Improving Brain Tumor Classification Efficacy through the Application of Feature Selection and Ensemble Classifiers

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***Abstract*—Accurate brain tumor detection is crucial due to its high mortality rate. However, existing automated methods suffer from limited accuracy and high false-positive rates. In this study, we aimed to improve brain tumor classification by comparing 17 different classifiers organized into six groups: Decision Tree (DT) Model, Support Vector Machine (SVM), Naive Bayes Classifier, Logistic Regression, Generalized Linear Model (GLM) Classifier, and Neural Network. We utilized a dataset of 3,762 Magnetic Resonance Imaging (MRI) scans of brain tumors from Kaggle, with each image having dimensions of 240 × 240 pixels and labeled as tumor or non-tumor. Our approach involved three main steps: extracting visual information using 17 predictor classes, optimizing feature extraction through weight optimization, and comparing different sets of classifier models. We evaluated the models' performance using the confusion matrix and Receiver Operating Characteristics (ROC) curves. Our results showed that optimizing feature selection and utilizing ensemble classifiers improved the accuracy of brain tumor classification. The DT Model with ensemble classifiers emerged as the best-performing classifier, achieving an accuracy of 98.11% and an AUC of 0.99. Notably, Random Tree (RT) exhibited the highest accuracy within the ensemble classifier set, with a significant increase compared to other models. Our proposed method outperformed the standard approach, demonstrating its potential for enhancing brain tumor detection accuracy. This study contributes to the field by providing a more accurate method for detecting brain tumors, potentially enabling earlier detection and improved patient outcomes. Future research should focus on further improving brain tumor diagnosis and treatment through the application of machine learning techniques.**

***Keywords*—brain tumor detection, machine learning, ensemble classifiers, feature selection, accuracy**

I. Introduction

Brain tumors are a complex and life-threatening condition that affects individuals of all ages and genders, causing damage to brain tissue and the central nervous system, leading to impaired cognitive abilities and reduced quality of life. The diagnosis and treatment of brain tumors present significant challenges due to the intricate nature of tumor biology, individual patient variability, and limited availability of patient data [1–4]. Artificial intelligence technology has emerged as a promising tool for processing medical data, creating precise predictive models, and aiding in the diagnosis and treatment of patients with brain tumors [5, 6]. Brain tumors are complex and life-threatening conditions that damage brain tissue and the central nervous system, leading to impaired cognitive abilities and a reduced quality of life, regardless of age or gender [7, 8]. Despite advancements in treatment, many patients still face challenges with diagnosis and effective therapy [9–11]. While imaging techniques such as Magnetic Resonance Imaging (MRI) and Computed Tomography Scan (CT Scan) are the primary methods of diagnosing brain tumors [12–14], the interpretation and diagnosis process can be arduous and requires a high level of proficiency [15, 16]. Moreover, in some instances, brain tumors can be difficult to detect using these methods, resulting in a delayed diagnosis [17–19].

To address these challenges, brain tumor research has utilized technologies such as artificial intelligence to make the analysis of medical data more effective and efficient [20, 21], thus aiding physicians in the diagnosis and treatment of brain tumor patients [22]. Additional research is necessary to improve the recognition and treatment of brain tumors and enhance the quality of life of affected individuals [23]. Several research topics can be explored concerning brain tumors, such as brain tumor segmentation from imaging images to assist with diagnosis and treatment planning [24–26], classification of brain tumor types based on imaging image attributes and clinical data [27–30], prediction of brain tumor growth [31, 32],

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and identification of risk factors and prevention of brain and other tumors [33, 34].

