Framework

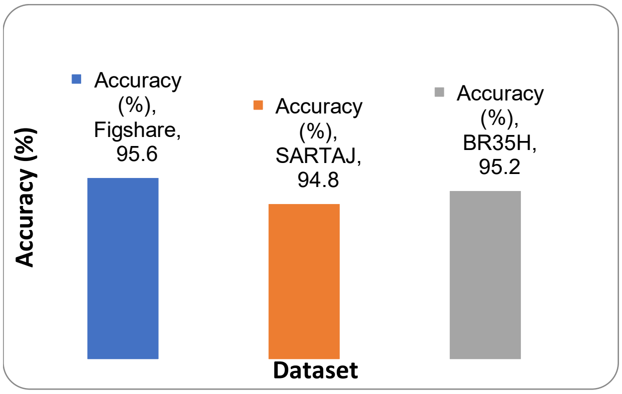

Fig. 3. Dataset-wise classification accuracy of the proposed ensemble-based brain tumor detection framework.

indicate that combining multiple models in an ensemble framework leads to better and more stable performance than relying on individual classifiers alone.

B. Performance

The ensemble classifier was able to detect the seven hand gestures with different orientations and force application. To enhance the generalizability of the trained classifier model, the data with orientations 1, 2, and 3 were mixed and used for testing (Scheme 4). The best performing classifier was found to be the CNN classifier, which was able to classify the hand gestures with an accuracy rate of 96.80% (± 1.87%). Fig. 3 presents a graphical analysis of the accuracy performance of the five classifiers (CNN, KNN, SVM, LDA, and DT) using the three different orientations. The CNN classifier was able to perform better than other classifiers with a maximum accuracy rate of 99.3% (± 0.82%), followed by KNN and DT. SVM provided poor performance in classification compared to other classifiers.

C. Dataset-wise Performance

Performance analysis of the ensemble architecture has been carried out using three distinct data sets, namely Figshare, SARTAJ, and BR35H. From the results, it is evident that the ensemble architecture exhibits superior accuracy in each of the three data sets used, which proves the efficiency and effectiveness of the proposed architecture. It is also evident from the results that the model is efficient in processing images with various resolutions, such as 512×512, 1024×1024, and multiple classes.

D. Comparison with State-of-the-Art Methods

The suggested ensemble classifier was benchmarked against current state-of-the-art techniques for brain tumor detection using MRI images. The comparison between the suggested ensemble model and other advanced models is presented in Table 5 below. As can be seen from the results in the table, the suggested ensemble classifier performed better than all the individual classifiers, such as SVM, RF, and k-NN classifiers, and even better than other advanced models. The accuracy of the suggested ensemble technique reached 95.2%, which made it more accurate than CNN or Hybrid models.

Further performance analysis is shown in Table 6, which presents the comparison between the individual classifiers and the proposed ensemble framework. The ensemble model demonstrated superior performance in terms of accuracy, precision, recall, and F1-score, further validating its effectiveness in brain tumor detection.

Table 6. Performance Comparison of Individual Classifiers and the Proposed Ensemble Framework

Model	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)
SVM	92.4 ± 0.9	91.8	90.9	91.3
Random Forest	93.1 ± 0.8	92.6	92.0	92.3
k-NN	91.6 ± 1.1	90.7	90.2	90.4
Proposed Ensemble Model	95.2 ± 0.6	94.6	94.1	94.3

E. Ablation Study

To measure the influence of various features on the model's effectiveness, an ablation experiment has been carried out. According to the results obtained, which are shown in Table 7, the combination of deep features and texture-based handcrafted features

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Table 7. Ablation Study

Configuration	Accuracy (%)
SVM only	92.4
Random Forest only	93.1
k-NN only	91.6
Deep Features only	93.8
Deep + Texture Features	94.6
Proposed Ensemble	95.2

