Optimized Multi-model Framework for Enhanced and Timely Brain Tumor Classification Leveraging DeepLoc, Machine Learning Architectures, and Ensemble Learning Technique

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***Abstract*—Brain Tumors (BT) is one of the major global health concerns with which diagnosis and treatment challenges are associated. Current techniques for BT identification and classification are time consuming and subjective due to manual expert interpretation of Magnetic Resonance Imaging (MRI) scans. The present research work focuses on Optimized Multi-Model Framework that incorporates DeepLoc, Machine Learning Architectures, and Ensemble Learning Technique for Enhanced Brain Tumor Classification. The framework uses DeepLoc algorithm for MRI images and exploits ML techniques including Support Vector Machine (SVM), k-Nearest Neighbor (kNN), and Naive Bayes (NB). By linking these models through ensemble techniques, we aim to attain higher classification performance. The effectiveness of approach is identified using key evaluation metrics including Training Time (TT:1.3 s), Testing Time (TET:1.9 s), Area Under Curve (AUC:88%), Classification Accuracy (CA:71%), F1-Score (F1:70%), and Recall (71%). Experimental results when compared with the previous approaches have shown a substantial increase in the values of evaluation parameters. Comprehensive validation is done using Confusion Matrix (CM), Calibration Plots (CP) and Receiver Operating Characteristic (ROC) Analysis. Ultimately, this research work intents to provide an efficient and reliable tool for early brain tumor classification, enabling timely treatment interventions for patients.**

***Keywords*—Deep Learning (DL), Machine Learning (ML), Ensemble Learning (EL), brain tumor, DeepLoc**

I. Introduction

Brain is one of the most important parts of the human body and is crucial for human functioning. Any kind of damage done to brain, can be life threating [1]. Four core sub-parts of brain include the Frontal Subpart (FS), Parietal Subpart (PS), Temporal Subpart (TS) and Occipital Subpart (OS) [2]. Few of body functions like thinking, planning, movement, speech and emotions are handled by FS. Touch, pain sensation, taste, stress and body temperature body functions and are handled by PS. Functions like listening, seeing and understanding are done by TS. OS is responsible for remembering the things. These four subparts are majorly responsible for the way we see and interact with world around us.

The existence of lump or abnormal tissue growth in any part of brain is termed as brain tumor [3]. The presence of tumor has adverse effects on the functions of brain. Tumor can be benign or malignant. Benign tumor is the one that is non-cancerous and it does not spread to other parts of the body. Malignant tumor is the one that is cancerous and it spreads to other parts of the body. Stage 1 to Stage 4 cancer ranges from localized area to widespread distribution of cancer [4]. Gliomas arises from the glial cells present in brain [5]. Primary brain tumor initiates in brain while Secondary brain tumor starts in other body parts and is spread [6].

BT is extra mass in the brain. This mass collides with nearby skull cells and create pressure in the brain. The function of the normal brain cells gets disturbed. Reasons of brain tumor include lifestyle, environmental and occupational factors [7] etc. Symptoms of brain tumor [8] include headache, vomiting, blurred vision, mood swings, hearing problem, speech problem, decline in cognition and seizures etc.

Brain tumor can be identified by consultation and diagnosis done by a neurologist. In this process, tests are performed [9] like, Like Magnetic Resonance Imaging (MRI), Computed Tomography (CT) Scan, Complete Blood Count (CBC), Erythrocyte Sedimentation Rate (ESR), Biopsy and Molecular tests. The type of test to be performed depends on the patient and diagnosis by the doctor. A person suffering from brain tumor is advised to eat healthy food [10]. Common approaches of Brain Tumors (BT) treatment [11] include Surgery, Radiation, Chemotherapy and Gene therapy.

In this paper we will do identification and classification of BT in an automated manner using Artificial Intelligence (AI) algorithms. The research work is organized by laying Introduction in the Section I. Literature review is specified

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in Section II. Multi-model approach is discussed in Section III. The projected methodology is laid in Section IV. Experimental findings are represented in Section V. The concluding remarks are given in Section VI.

II. Literature Review

A technique for classification of BT using Deep Learning (DL) was proposed by Das *et al.* [12]. The model utilized a number of Machine Learning (ML) algorithms. These algorithms include SVM, Random Forest (RF), YOLOv5, and Neural Network (NN) for the classification purpose. An accuracy of 99% was achieved using the RF classifier. Thakur *et al.* [13] projected an ensemble-based approach for prediction of gliomas disease. The paper suggested gliomas to be the most common types of tumors. It is identified in this paper that accurate prediction of glioma is necessary for treating the disease.