The previous research focuses on the classification of brain tumors, which involves grouping brain tumor types based on specific features such as size, location, and cell type [35–38]. Previous studies on brain tumor classification have utilized various techniques such as k-means clustering, Principal Component Analysis (PCA), Support Vector Machine (SVM), Decision Tree, Random Forest, and Neural Networks. For instance, Kumar *et al.* [39] described a hybrid method that combines deep learning techniques and conventional machine learning algorithms for classifying MRI images of brain tumors. The hybrid technique achieved a classification accuracy of 95.71% for the Brain Tumor Segmentation (BraTS) dataset and 94.6% for The Cancer Imaging Archive (TCIA) dataset. Jayapal *et al.* [40] presented Active Contour Model and Support Vector Machine (SVM) algorithms for tumor categorization, and their proposed intelligent system outperformed conventional techniques of categorization, achieving an accuracy of 92.48% and a sensitivity of 95.12%. Similarly, Huml *et al.* [41] utilized Atomic Force Microscopy (AFM) technology and data mining approaches for the categorization of brain cancers, and the proposed technique accurately classified brain tumors with an accuracy of 89.28%, but there is still a need for improved accuracy and dependability of brain tumor classifiers.

To develop a more accurate and dependable brain tumor classification model, it is crucial to consider various criteria such as data quality, feature selection, and data mining approaches. Additionally, model validation and evaluation must be conducted regularly to ensure the best performance of categorization models [42]. So that to improve the accuracy of brain tumor classification, this study utilized Confirmatory Factor Analysis (CFA) for feature extraction. The classification stage was then divided into training and testing and subjected to k-fold cross-validation with k = 10. During the training process, 17 classifiers were compared using three different models: (1) 17 standard classifier models (model CS); (2) 17 classifier models with feature selection (model C+FS); and (3) 17 classifier models with ensemble classifier (model C+ES). Our proposed method demonstrated improved accuracy and dependability, providing a significant contribution to the field of brain tumor classification. By combining feature selection approaches or ensemble classifiers, we were able to achieve better results than the standard methods used in previous studies. These findings have important implications for the development of more accurate and dependable methods for diagnosing brain tumors, ultimately leading to earlier detection and treatment. Additionally, our research can aid in identifying critical areas for future research in improving brain tumor diagnosis and treatment using machine learning techniques.

II. Research Method

Due to the potential danger of brain tumors and their ability to impair brain function and threaten lives, it is important to conduct studies on tumor classification [43]. According to [44], timely detection and classification of brain tumors are critical for effective treatment. With advances in technology, data mining techniques can be used to classify brain tumors. However, careful consideration must be given to the choice of algorithm, as each method has its unique strengths and weaknesses depending on the data used. For instance, DT is prone to overfitting and not suitable for imbalanced data [45], while k-NN struggles with high-dimensional data, is susceptible to outliers, and requires a large amount of memory to hold the complete dataset [46]. SVM approach is particularly sensitive to parameter values and kernel functions [47], and Neural Network requires large amounts of data to train effectively [48]. To overcome these challenges, the proposed model in this study compares 17 classifiers across six groups, including DT Model, SVM, Naive Bayes Classifier, Logistic Regression, GLM Classifier, and Neural Network, with feature selection or ensemble classifier optimization, aiming to improve classification accuracy [49]. It is hoped that the advancement of data mining techniques can overcome these limitations and improve accuracy in the classification of brain tumors, enabling doctors to better identify appropriate treatment options for patients. The flowchart of the proposed model is shown in Fig. 1.

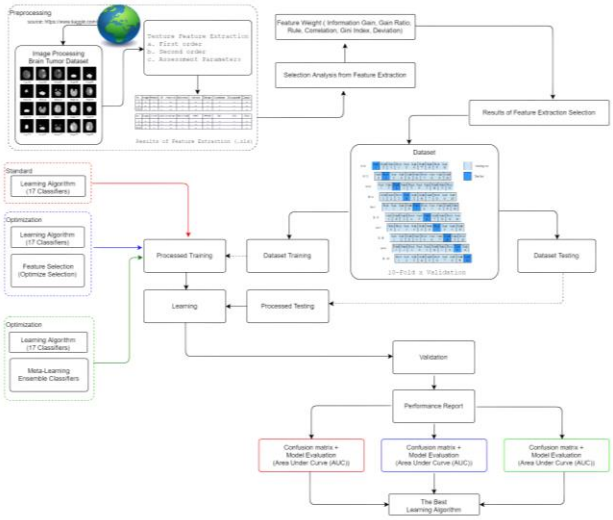


Figure 1. Proposed model.

