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Brain Tumor Classification based on Convolutional Neural Networks with an Ensemble Learning Approach through Soft Voting

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***Abstract*—The brain is a vital organ that serves various purposes in the human body. Processing sensory data, generating muscle movements, and performing complex cognitive tasks have all historically relied heavily on the brain. One of the most common conditions affecting the brain is the growth of abnormal tissue in brain cells, leading to the development of brain tumors. The most common forms of brain tumors are pituitary, glioma, and meningioma, which are major global health issues. From these issues, there is a need for appropriate and prompt handling before the brain tumor disease becomes more severe. Quick handling is through an early disease detection approach, and computer vision is one of the trending early disease detection methods that can predict diseases using images. This research proposes a model in computer vision, namely the Convolutional Neural Network (CNN), with a soft voting ensemble learning strategy to classify brain tumors. The dataset consists of 7,023 images without tumors and MRI brain tumors such as glioma, meningioma, and pituitary with a resolution of 512x512 pixels. This experiment investigates classifier models such as VGG16, MobileNet, ResNet50, and DenseNet121, each of which has been optimized to maximize performance. The proposed soft voting ensemble strategy outperformed existing methods, with an accuracy of 97.67% and a Cohen's Kappa value of 0.9688. The proposed soft voting ensemble method approach has proven effective in improving the accuracy.**

***Keywords*— Brain tumor; soft voting; ensemble learning; CNN; classification.**

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I. INTRODUCTION

Comprising multiple complex neuronal networks, the human brain is the most complicated organ in the body. These interconnected neurons function in response to signals from other parts of the body. The malfunctioning of these neurons leads to brain cancer. About 10% of all deaths in 2018 were caused by brain tumors, which accounted for 9.6 million deaths, the cause of death globally [1], [2].

Brain tumors can be categorized as benign (non-cancerous) or malignant (cancerous) [3], [4], [5]. While malignant tumors can spread throughout the body and pose a life-threatening risk, benign tumors do not spread or damage other parts of the body, with gliomas, meningiomas, and pituitary tumors being among the types of brain tumors [6], [7]. The three brain tumor diseases, glioma is one of the brain or spinal cord tumor diseases originating from glia cells. In contrast, meningioma originates from the protective membrane of the brain and spinal cord, and pituitary tumors originate from the pituitary gland [8], [9]. Although brain tumors can be treated through surgery or with radiation therapy and chemotherapy, early detection is considered very important to prevent the disease so that patients with the disease do not experience worsening symptoms [10].

Symptoms affecting brain tumors can be determined by their type, location, and size. Symptoms of nausea, vomiting, headache, difficulty thinking or speaking, and seizures are common [11]. The most well-known diagnostic methods for brain tumors that use a combination of image tests include Magnetic Resonance Imaging (MRI) and Computerized Tomography (CT) scans, or commonly known as biopsy procedures, depending on the type and stage of the tumor [12], [13]. Additional treatment options in brain tumors are radiation therapy, chemotherapy, and surgery [14], [15]. These treatments aim to reduce symptoms, limit tumor

growth, and extend the life expectancy of patients with brain tumors.

Among the conventional brain tumor detection, MRI techniques are considered to provide comprehensive information and are commonly used by medical personnel [16], [17]. However, the drawback of conventional MRI image processing is that it is time-consuming and prone to errors. As artificial intelligence technology develops, medical image categorization can be handled using machine learning and deep learning. With Convolutional Neural Networks (CNN), images can be extracted automatically to obtain image information and can classify them with high accuracy [18], [19]. However, using only one CNN model is sometimes not enough to get optimal results. As an alternative, the use of ensemble learning techniques, such as soft voting, can increase the accuracy value in the classification because it combines predictions from several models.