A technique for detection of BT using hybrid ML models was given by Ishaq *et al.* [14]. kNN and Gradient Boosting algorithm are used for the prediction purpose. A hybrid technique makes use of the advantages of both the algorithms. Segmentation based accuracy achieved using the given approach was 71% for 3D-UNet. While for 2D-UNet the accuracy came out to be 64%. Zurfi *et al.* [15] identified a technique of Glioma Grading (GG) using 3D texture analysis and ML. MRI images taken are observed for different angles. In this paper, it is suggested that the more is the Glioma, higher are the chances of mortality.

A multi-level ensemble learning technique for classification of BT was proposed by Xenya and Wang [16]. Two main techniques utilized for BT detection include segmentation and classification. Segmentation based on region properties is utilized. And for classification a three-class architecture is followed. BT classification technique using EL was proposed by Remzan *et al.* [17]. The paper mentions that children and the old people are the ones in which chances of BT existence is common. The nature of BT is identified to be heterogeneous. A transfer-based learning approach is suggested in this paper.

Hossain *et al.* [18] suggested an approach of BT detection and classification using three modules. First module includes transfer learning, second module includes ensemble model and the third module is of vision transformers. Attention-based model for identification and classification of BT was given by Shah *et al.* [19]. Convolutional auto encoders and Bayesian based ensemble voting mechanism is used for identifying the abnormalities. The primary objective of this paper is to create an automated system that could segment and classify the BT.

Classification and grading of BT was proposed by Ullah *et al.* [20]. The paper identifies that the survival rate of this dangerous disease is nearly 70%. ML algorithms can help a lot in this area. A lightweight ensemble model corresponding to XGBoost is adopted in this paper. Behera *et al.* [21] proposed a DL technique of transfer learning for BT classification. Magnetic Resonance (MRI) scans are taken into consideration in this paper. Clustering is done using superpixel algorithm. A dual approach of BT Classification was proposed by Asiri *et al.* [22]. MRI images are suggested to be the most common way of identification of BT in comparison to other imaging techniques.

A review on BT classification using DL is given by Neamah *et al.* [23]. MRI images are suggested to be used for BT classification in this paper. DL strategies for BT are identified within a period of 2019 to 2022. Advantages and disadvantages of each approach is discussed by the authors. A Fuzzy C-Means (FCM)-SVM based technique of BT classification is suggested by Alqhtani *et al.* [24]. The paper reveals that the leading cause of death world-wide is cancer and nervous system disorders.

In spite of the considerable efforts dedicated by many researchers in BT classification, still a standardize approach is lacking in this field of study. In the subsequent segment, we investigate into the EL, ML and DL models along with the types of BT classified by our proposed approach.

III. The Multi-Model Approach

DeepLoc algorithm [25] is used in image embedding by which vector of numbers are used to represent images. Complex visual data from MRI scans is interpreted and converted into numerical form. DeepLoc is a Convolutional Neural Network (CNN) that is trained on nearly 22 K images containing diverse cell structure. In this proposed research we will differentiate between different types of BT using DeepLoc. Thus, the algorithm is well suited for multi-classification of BT. DeepLoc algorithm is stated below:

(1) BT based MRI scans are taken as input.
(2) VGG16 Pretrained model is chosen for feature extraction tasks including colour moments, texture, shape, spatial features, complex patterns, frequency components, edge and object detection features.
(3) Model is initialized using pre-trained weights.
(4) Last layer of classification is removed to obtain penultimate feature representation for transfer learning.
(5) For each image I, the model is utilized for feature extraction so as to obtain output in a multi-dimensional tensor form.
(6) Flattening is done to convert tensor into one dimensional vector.
(7) Extracted numerical features are then used for training the classification models.

SVM is a Supervised Learning Algorithm (SLA) that is used for both classification and regression. In our proposed research work we will be using the technique for BT Classification. In SVM hyperplane is used for identifying the classes as shown in Fig. 1 [26]. Four classes identified by SVM for BT includes Glioma Tumor (GT), Meningioma Tumor (MT), No Tumor (NT), and Pituitary Tumor (PT).