A. Data Collection

To evaluate the effectiveness of feature selection and ensemble classifiers in brain tumor classification, we used a dataset obtained from Kaggle (https://www.kaggle.com). The dataset comprised 3,762 images categorized as "Tumor" and "Non-tumor" and saved in either .jpg or .jpeg format. Each image had dimensions of 240×240 pixels and a depth of 24 bits, allowing for processing of RGB colors with 8 bits for each of the red (R), green (G), and blue (B) components. The images also had a density of 300 dpi (horizontal and vertical), which is a measure of density from one point to another in a unit of an inch (dots per inch). Examples of brain imaging samples with and without tumors are shown in Fig. 2.

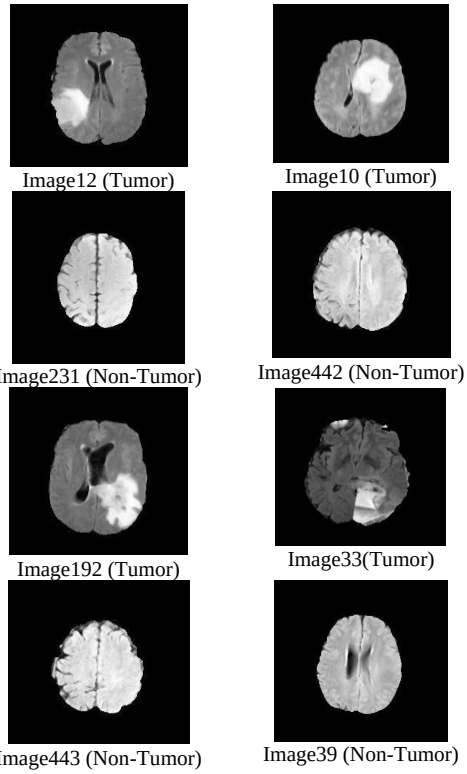


Figure 2. Sample brain image with size 240×240 pixels Complete file: shorturl.at/asZ02.

B. Preprocessing

To enhance the accuracy of brain tumor classification, we conducted a feature extraction process using the Confirmatory Factor Analysis (CFA) technique on the brain tumor dataset obtained from Kaggle (https://www.kaggle.com). The CFA technique comprised of first-order and second-order predictor classes, which were summarized in an excel spreadsheet (.xls) containing 17 predictor classes per image. We compared and selected the best predictor class using feature weights such as information gain, gain ratio, rule, correlation, Gini index, and deviation to improve model accuracy. This preprocessing step was followed by developing a model that compared 17 classifiers from six groups, including DT Model, SVM, Naive Bayes Classifier, Logistic Regression, GLM Classifier, and Neural Network, with 12 predictor classes to classify images as "tumors" or "non-tumors". The planned workflow diagram based on Fig. 1 is depicted in Fig. 3.

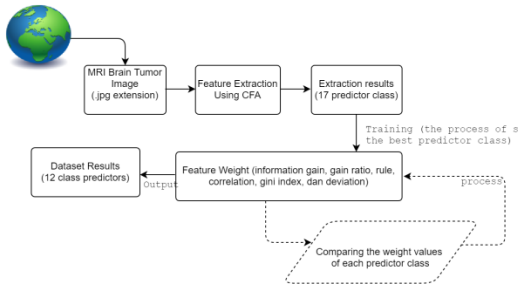


Figure 3. Preprocessing phases completed.

C. Classification Process

After the preprocessing phase, the next step involves the classification stage, which is further divided into two parts —training and testing, and subjected to k-fold cross-validation with k = 10. During the training process, 17 classifiers were compared using three different models, namely: (1) 17 standard classifier models (model CS); (2) 17 classifier models with feature selection (model C+FS); and (3) 17 classifier models with ensemble classifier (model C+ES). The accuracy of each model was then evaluated using the test dataset, and the results of the classification methods for each model can be found in Table I.