The CNN method for categorizing brain tumor MRI scans was performed in Reyes' study [20]. A total of two sets of MRIs were evaluated using several CNN architectures, including ConvNeXt, EfficientNet, ResNet, and VGG. The results of this study show that the best-performing model has an accuracy of 95.3%. Takahashi et al. [21] conducted another study to reduce inconsistent images caused by variations in various medical facilities. This study used machine learning-based fine-tuning techniques to classify images on brain MRI. The advantage of using the fine-tuning method in this study is that it increases the accuracy of glioma segmentation with an accuracy rate of 87.5%. However, some limitations must be considered, because the performance of fine-tuning methods is highly dependent on the quality and availability of data and can consume large resources in the computational process.

In classifying brain tumors, CNN models are able to perform well, but managing different datasets requires multiple models [22]. If only one model is used, sometimes CNN fails to get accurate prediction results on unseen data [23], [24]. Therefore, in this study, an ensemble soft voting technique is used to classify brain tumors by combining several optimized CNN models, to maximize predictive power.

Furthermore, in the ensemble technique, hyperparameter adjustments is applied to each CNN model. The performance of the soft voting approach on the MRI dataset is evaluated using metrics such as f1-score, recall, accuracy, and precision. To assess the effectiveness of this strategy, this study compared the classification results of the single model technique with the soft voting method.

II. MATERIAL AND METHODS

This research methodology has several steps that can overcome the challenges of brain tumor classification. The steps start with data preparation and end with ensemble model evaluation. This method integrates several CNN models, including DenseNet121, ResNet50, VGG16, and MobileNet, using ensemble soft voting techniques. Figure 1 shows the flowchart of the research model.

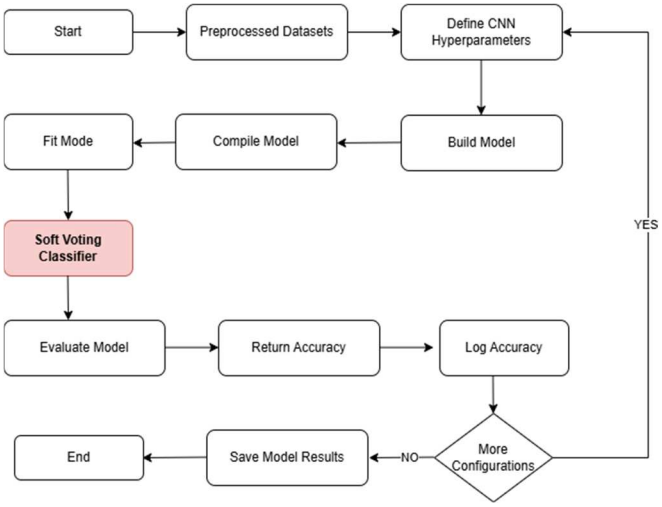
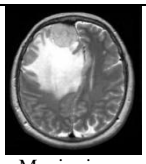


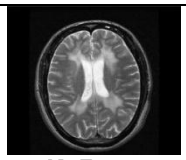
Fig. 1 Flow diagram for the suggested method

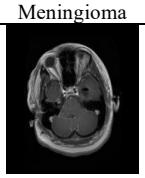
A. Dataset

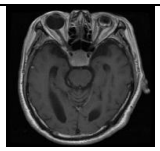
The experiments used the MRI dataset [25] to evaluate the performance of the proposed scheme. The MRI dataset consists of 7,023 images with a size of 512x512 pixels. It comprises the four classes: pituitary (1,757 images), meningioma (1,645 images), glioma (1,621 images), and no tumor (2,000 images). The different dataset categories, such as no tumor, meningioma, pituitary, and glioma, are shown in Table I.

TABLE I
SAMPLE IMAGES FROM THE DATASET


Meningioma


No Tumor


Glioma


Pituitary

B. Pre-processing

The dataset, originally 512x512 pixels in size, was reduced to 128x128 pixels to facilitate the computation process and improve results. The reduced dataset is then separated into three parts, including training data, validation data, and testing data. Using the training data, the model was trained during the training period using the validation data, and then its capacity for generalization ability was assessed using the testing data. A detailed description of the dataset, including the distribution of images in each subset, is provided in Table II.