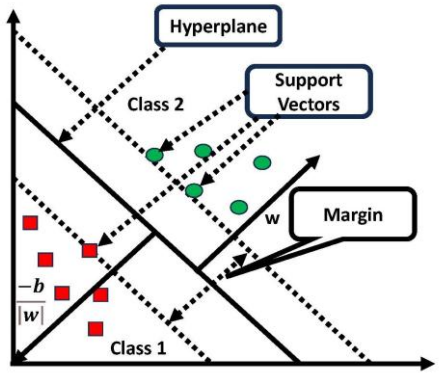

Fig. 1. Support Vector Machine (SVM).

Naive Bayes Algorithm (NBA) is SLA that is used for BT classification. In this work, we will use the algorithm to predict as to which class the tumor belongs to. The primary basis of NBA is Bayes' Theorem as given in Eq. (1). Probability plays an important role in NBA. In NBA there is an assumption that all the variables that are being used are independent to each other. This feature makes the algorithm unique as there is no differentiation as to which feature is important and which one is less.

$$P(A|B) = \frac{P(B|A).P(A)}{P(B)} \quad (1)$$

where, P(A|B) is probability of happening of event A such that B has already occurred; P(B|A) is probability of happening of event B such that A has already occurred; P(A) is probability of happening of event A; P(B) is probability of happening of event B; kNN is also SLA that is principally used for the classification tasks as shown in Fig. 2 [27]. kNN is a statistical technique, as in this predicting the class of new point depends on the Euclidean Distance (ED). Nearest neighbors are identified using the ED. k is the hyperparameter. Identifying the right value of k is significant in this algorithm. In the present research work we will be identifying the class of tumor on the basis of k Nearest Neighbors.

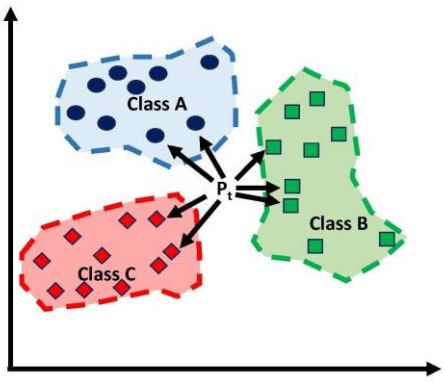

Fig. 2. k-Nearest Neighbor (kNN).

Ensemble Learning (EL) is a group learning technique in which multiple models are used, so to take the most appropriate decision corresponding to the problem. In our proposed research, we will be using three different algorithms which include SVM, Naive Bayes and kNN. Each algorithm independently processes the features extracted by the DeepLoc algorithm, generating predictions for each tumor class. The ensemble method aggregates these predictions, leveraging the strengths of each model to improve overall performance. By maintaining diversity among the algorithms, the ensemble approach reduces the risk of overfitting and increases robustness. The final classification is determined by selecting the optimized output from this diverse set of models. Evaluation metrics will be identified corresponding to each of these algorithms and the algorithm with the optimized output is selected. Diversity is getting maintained in the algorithms generating heterogeneous ensembles.

IV. Methodology

A. Categories of BT

Brain Tumors identified in this research work are categorized into 4 different classes such as Glioma Tumor (GT), Meningioma Tumor (MT), No Tumor (NT) and Pituitary Tumor (PT). GT is a class of tumor that generally happens in brain and spinal cord. MT is the tumor of meninges. This tumor is the one that is usually benign i.e. it does not spread and is localized. MT grow slowly over a period of time. It is for this reason that people do not know that they have MT. A NT class is the one in which there is abnormal growth of cells but it is not cancerous. It is benign in this class. PT is the one that is present in the Pineal Gland (PG) of the brain. There are two possibilities for PT. The first case is of Null cell Adenoma. Here the tumor is not arising from the cells that form hormones. The second case of PT is the one where tumor arise from the cells that form hormones. A comprehensive state of art facilities is required for BT as the patient may be referred to multiple departments like dedicated neurosurgery, postoperative psychotherapy, endocrinology department and other patient care units.

B. Dataset

The publicly available Brain MRI scans dataset is utilized in this study [28]. The dataset comprises of 3264 scans is divided into training and testing sets. The training set contains 2870 MRI scans, while the testing set contains 394 scans. The training set includes 826 images of GT, 822 images of MT, 395 images of NT and 827 images of PT. One image from each category is depicted in Fig. 3. Testing set includes 100 images of GT, 115 images of MT, 105 images of NT and 74 images of PT. The MRI scans in the dataset are in JPEG format, with dimensions of 512×512 pixels. This standard resolution ensures adequate detail for analysis while maintaining manageable file sizes. The dataset encompasses a diverse range of brain pathologies, enhancing its utility for training and evaluating diagnostic models. Each category's representative images are selected to provide a true foundation for analysis.