D. Evaluation Method

In the evaluation phase, the performance of all 17 classifiers in classifying brain tumor datasets into "tumors" and "non-tumors" was assessed. This process involved utilizing the confusion matrix, ROC curve, and Eqs. (1)–(5). The ROC curve was constructed using the False Positive Rate and True Positive Rate derived from computations with the confusion matrix. The performance was determined by the AUC of the ROC curve, as shown in Algorithm 1 and Algorithm 2. It can be concluded that a larger area under the curve indicates better performance.

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

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

$$\text{Recall} = \frac{TP}{TP+FN} \quad (3)$$

$$\text{False Positive Rate (FPR)} = \frac{FP}{FP+TN} \quad (4)$$

$$\text{True Positive Rate (TPR)} = \frac{TP}{TP+FN} \quad (5)$$

Accuracy is a metric that measures how well a model predicts overall, expressed as the percentage of correct predictions (True Positives and True Negatives) compared to the total number of predictions (True Positives, False Positives, False Negatives, and True Negatives). Precision, on the other hand, quantifies the proportion of true positive predictions out of all positive predictions made by the model, indicating its "precision" or accuracy in classifying positive labels. Recall, also known as sensitivity, measures the proportion of all positive cases successfully detected by the model, reflecting its ability to "recall" or "detect" positive cases. The False Positive Rate (FPR) calculates the ratio of false positive predictions to the actual total negative cases, informing us about how often the model incorrectly identifies negative class as positive. Lastly, the True Positive Rate (TPR) or Sensitivity gauges how well the model detects true positive cases or how sensitive it is to positive cases. These metrics provide valuable insights into the performance of classification models in terms of accuracy, precision, recall, false positive detection, and true positive detection.

TABLE I: THE RESULTS OF THE COMPARISON OF THE MODEL ACCURACY AND AREA AUC VALUES

Classifiers		H1	H2	H3	H4	H5	H6
Decision Tree (DT) Model	Decision Tree (DT)	97.22	0.985	98.93	0.983	97.95	0.989
	Random Forest (RF)	97.03	0.994	98.64	0.997	98.51	0.997
	Gradient Boosted Tree (GBT)	96.11	0.995	98.51	0.995	98.41	0.995
	Random Tree (RF)	92.85	0.925	91.12	0.906	97.58	0.991
Support Vector Machine (SVM)	SVM	95.03	0.966	97.93	0.995	98.06	0.995
	SVM (LibSVM)	83.21	0.945	89.95	0.964	86.84	0.991
	SVM (Linear)	97.09	0.996	98.01	0.995	98.06	0.996
	SVM (Evolutionary)	55.79	0.743	57.79	0.743	55.79	0.743
Naive Bayes Classifier	Naive Bayes	96.89	0.990	96.68	0.992	96.68	0.991
	Naive Bayes (Kernel)	93.59	0.979	96.2	0.991	95.7	0.979
Logistic Regression	Logistic Regression	98.43	0.997	98.01	0.997	98.38	0.998
	LR (SVM)	96.97	0.997	97.82	0.995	98.22	0.997
	LR (Evolutionary)	44.74	0.531	44.74	0.531	44.74	0.526
GLM Classifier	Generalized Linear Model	94.14	0.966	98.01	0.996	98.11	0.996
Neural Network	Neural Net	96.17	0.995	97.9	0.995	98.22	0.995
	Deep Learning	96.51	0.998	98.19	0.997	98.46	0.998
	AutoMLP	95.17	0.995	97.71	0.991	98.17	0.995

Explanation of table headers: **H1**: represents the accuracy of the model CS, **H2**: represents the AUC of the model CS, **H3**: represents the accuracy of the model C+FS, **H4**: represents the AUC of the model C+FS, **H5**: represents the accuracy of the model C+ES, and **H6**: represents the AUC of the model C+ES.