TABLE II
DETAILS AND DISTRIBUTION OF THE MRI BRAIN TUMOR DATASET

Class Name	Number of Images	Training	Validation	Testing
Glioma	1,621	1,321	300	300
Meningioma	1,645	1,339	306	306
No Tumor	2,000	1,595	405	405
Pituitary	1,757	1,457	300	300
Total	7,023	5,712	1,311	1,311

C. Convolutional Neural Network

One of the commonly used CNN methods is the transfer learning method. The transfer learning method used to classify brain tumors from the available datasets, in other words, using transfer learning is using pre-trained models such as DenseNet121, ResNet50, VGG16, and MobileNet. However, for the top layer, the transfer learning method is not used by using the parameter include_top=False. Table III shows the top layer in this research model.

TABLE III
DETAILS OF THE TOP LAYER

No	Parameter	Weight/Loss	Activation/ Optimizer
1	GlobalAveragePooling2D	-	-
		Layer	
2	Dense	1024	ReLU
3	Dropout	0.3	-
4	Dense	4	Softmax

The GlobalAveragePooling2D layer, which reduces the output dimensions from the convolutional layer by averaging the features in each feature map, is the first layer of the top layers used in the model, as detailed in Table II. To provide non-linearity and enable the model to learn more complex correlations between features, a Dense layer with 1024 units and ReLU activation is then used. 30% of the neurons are randomly deactivated during training at a Dropout rate of 0.3 to minimize overfitting. For classification with four classes, the last layer is a Dense layer with four units and Softmax activation. The model is optimized using the Adam optimizer with a learning rate of 0.0001, and a kernel_regularizer with a value of 0.001 is applied to the Dense layer to reduce overfitting by penalizing large weights.

D. Soft Voting Classifier

In ensemble learning, the soft voting method bases the ultimate decision on the probability estimates from multiple transfer learning models. The result of soft voting is calculated by combining the average value of the projected probability of each model. Then, the model with the highest average value is used as the final prediction. By combining the benefits of multiple models, the accuracy of the models can be improved, the probability of error from one model is reduced, and the prediction results are more accurate. An overview of the ensemble model is shown in Table IV.

TABLE IV
SUMMARY ENSEMBLE MODEL

Layer (type)	Output Shape	Param #	Connected to
input_layer_9 (InputLayer)	(None, 128, 128, 3)	0	-
functional_5 (Functional)	(None, 4)	25,689,988	input_layer_9[0][0]
functional_6 (Functional)	(None, 4)	15,244,100	input_layer_9[0][0]
functional_7 (Functional)	(None, 4)	4,282,564	input_layer_9[0][0]
functional_8 (Functional)	(None, 4)	8,091,204	input_layer_9[0][0]
average_1 (Average)	(None, 4)	0	functional_5[0][0] functional_6[0][0] functional_7[0][0] functional_8[0][0]

E. Evaluation Model

The matrix used to evaluate the model is a confusion matrix which is divided into four parts, namely, false positive (FP), false negative (FN), true positive (TP), and true negative (TN). This matrix can show how well the model divides the data into correct and incorrect classes [26], [27], [28], [29], [30]:

1) Accuracy:

$$\frac{(TP + TN)}{(TP + TN + FP + FN)} \quad (1)$$

2) Precision:

$$\frac{TP}{(TP+FP)} \quad (2)$$

3) F1-score:

$$F1Score = 2 \times \frac{Precision \times TP}{Precision + TP} \quad (3)$$

III. RESULTS AND DISCUSSION

In this study, the ensemble soft voting method is used which combines 4 CNN models namely ResNet50, VGG16, MobileNet, and DenseNet to classify brain tumors. The proposed confusion matrix table can be seen in Fig. 2.