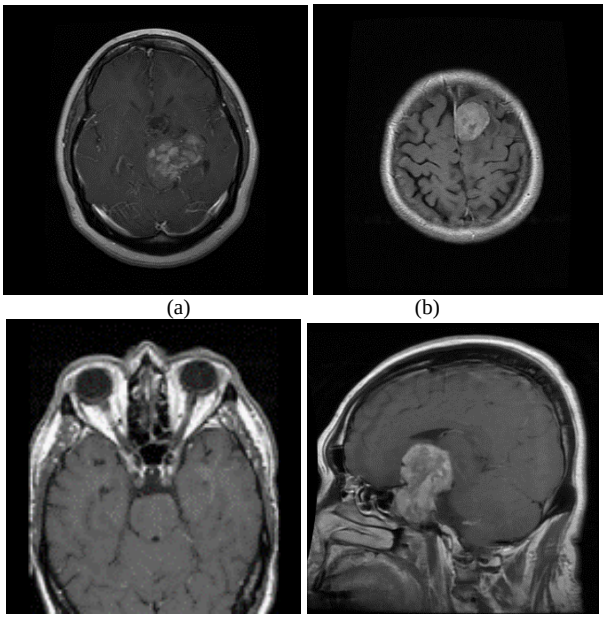

Fig. 3. MRI Scans of BT.

C. Proposed Model

This work employs a multi-model approach of brain tumor classification. The output of the DeepLoc algorithm is processed by ML algorithms. The algorithms used are SVM, Naive Bayes, and kNN. Ensemble learning selects the optimal output for classification. The model supports two outcomes. One is model learning and the other is prediction. Evaluation metrics include Confusion Matrix (CM), Calibration Plots (CP), and ROC Analysis. The second outcome involves predictive analysis on test data for classification. Fig. 4. illustrates the proposed Experimental Model Architecture (EMA).

D. Stages of EMA

Various Stages(S) of EMA include:

S1: In first stage MRI scans are imported from the directory and organized into training and testing sets.

S2: In second stage image viewer displays images in comparative mode, alongside a data table displaying dimensions. Columns are selected to define the target feature using select column widget.

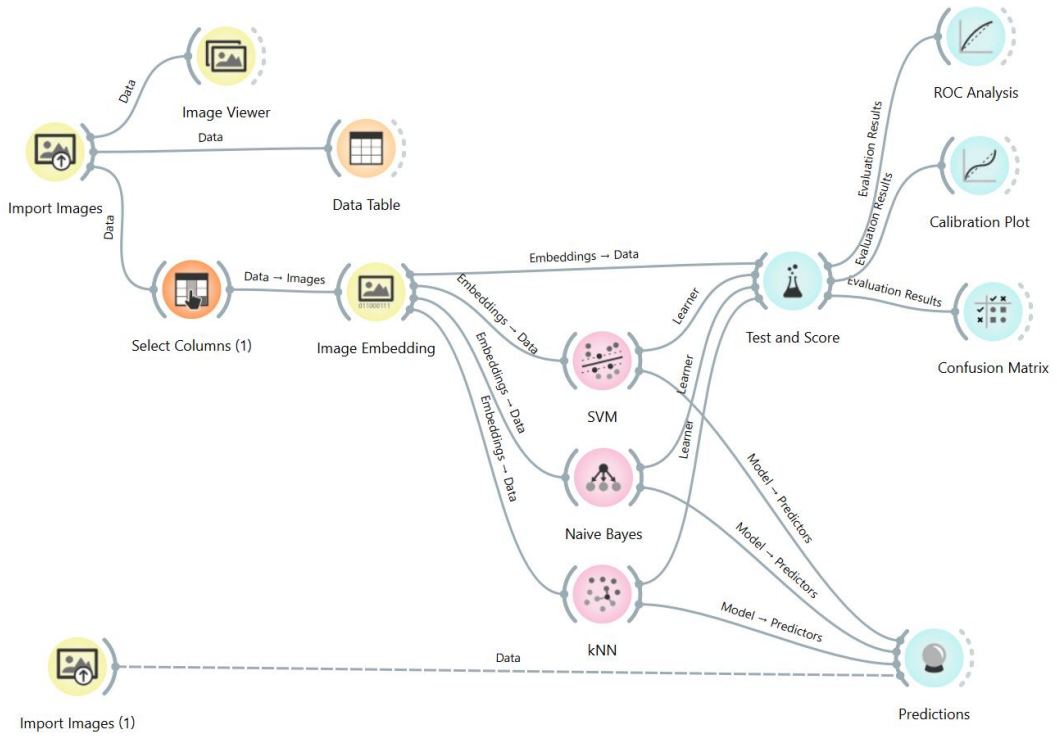

Fig. 4. Experimental model architecture.