TABLE II. INTERPRETATION OF AUC VALUES

AUC value	Connotation
0.9< **AUC**< 1.0	Excellent
0.8< **AUC**< 0.9	Good
0.7< **AUC**< 0.8	Fair
0.6< **AUC**< 0.7	Poor
0.5< **AUC**< 0.6	Insignificant

Algorithm 1: Generating ROC Curve

```
Input:
- predicted values: y_pred (array)
- true values: y_true (array)
Output:
- fpr (false positive rate) values (array)
- tpr (true positive rate) values (array)
- area under the curve (AUC) measure (float)
# Step 1: Compute True Positive Rate (TPR) and False
Positive Rate (FPR) for different thresholds
fpr = []
tpr = []
thresholds = sorted(y_pred, reverse=True)
num_positive_cases = sum(y_true)
num_negative_cases = len(y_true) - num_positive_cases
for threshold in thresholds:
    predicted_positive = [int(x >= threshold) for x in y_pred]
    true_positives = [x*y for x,y in zip(predicted_positive,
y_true)]
    false_positives = [(1-x)*y for x,y in zip(predicted_positive,
y_true)]
    tp_rate = sum(true_positives)/num_positive_cases
    fp_rate = sum(false_positives)/num_negative_cases
    tpr.append(tp_rate)
    fpr.append(fp_rate)
```

Algorithm 2: Calculating the AUC measure

```
auc = 0.0
for i in range(1, len(fpr)):
    auc += (fpr[i] - fpr[i-1]) * (tpr[i] + tpr[i-1]) / 2.0
return fpr, tpr, auc
```

The pseudocode assumes that the input y_pred and y_true are arrays of predicted and true binary labels, respectively. The output includes two arrays of false positive rate (fpr) and true positive rate (tpr) values, along with the area under the curve (auc) measure. The ROC curve can be plotted using the fpr and tpr arrays, which represent the x and y axes, respectively. The AUC measure represents the area under the ROC curve and serves as a metric for evaluating the performance of a binary classifier.

III. RESULTS AND DISCUSSION

Based on the evaluation results, it can be concluded that optimizing the classification models through feature selection or ensemble classifiers has led to improved accuracy in the classification of brain tumors. On average, the improvement in accuracy ranged from 1% to 2%. However, it was observed that SVM (Evolutionary) and LR (Evolutionary) classifiers were not suitable for brain tumor classification, as they produced accuracy values below 50% in both standard and optimization model testing.

Fig. 4 shows the results of the tests conducted on three models (Model CS, Model C+FS, and Model C+ES), it can be observed that Model C+FS and Model C+ES produce higher accuracy than Model CS for most classifiers. Overall, Model C+FS performs the best among the three models with an accuracy improvement of 1%–3% for most classifications compared to Model CS. On the other hand, Model C+ES provides an accuracy increase of 0.5%–2% compared to Model CS. The accuracy improvements of Model C+FS can be seen in the tests on Decision Tree Model, Support Vector Machine, Naive Bayes Classifier, Logistic Regression, GLM Classifier, and Neural Network. Similarly, Model C+ES shows an increase in accuracy in the tests on Decision Tree Model, Support Vector Machine, Naive Bayes Classifier, Logistic Regression, and Neural Network. Based on these test results, it can be concluded that using feature selection or ensemble classifiers can improve accuracy in brain tumor classification. However, the effectiveness of using feature

selection or ensemble classifier depends on the type of classifier chosen.

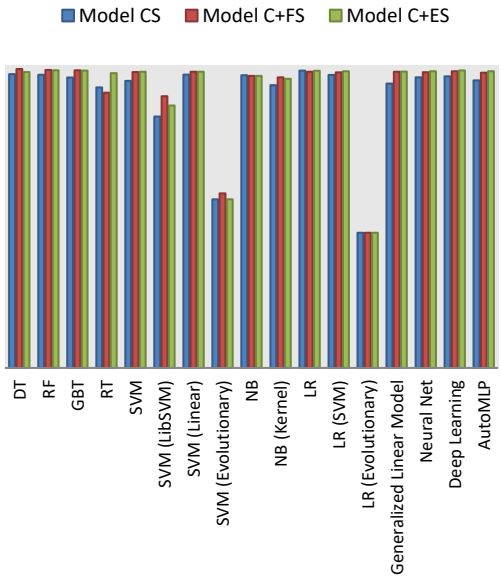


Figure 4. The graph shows the model's accuracy scores for 17 classifiers.