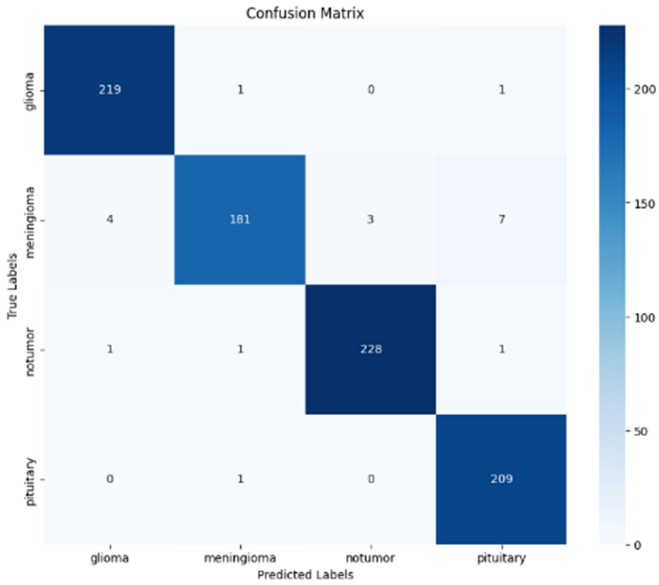


Fig. 2 The confusion matrix obtained from the proposed model

Fig. 2 shows the confusion matrix results divided into 4 classes, including glioma, meningioma, no tumor and pituitary. The model can correctly classify most of the images. In the glioma class, the model can predict 219 images correctly, the meningioma class can predict 181 images, the no tumor class can predict 228 images, and the pituitary class can predict 209 images. However, in all four classes, the model made several errors in predicting images, such as the pituitary class was incorrectly predicted as a meningioma class for 7 images. In general, the performance of the model has been considered quite good based on the True Positive (TP) label on the main diagonal. The evaluation of soft voting ensemble model and comparison with the existing methods are shown in Tables V and VI, respectively.

TABLE V
EVALUATION OF SOFT VOTING ENSEMBLE MODEL FOR VARIOUS DATASET

Class Name	Precision	Recall	F1-Score	Support
Glioma	98%	99%	98%	221
Meningioma	98%	93%	96%	195
No Tumor	99%	99%	99%	231
Pituitary	96%	100%	98%	210
Average	98%	98%	98%	857

TABLE VI
COMPARISON OF SOFT VOTING ENSEMBLE MODEL WITH THE EXISTING CLASSIFIER

Model	Accuracy	Precision	Recall	F1-Score	Support
ResNet50	51.34%	66%	48%	40%	857
VGG16	96.97%	97%	97%	97%	857
MobileNet	97.08%	97%	97%	97%	857
DenseNet	92.77%	93%	93%	93%	857
Soft voting ensemble model	97.67%	98%	98%	98%	857

Table V shows the evaluation of the ensemble soft voting model based on precision, recall, f1-score, and support. Notably, the model achieves a high average precision of 98% and an equally strong recall of 98%. The precision and recall scores for the "No Tumor" category are particularly noteworthy, with both metrics reaching 99%. This indicates that the model is highly effective at accurately identifying patients without tumors while also minimizing false negatives. The only category with slightly lower precision is the Pituitary tumor classification at 96%, though it maintains a perfect recall of 100%, underscoring its effectiveness in identifying all relevant cases.

In the comparative analysis shown in Table VI, the soft voting ensemble model outperforms existing classifiers across several key metrics, including precision, recall, and f1-score. While ResNet50 displays significantly lower performance, both in accuracy 51.34% and recall 48%, models like VGG16 and MobileNet also yield high precision and recall scores but fall short of the soft voting ensemble model's results. The soft voting ensemble model achieves a precision of 98% and a recall of 98%, indicating its superior ability to balance both false positives and false negatives when classifying tumors. The evaluation metrics of the existing CNN model is listed in Table VII.