S3: In third stage, DeepLoc embedder converts images into vectors identifying 512 features from each image resulting in nearly 1.4 million numerical values.

S4: In fourth stage, three ML models are incorporated including SVM, Naive Bayes and kNN.

S5: In fifth stage, results are evaluated using evaluation metrics.

S6: In the sixth stage, results are validated visually using CM, CP and ROC Analysis.

S7: In the last stage final tumor predictions are done using the trained model.

V. Experimental Findings

A. Evaluation Results

Results for BT classification is depicted in Table I. The table shows performance of three ML models which include SVM, kNN and NB. Various parameters for consideration include Training Time (TT), Testing Time (TET), Area Under Curve (AUC) [29], Classification Accuracy (CA) [30], F1-Score [31], and Recall [32]. A lower value of TT and TET is considered good as the time

taken is less by the model for both training and testing. A higher value of AUC indicates better performance as it shows how correctly the model can classify. CA is the ratio of correctly identified cases to the total number of cases. Harmonic mean of precision and recall generates the F1-Score. Recall is the ratio of correctly recognized positive cases to the total number of positive cases. Analytical equations used for the various evaluation metrics are given in Eq. (2)–(6).

TABLE I. RESULTS OF BRAIN TUMOR CLASSIFICATION

Model	TT(s)	TET(s)	AUC	CA	F1	Recall
SVM	14.1	7.8	0.85	0.59	0.57	0.57
kNN	1.3	1.9	0.88	0.71	0.70	0.71
NB	2.1	0.61	0.80	0.58	0.55	0.56

$$\text{TT} = \text{Time per iteration} \times \text{Number of Iterations} \quad (2)$$

$$\text{TET} = \text{Time per Sample} \times \text{Number of Samples} \quad (3)$$

$$CA = \frac{TP + TN}{TP + TN + FP + FN} \quad (4)$$

$$F1\ Score = \frac{Precision \times Recall}{Precision + Recall} \quad (5)$$

$$Recall = \frac{TP}{TP + FP} \quad (6)$$

where, True Positives (TP): Correctly predicted positive cases; True Negatives (TN): Correctly predicted negative cases; False Positives (FP): Incorrectly predicted positive cases; False Negatives (FN): Incorrectly predicted negative cases. Area Under the Curve (AUC) is calculated from the Receiver Operating Characteristic (ROC) curve, representing the trade-off between sensitivity and specificity across different thresholds.

To prevent overfitting, we employed dropout regularization technique, and early stopping during training. Hyperparameters such as batch size, learning rate, and optimizer were initially set based on common practices in literature, with a batch size of 32 and a learning rate of 0.001 being standard starting points.

We applied grid search hyperparameter optimization to fine-tune these values, ensuring the best model performance. For cross-validation, we utilized k-fold cross-validation, which allowed us to divide the dataset into k subsets, training the model on k–1 subsets and validating on the remaining one. This process was repeated k times to ensure that each data point was used for both training and validation, providing a robust evaluation of the model's performance.

Analysing the three models suggest that kNN has the least TT of 1.3 s and second lowest TET of 1.9 s. The lowest TET is of 0.61 s for NB. AUC parameter of 0.88 is the highest for kNN among all three algorithms. CA, F1-Score and Recall parameters are also high in case of kNN and it comes to be 0.71, 0.70, and 0.71.

B. Comparative Analysis

Comparative Analysis of CA of the proposed technique with former methods are portrayed in Table II. A rise of 30.98% is achieved for CNN when compared with our proposed approach. Similarly, a rise of 33.80%, 30.98% and 45.07% is achieved for Long Short-Term Memory (LSTM), Gated Recurrent Unit (GRU), Deep Neural Network (DNN). This shows that the. model is quite efficient in its performance of BT Classification. Percentage improvement formula of CA is given in Eq. (7).