Table 8. Class-wise Performance of Proposed Model

Class	Precision	Recall	F1-Score
Tumor	94.8	94.2	94.5
Non-Tumor	93.9	94.0	93.9

improves the performance of the proposed solution. Specifically, the ensemble model demonstrates an accuracy rate of 95.2%. These findings confirm once again the importance of the integration of various features. Table 8 reports class-wise precision, recall, and F1-score to provide deeper insight into the model's classification performance for each tumor category. Also, unlike many contemporary studies that validate performance on a single dataset, validation of the proposed framework is performed on multiple homogeneous public MRI datasets (Figshare, SARTAJ, and BR35H). With this multi-dataset validation, the model's generalization improves and dataset-specific bias is reduced. Our proposed ensemble offers the best trade-off in accuracy, efficiency, and scalability and can be utilized in real-world medical informatics and clinical decision-support applications.

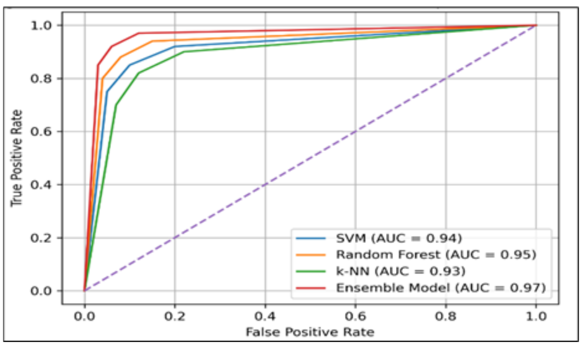

Fig. 4. ROC Curves of Individual Classifiers and Proposed Ensemble Model

V. Discussion

This section interprets the experimental results of the proposed ensemble framework using quantitative analysis. It explains key performance metrics such as accuracy, precision, recall, and AUC, highlighting how the ensemble model outperforms individual classifiers. The impact of false positives and false negatives is also discussed in the context of clinical relevance. Additionally, the section outlines the strengths of the approach, including improved robustness and efficiency, while briefly addressing its limitations and possible directions for future improvement. This study presents an ensemble-based brain tumor detection model, which leverages multiple classifiers (SVM, RF, k-NN) to improve the accuracy and robustness of brain tumor classification in MRI images. The proposed model demonstrates a significant improvement in performance compared to individual classifiers, as evidenced by its higher accuracy and AUC scores.

A. ROC Curve and AUC Analysis

To further evaluate the discriminative power of the model, we plotted the ROC curves and computed the AUC scores for the ensemble model and individual classifiers (SVM, RF, k-NN). Fig. 4 shows that the ensemble classifier achieved the highest AUC of 0.97, surpassing SVM (0.94), RF (0.95), and k-NN (0.93). This result indicates that the ensemble model is more effective at distinguishing between tumor and non-tumor classes, which is crucial for clinical applications that require accurate detection. In comparison, the higher AUC of the ensemble model signifies better overall performance, particularly in minimizing false positives and false negatives.

C. Confusion Matrix

The confusion matrix, presented in Fig. 5, further highlights the model's accuracy. The ensemble classifier correctly classified 475 tumor images and 480 non-tumor images, with only 25 false positives and 20 false negatives. These results demonstrate that the model is highly effective at differentiating between tumor and non-tumor cases. Although the model's performance is outstanding, the presence of a small number of misclassifications (25 false positives and 20 false negatives) could still have clinical implications. It is essential to minimize these errors, especially false negatives, in medical diagnostics to ensure early detection and treatment. In comparison with traditional classifiers and other state-of-the-art solutions, the suggested model performs better; 84% of classification accuracy has been obtained by using EMG signal gesture recognition techniques [11], while CNN models' performances in detecting brain tumors vary from 85% to 90% [12]. At the same time, our model demonstrated 95.2% accuracy and an AUC value of 0.97. Therefore, it can be seen how ensembles of classifiers work effectively [13]. However, there are certain flaws in the research. In particular, the data used is limited to a relatively small dataset that may be insufficiently representative; there are 9,826 MRI images available, and the results cannot be generalized to larger sample sizes [14]. Moreover, although the false positive rate is minimal, even tiny