Fig. 5 shows the average accuracy values for each group of classifiers. The DT model had the highest increase in accuracy, with a 2.31% increase for ensemble classifier optimization and a 1% increase for feature selection optimization. The neural network model also had significant improvements in accuracy, with a 2.33% increase for ensemble classifier optimization and a 1.98% increase for feature selection optimization. The SVM, Naive Bayes Classifier, Logistic Regression, and GLM Classifier models had more modest increases in accuracy, ranging from 0.1% to 0.98% for all optimization methods.

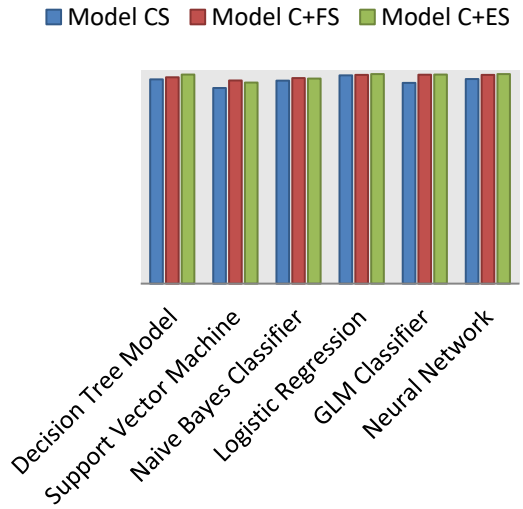


Figure 5. The graph shows the model's average accuracy scores.

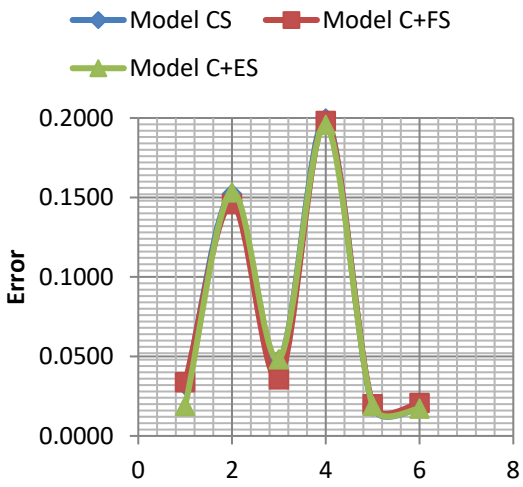


Figure 6. The graph shows the model's error accuracy scores.

Fig. 6 illustrates the errors that occurred during the classification tests. When optimization was applied, errors were reduced in all models. The DT model had the largest reduction in error, with values of 0.0320, 0.0338, and 0.0189 for model CS, model C+FS, and model C+ES, respectively. Compared to model CS, the difference in value was around 0.0131. The other classifier groups had smaller reductions in error, with values ranging from 0.001 to 0.0003 when compared to model CS.

To analyze the comparison between Model CS and Model C+FS, as well as Model CS and Model C+ES, we can utilize the Receiver Operating Characteristic (ROC) curve. The ROC curve is used to visualize and compare the classification performance at various thresholds. Based on the given table, we can create ROC curves for both comparisons. Analyzing the results, it can be observed that Model C+FS consistently outperforms Model CS in all classifications except for Support Vector Machine. Similarly, Model C+ES demonstrates better performance than Model CS across all classifications except for Support Vector Machine. This suggests that both Model C+FS and Model C+ES generally provide superior results compared to Model CS in terms of classification performance. However, it's essential to consider additional factors and examine more detailed information when evaluating model performance.

Based on the information provided, it seems that the ROC curve value for all classifier models has increased by 0.004 to 0.01, which is associated with the improvement in various performance metrics such as accuracy, precision, recall, and sensitivity values. The DT, RF, SVM, SVM (LibSVM), and SVM (Linear) classifiers showed significant improvement, as seen in Fig. 7. Fig. 8 indicates that DT outperforms the other groups based on the average value of the ROC curve, with an increase in value by 0.0183 for Model C+ES. The ROC curve graph for DT with ensemble classifier optimization is also shown.