TABLE II. COMPARATIVE ANALYSIS OF CA WITH FORMER METHODS

Model	CA	% Inc.
CNN	0.49 [14]	30.98
LSTM	0.47 [14]	33.80
GRU	0.49 [14]	30.98
DNN	0.39 [14]	45.07
Our Multi-model Approach	0.71	--

$$\%\ \text{Improvement} = (\text{Inc.} / \text{Org. CA}) \times 100 \quad (7)$$

Comparative Analysis of F1-Score of the proposed technique with former methods are portrayed in Table III. A rise of 53.52% is achieved for CNN when compared with our proposed approach. Similarly, a rise of 50.70%, 49.30% and 45.07% is achieved for LSTM, GRU and DNN. This shows that the model is quite efficient in classifying the brain tumor. Percentage improvement formula of F1 is given in Eq. (8).

$$\%\ \text{Improvement} = (\text{Inc.} / \text{Org. F1-Score}) \times 100 \quad (8)$$

TABLE III. COMPARATIVE ANALYSIS OF F1 WITH FORMER METHODS

Model	F1	% Inc.
CNN	0.33 [14]	53.52
LSTM	0.35 [14]	50.70
GRU	0.36 [14]	49.30
DNN	0.39 [14]	45.07
Our Multi-model Approach	0.71	--

C. Confusion Matrix

The Confusion Matrix (CM) provides a detailed breakdown of classification performance, allowing for an assessment of both accuracy and types of errors made by each model. The true positive, false positive, true negative, and false negative rates can be derived from the matrix, offering insights into where each classifier excels or struggles. Additionally, the overall accuracy for each model can be calculated by summing the diagonal elements and dividing by the total number of predictions. This comprehensive analysis underscores the importance of model selection in clinical applications, where accurate classification is crucial for effective diagnosis and treatment planning.

Confusion Matrix for SVM, kNN and NB is depicted in Figs. 5–7. The diagonal part of CM shows the correct classifications while other cells show the misclassification. Comparing all the three CM shows that kNN is working best in classification for GT and MT with the highest values of 1950 and 1639. Similarly, for NT case SVM is showing promising results with 1112 correct classifications. Again, for PT, SVM is showing best result with a value of 2625. But here kNN prediction is not for behind with a value of 2538. An average of all the cases makes kNN a successful winner over SVM with an increase of 19.49%.

		Predicted				
		glioma_tumor	meningioma_tumor	no_tumor	pituitary_tumor	Σ
Actual	glioma_tumor	1108	929	27	746	2,810
	meningioma_tumor	849	972	174	805	2,800
	no_tumor	86	56	1112	86	1,340
	pituitary_tumor	51	66	68	2625	2,810
	Σ	2,094	2,023	1,381	4,262	9,760

Fig. 5. Confusion matrix for SVM.

		Predicted				
		glioma_tumor	meningioma_tumor	no_tumor	pituitary_tumor	Σ
Actual	glioma_tumor	1950	692	10	158	2,810
	meningioma_tumor	718	1639	115	328	2,800
	no_tumor	117	210	824	189	1,340
	pituitary_tumor	105	157	10	2538	2,810
	Σ	2,890	2,698	959	3,213	9,760

Fig. 6. Confusion matrix for kNN.

		Predicted				
		glioma_tumor	meningioma_tumor	no_tumor	pituitary_tumor	Σ
Actual	glioma_tumor	1933	363	52	462	2,810
	meningioma_tumor	1238	646	321	595	2,800
	no_tumor	81	82	936	241	1,340
	pituitary_tumor	248	218	182	2162	2,810
	Σ	3,500	1,309	1,491	3,460	9,760

Fig. 7. Confusion matrix for NB.

D. *Calibration Plot (CP)*

Calibration plot for F1-Score with the Threshold Probability (TP) to classify as positive for all four classifications i.e. GT, MT, NT, and PT is shown in Fig. 8. The red lines in CP are for kNN, green lines for SVM and blue lines for NB. A threshold of 0.50 is set for all the 4 classes. For GT, CP is predicting probabilities of 0.039 for SVM, 0.680 for kNN and, 0.613 for NB. This shows that the best predictive probability in this case is of kNN. For MT, CP is predicting probabilities of 0.080 for SVM, 0.590 for kNN and, 0.315 for NB. This again shows that the best predictive probability in this case is of kNN. For NT, CP is predicting probabilities of 0.813 for SVM, 0.696 for kNN and, 0.661 for NB. This shows that the best predictive probability for no tumor is of SVM. For MT, CP is predicting probabilities of 0.648 for SVM, 0.845 for kNN and, 0.690 for NB. This shows that the best predictive probability in this case is of kNN. Calibration plot suggests kNN is the best model for predicting the brain tumor.