TABLE VII
EVALUATION METRICS OF THE PERFORMING CNN MODEL

Model	Cohen's Cappa
ResNet50	0.3243
VGG16	0.9595
MobileNet	0.9611
DenseNet	0.9035
Soft Voting Ensemble model	0.9688

The Cohen's Cappa scores for each CNN model and the suggested soft voting ensemble model for brain tumor classification are shown in Table VII. The findings show that there was a strong correlation between the predicted and actual labels, with the ensemble model achieving the highest Kappa score of 0.9688. With Cappa scores of 0.9611 and 0.9595, respectively, MobileNet and VGG16 outperformed the other models in terms of classification performance with a score of 0.9035, DenseNet likewise produced dependable results, but ResNet50 had the lowest agreement 0.3243, indicating less predictive reliability. The effectiveness of combining predictions through soft voting was confirmed when the ensemble model performed better overall than any of the individual models.

Table VI displays the classification performance metrics of the soft voting ensemble model, which combines ResNet50, VGG16, MobileNet, and DenseNet. The model performs exceptionally well across all tumor classifications, with consistently high Precision, Recall, and F1-Score values. The metrics, which range from 96% to 99% for specific classes like pituitary, glioma, and no tumor, show how well the model can classify these groups. The average metrics for F1-Score, Precision, and Recall are 98% for all classes, indicating strong overall performance. With a total support of 857 samples, the soft voting ensemble model achieves a robust classification capability, proving its effectiveness as a comprehensive approach to tumor identification. Fig. 3 displays the brain tumor classification graph accuracy.

This outcome demonstrates the benefit of employing ensemble methods to improve the robustness and stability of classification. It also illustrates how individual model flaws can be lessened by combining complementary feature representations from various architectures. High reliability is essential in medical diagnosis, where the enhanced performance is particularly beneficial. Consequently, the suggested ensemble approach offers a viable way to classify brain tumors with greater accuracy and consistency. The graph accuracy of the proposed model is shown in Fig. 3.

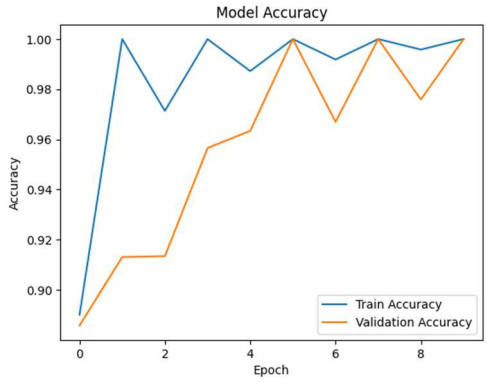


Fig. 3 Graph of accuracy

Fig. 3 illustrates how the model's accuracy for classifying brain tumors improved across ten epochs on both the training (blue line) and validation (orange line) data. The model performs best when it comes to correctly diagnosing different types of brain tumors, as seen by training accuracy reaching over 100% as early as the second epoch and staying steady, while validation accuracy progressively rises to almost 98% by the last epoch. This shows that the model retains its great generalization abilities while efficiently learning from the training data. The training accuracy's steady stability demonstrates the resilience of the model's architecture. In the meantime, the consistent rise in validation accuracy shows how well the model can adjust to new data. The model loss value for the validation data is shown in Fig. 4.

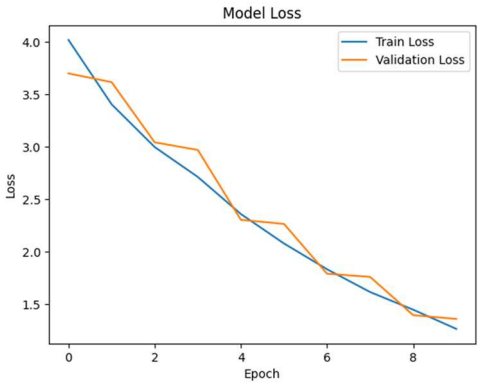


Fig. 4 Graph of loss

As the epochs rise, the graph in Fig. 4 displays a decline in the loss values for the validation data (orange line) and training data (blue line). The model is learning from the data without showing any discernible signs of overfitting or underfitting, as evidenced by the training loss drastically decreasing to a value near 1.5 at the end of the epoch and the validation loss likewise decreasing in a similar manner. When these two graphs are combined, it appears that the model is stable and performs exceptionally well on both training and validation data. The illustration of false and true prediction from the proposed model is shown in Fig. 5.