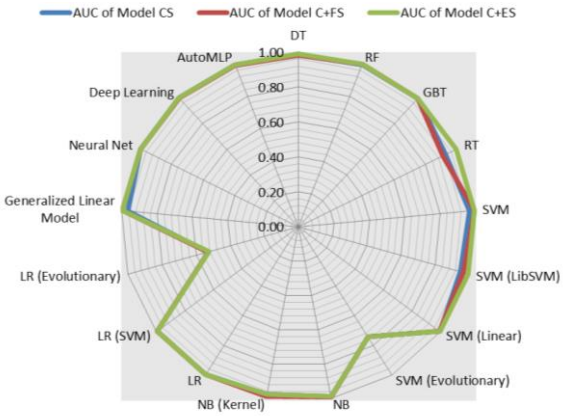


Figure 7. ROC curve values graph for all classifiers.

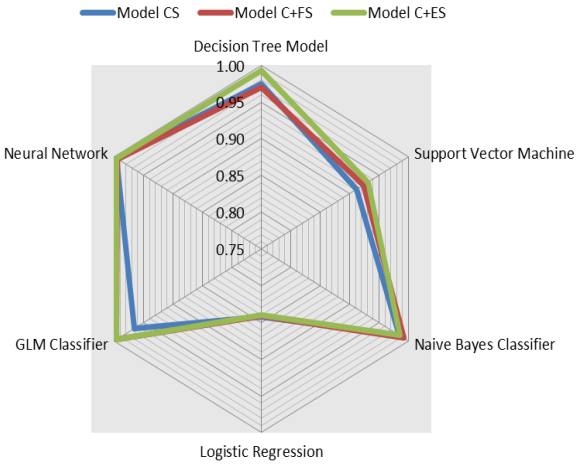
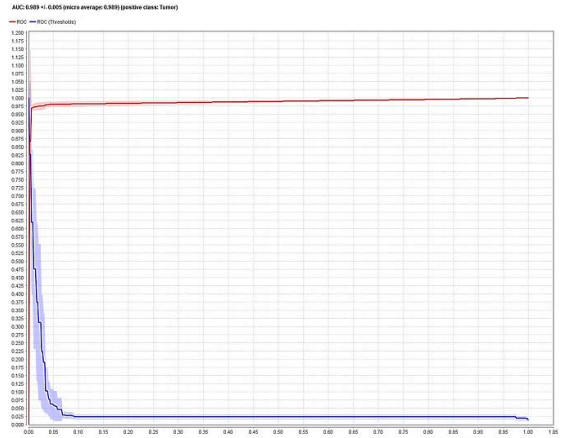
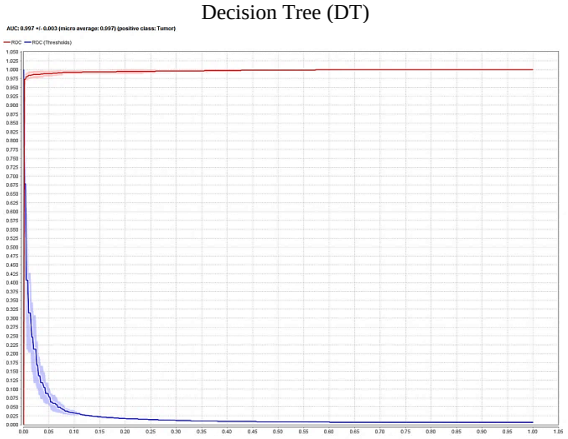


Figure 8. ROC curve values graph by group.