E. *ROC Analysis*

ROC Analysis is another measure used to estimate the performance of our multi-model approach. In this a curve is drawn between Sensitivity, i.e., True Positive Rate and Specificity, i.e., True Negative Rate as shown in Fig. 9. A trade-off is maintained between Sensitivity and Specificity. On x-axis Specificity is there while on y-axis Sensitivity is there. The curve shows a high True Positive Rate with a low False Positive Rate. The red lines in ROC Analysis are for kNN, green lines for SVM and blue lines for NB. This summarizes that the inclusive performance of the multi-model technique is good with kNN being the best choice for BT classification.

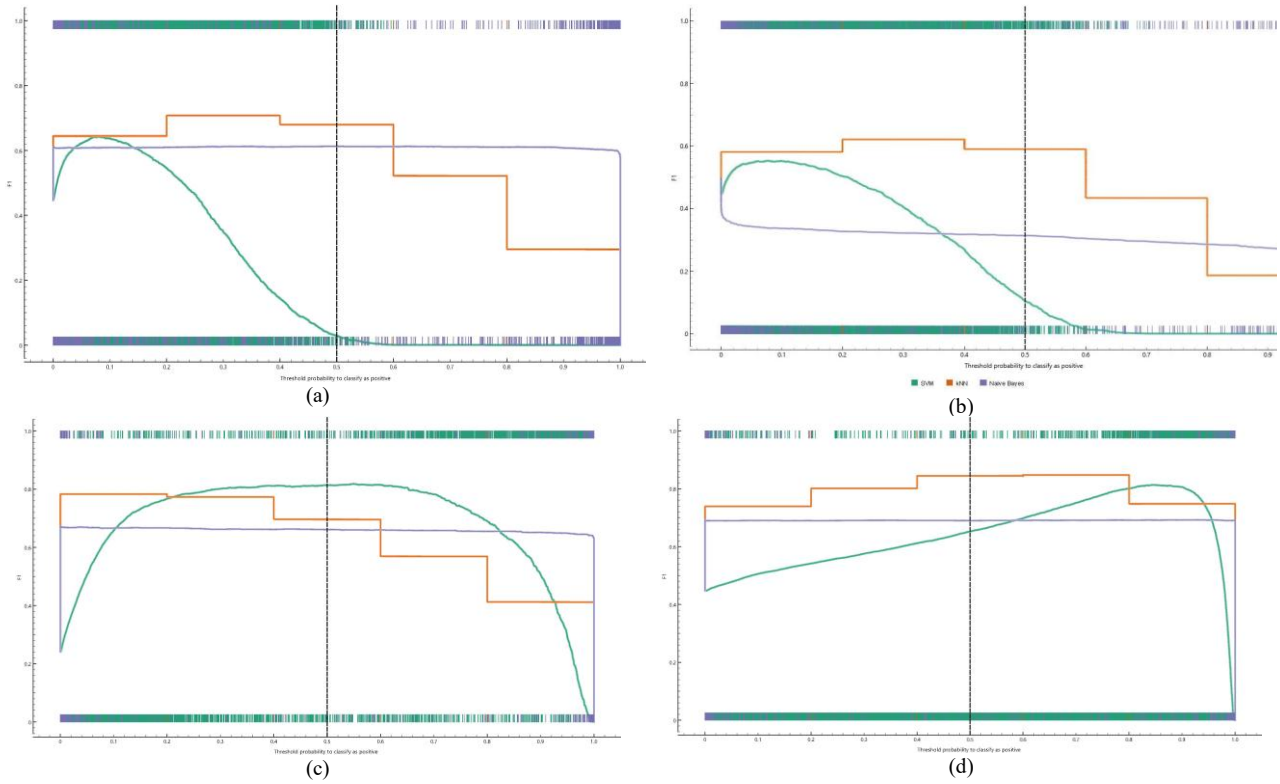

Fig. 8. CP for F1 vs TP with GT, MT, NT and PT.