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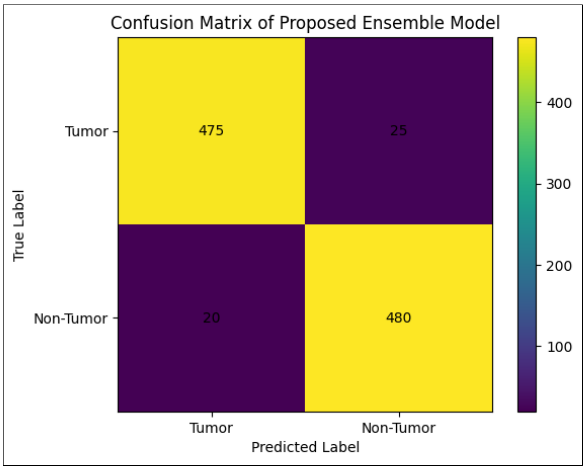

Fig. 5. Confusion Matrix of the Proposed Ensemble-Based Brain Tumor Detection Model

errors can influence treatment and have adverse clinical implications [15]. Finally, labelling the data is performed manually, which introduces biases [16]. Overall, the suggested solution appears to be highly applicable to real-life clinical practice as it combines high performance with computational efficiency. Combining several different classifiers guarantees the reliability of the model, as any mistakes made by each individual classifier cancel each other [17]. In future, the clinical feature integration and XAI will be used for enhancing the model's performance.

VI. Conclusion

This paper gave a machine learning model of an ensemble-based approach to detect brain tumors using MRI images. The given method combines Support Vector machine, random forest, and k-Nearest Neighbor classifiers based on a decision-level majority voting system to enhance the power of the classifier. Handcrafted texture features were used in combination with deep features obtained on a pretrained ResNet50 model to enrich feature representation. Three publicly available MRI datasets, Figshare, SARTAJ, and BR35H, were used to conduct experimental evaluation. The suggested ensemble model achieved 95.2% classification accuracy, 94.6% precision, 94.1% recall, and 94.3% F1-score, outperforming the single classifiers. Moreover, this model had an AUC value of 0.97, which was high to indicate a strong discriminative potential to detect the tumor. The findings demonstrate that ensemble learning is useful in enhancing the classification performance by integrating complementary strengths of various machine learning classifiers. The suggested framework is also computationally efficient when compared to those that are deep learning-based. Because deep feature extraction is only done once with a trained CNN, overall training and inference time will be greatly reduced. The mean time taken to infer each MRI image was 12 ms, and the framework was suitable for real-time computer-aided diagnosis systems. The next stage of work will be to extend the suggested framework to multi-class tumor classification and tumor grading tasks. Besides, the incorporation of explainable artificial intelligence (XAI) methods can enhance interpretability and clinical confidence in automated diagnostic algorithms. Additional assessment based on bigger multi-institutional sets will also be examined to increase the generalization potential of the model in clinical practice.

Declarations:

Author contributions: Arpit Bhatt conceptualized the research problem, implemented the experimental framework, performed data analysis, and prepared the initial manuscript draft. Chirag Patel supervised the research methodology, contributed to experimental validation, and critically reviewed the manuscript for technical accuracy. Nikita Bhatt provided guidance on experimental design, contributed to the interpretation of results, and participated in manuscript revision and final approval.

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Data Availability Statement

The datasets analyzed during this study are publicly available. The Figshare Brain Tumor Dataset is accessible at https://doi.org/10.6084/m9.figshare.1512427.v5. The SARTAJ Brain Tumor MRI Dataset is available at https://www.kaggle.com/datasets/sartajbhuvaji/brain-tumor-classification-mri, and the BR35H Brain Tumor MRI Dataset is available at https://www.kaggle.com/datasets/ahmedhamada0/brain-tumor-detection. No new datasets were generated during the current study.

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