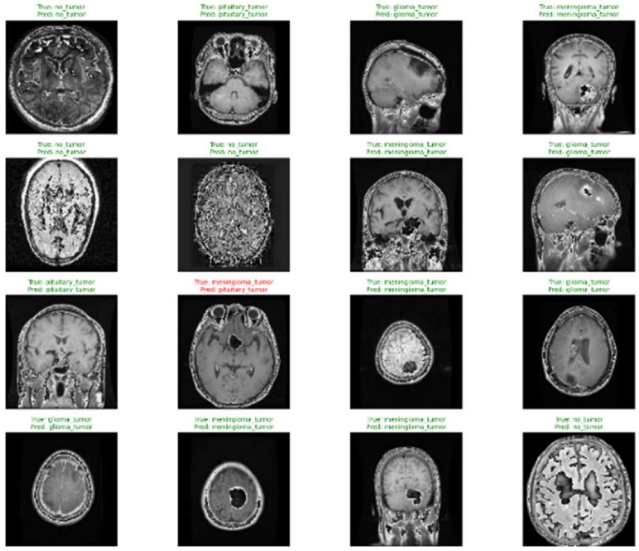


Fig. 5 Illustration of the true and false predictions made by the model for the image classification

Color indications are used to illustrate the prediction findings for brain tumor categorization in Fig. 6, where green indicates correct predictions, while red indicates incorrect predictions. This method offers an easily understandable and straightforward technique to assess model performance by facilitating the search for accurate classifications and quickly identifying errors. With this color prediction, evaluation efficiency is improved, especially when examining large datasets. The visualization of the predicted meningioma tumor is shown in Fig. 6.

Fig. 7 shows that one of the brain tumor images in the meningioma class in the testing data was predicted using the trained model. After being predicted by the model, the image was predicted to be glioma at 9.73%, meningioma at 62.05%, no tumor at 0.90%, and pituitary at 27.35%, as shown in Figure 8. From the results, it shows that the image is predicted to belong to the meningioma class, with the trained model being able to predict the image according to its actual class. This can also be repeated to predict a single image with other tumor images. The model's adaptability and resilience in differentiating across tumor kinds are demonstrated by its capacity to forecast probabilities across all classes. The image's actual class further supports the model's confidence in its prediction, which is indicated by the highest probability value, 62.05% for meningioma. This demonstrates the model's sensitivity to minute details in the image, even if other classes, such as pituitary and glioma, were given lower probabilities.