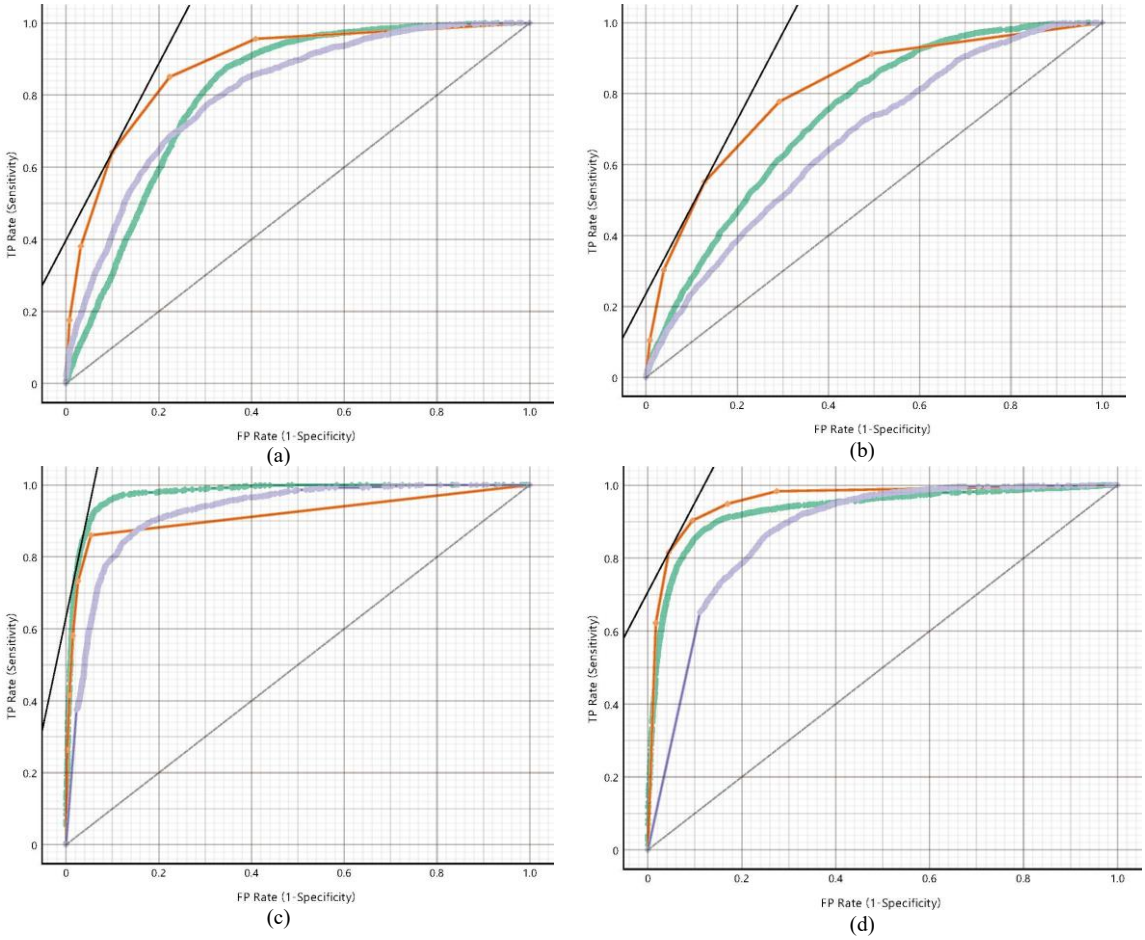

Fig. 9. ROC Analysis for Sensitivity vs Specificity with GT, MT, NT and PT.

VI. Conclusion

This research presents a robust multi-model framework for the automated classification of brain tumors, integrating Deep Learning, Machine Learning, and Ensemble Learning techniques. By using the DeepLoc algorithm with SVM, kNN, and Naive Bayes models, we attained substantial enhancements in classification accuracy and efficiency compared to existing methodologies. The experimental results established that the kNN model outperformed others in terms of key metrics such as Area Under Curve (AUC) and Classification Accuracy (CA), confirming its effectiveness in distinguishing between various tumor types. Comprehensive evaluation through Confusion Matrices, Calibration Plots, and Receiver Operating Characteristic (ROC) analysis further validated the robustness of our approach. While the findings are promising, collaboration with neurosurgeons and clinical experts will be crucial to facilitate the practical implementation of this framework in clinical settings. By enabling timely and accurate brain tumor classification, this research aims to contribute to improved patient outcomes and pave the way for early intervention strategies.

Conflict of Interest

The authors declare no conflict of interest.

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