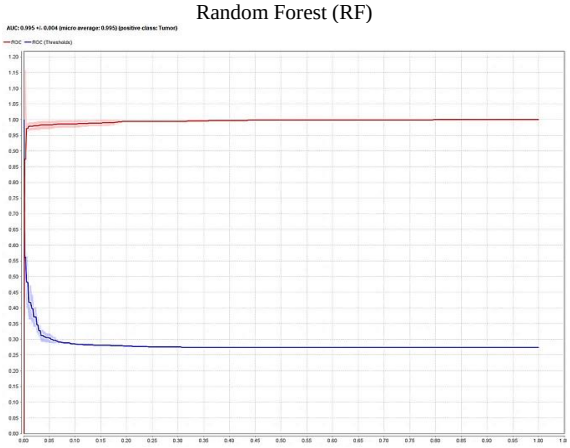
Fig. 9 explains that the evaluation of the classification models using ROC curve analysis showed that the Random Tree (RT) classifier outperformed other classifiers, such as Decision Tree (DT), Random Forest (RF), and Gradient Boosting Tree (GBT) classifiers. The ROC curve graph indicated that RT has the highest Area Under Curve (AUC) value of 0.999, indicating excellent performance. Moreover, RT achieved a maximum accuracy of 97.58%, which is higher than the other classifiers evaluated. The precision level of the accuracy data obtained by the RT classifier was good, with a value of 0.9872, indicating that the classifier produced a low number of false positives. Additionally, the recall was 0.9584, meaning that the RT classifier identified almost all of the positive cases in the dataset. The sensitivity level of the RT classifier was also extremely high compared to the DT, RF, and GBT classifiers, with a value of 0.9584. Furthermore, the optimization of the ensemble classifier with feature selection (C+ES) resulted in a very low error rate, with the smallest error margin being 0.0242 for the RT classifier. This finding implies that the optimization of the ensemble classifier with feature selection can improve the performance of the classification models. Overall, the results indicate that the RT classifier with the C+ES model is the most accurate and efficient classifier for brain tumor classification.



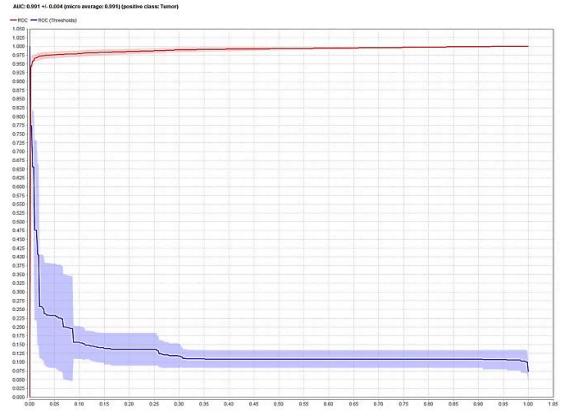
Decision Tree (DT)



Random Forest (RF)



GBT



Random Tree (RT)

Figure 9. ROC Curve Graph for Decision Tree Model (model C+ES) classifier.

IV. Conclusion

In this article, we presented a comparative study of ensemble classifiers with feature selection techniques for enhancing brain tumor classification performance. The study involved the classification of brain tumors using 17 classifiers from six different groups, namely Decision Tree Model, Support Vector Machine, Naive Bayes Classifier, Logistic Regression, GLM Classifier, and Neural Network. The dataset used for the study was a collection of brain tumor images available on Kaggle. We first preprocessed the data using Confirmatory Factor Analysis (CFA) and feature weight to extract meaningful features from the images. We then compared the performance of three different models: 17 standard classifiers, 17 classifiers with feature selection, and 17 classifiers with ensemble classifiers. The evaluation was carried out using k-fold cross-validation (k = 10) to ensure the robustness of the results. Our findings revealed that the ensemble of classifiers in the Decision Tree Model group was the best classifier, with an accuracy of 98.11% and an AUC of 0.993. Specifically, the Random Tree method within the Decision Tree Model group with ensemble classifiers showed an accuracy of 97.58%, which was 4.73% higher than the standard classification model and 6.46% higher than the feature selection optimization model. Furthermore, our proposed method (feature selection optimization or ensemble classifiers) showed superior classification performance compared to the standard method. Our study suggests that future research can focus on combining optimization with other classification models to further enhance brain tumor classification performance. Additionally, addressing the main issues in this study, such as limited memory and slow training speed, can be a potential avenue for future research.

Conflict of Interest

The authors declare no conflict of interest.

Author Contributions

Yuhandri devised and supervised the research while providing suggestions and recommendations along the way include wrote the revision of papers. Agus Perdana Windarto conducted the experiment, analyzed the resulting data, and wrote the paper with support from Muhammad Noor Hasan Siregar. All authors approved the final version of this paper.

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