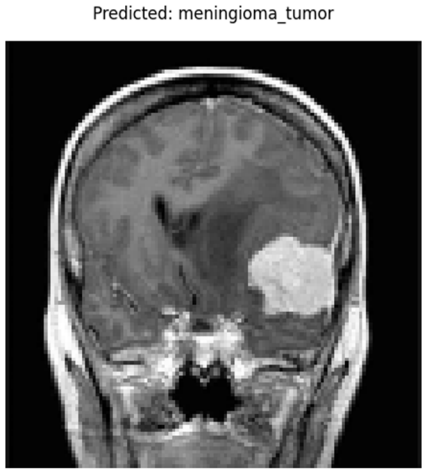


Fig. 6 Predicted image meningioma tumor

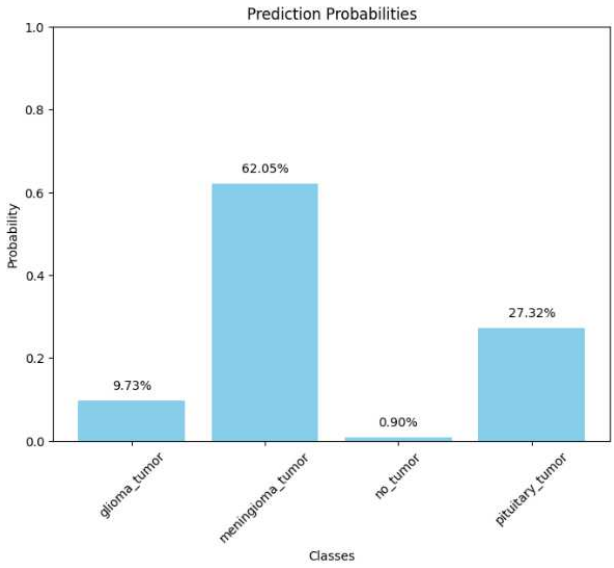


Fig. 7 Prediction probabilities graph

The proposed soft voting ensemble model is compared with related research in terms of its accuracy level, as shown in Table XIII. It is expected to be feasible to ascertain whether the new model provides any improvements or optimizations over earlier techniques by examining the outcomes. The accuracy comparison with the existing method is shown in Fig. 8.

TABLE XIII
COMPARISON OF MODEL PERFORMANCE WITH PRIOR RESEARCH

Author	Dataset	Method	Accuracy
Mahmud et al. 31]	MRI	CNN	93.3%
Asiri et al. [8]	MRI	Hyperparameter CNN (HPCNN)	96%
Alsaif et al. [32]	MRI	VGG19	93%
Filatov et al. [33]	MRI	CNN	89.55%
Ravinder et al. 34]	MRI	GCNN	95.01%
Proposed soft voting ensemble model	MRI	Soft Voting (DenseNet121, ResNet50, VGG16, and MobileNet)	**97.67%**

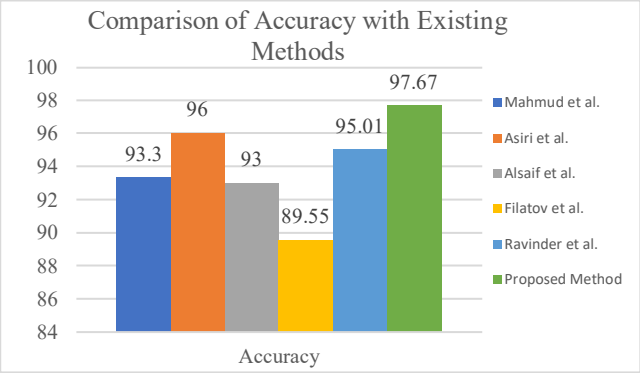


Fig. 8 Comparison of Accuracy with Related Research

Researchers have shown how well different deep learning models classify brain tumors from MRI scans. Using a CNN model, Mahmud et al. [31] obtained an accuracy of 93.3%, and Asiri et al. [8] used a hyperparameter-tuned CNN (HPCNN) to increase performance to 96%. Filatov et al. [33] obtained 89.55% accuracy with a CNN model, whereas Alsaif et al. [32] claimed 93% accuracy with the VGG19 model. Using a GCNN model, Ravinder et al. [34] achieved a high accuracy of 95.01%. The suggested approach, which used Soft Voting with models like DenseNet121, ResNet50, VGG16, and MobileNet, obtained the maximum accuracy of 97.67%.

IV. CONCLUSION

This study presented a soft voting ensemble learning strategy that combines DenseNet121, ResNet50, VGG16, and MobileNet to classify brain tumors. By utilizing the advantages of each base model, the model surpasses earlier research when optimized using the Adam optimizer (learning rate 0.0001, kernel_regularizer 0.001). The proposed soft voting ensemble learning achieved an accuracy of 97.67% for classifying brain tumors from MRI scans. In future research, the authors suggest investigating bigger datasets, hyperparameters, and transfer learning. Additionally, integrating explainable AI approaches could enhance the model's interpretability for clinical applications.

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