Robust Classification for Sub Brain Tumors by Using an Ant Colony Algorithm with a Neural Network

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Abstract

A brain tumor is responsible for the highest number of fatalities across the globe. Identifying and diagnosing the tumor correctly at an early stage can significantly improve the chances of survival. Classifying a brain tumor can be aided by factors like type, texture, and location. In this research, we propose a robust technique for detecting sub-brain tumors using an ant colony algorithm coupled with a neural network. To achieve this, we employ an ant colony optimization algorithm (ACO) to eliminate extraneous features extracted from the image, enabling us to find the most effective representation of the image. This, in turn, assists the Neural Network (NN) in the process of classification. Our system involves a series of five steps. Initially, we perform cropping processing as the initial step to eliminate unnecessary background from the original MRI images. This enhances the overall quality of the images, thereby improving the performance of the classification method. In the next step, we conduct image preprocessing to enhance image quality, making it easier for the feature extractor to accurately extract features. The third step involves employing a feature extractor for each image. In the fourth step, we utilize the ant colony optimization algorithm (ACO) to identify the most suitable representation of the image, which further aids the NN in classification. In the fifth and final step, we utilize an NN method to classify the vector obtained from the fourth step (optimization method) to determine the subtype of the brain tumor (normal, glioma, meningioma, and pituitary). Our model's performance is evaluated using the publicly available BT-large-4c dataset, and it surpasses current state-of-the-art methods with exceptional accuracy, attaining a rate of 87.7%. The effectiveness of our approach is particularly evident in maintaining accurate classifications within MRI input images.

Index Terms: Image Classification, Artificial Neural Network, MRI, Cropping, Feature Extraction, HOG, LBP, Optimization Method.

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1 Introduction

Brain tumors, being a lethal form of cancer, pose significant challenges due to their diverse and often acute characteristics, along with a low survival rate among patients (Sargunapathi et al., 2020). Various factors such as location, type, and tissue properties contribute to the complexity of classifying brain tumor types, which include meningioma, central nervous system lymphoma, glioma, acoustic neuroma, and pituitary adenoma. The distribution of these tumor types is approximately 45%, 15%, and 15%, respectively, as indicated (Gaikwad & Joshi, 2015). Treatment decisions, typically starting with chemotherapy or radiotherapy, greatly influence patient survival rates and depend on the specific tumor type (Sharif et al., 2022). Proper planning and monitoring are essential in managing brain tumors, and classification of their subtypes remains challenging due to multiple factors (Yadav et al., 2024). Utilizing a neural network as a supervised machine learning algorithm aids in this classification task (Camgözlü & Kutlu, 2023). Neural networks, composed of interconnected modules known as neurons arranged in layers, process input data using non-linear functions to generate output. Each module receives input, applies a function to it, and passes the resulting output to the next layer (Liu, 2020). Typically, neural networks are described as feed-forward, meaning that each module forwards its output to all modules in the next layer without feedback to the previous layer (Kutlu & Camgözlü, 2021). Weights are assigned to signals moving between units, and during the training phase, these weights are adjusted to tailor the neural network to the particular task at hand, constituting the learning phase (Mavrovouniotis & Yang, 2013) Despite ongoing efforts by experts to enhance detection accuracy through advancements in technology, challenges persist. Various methods are necessary for the identification of brain tumors (Acharya et al., 2019). Brain tumors can be diagnosed by Image processing for brightness uniformity (Nayak & Dash, 2016; Qusef et al., 2023; Al-Dawoodi, 2015; Mahmuddin & Al-dawoodi, 2017). The tumor may be separated manually into an area in the brain where MRI can be considered a very difficult and complex process (Indrivani et al., 2023).

Nowadays, with advances in image processing algorithms, brain tumors can be diagnosed automatically (Lin et al., 2015). Brain tumor detection is now automated, and it reduces human error and operator work, making it easier to Storing information about tumor growth status has been highlighted (Afza et al., 2019). Over recent years, the utilization of computer-aided diagnosis (CAD) systems has surged, aiding clinicians in disease diagnosis and abnormality detection, including brain tumors. Despite extensive efforts in brain tumor detection, many methods have fallen short due to challenges in accurately identifying tumor areas amidst noise present in input images (Sadia et al., 2021). This limitation affects the differentiation between healthy tissue and tumors based on density and tissue distribution. Consequently, researchers are intensifying efforts to enhance CAD system diagnosis (Akram et al., 2024). Figure 2 illustrates the proposed system devised for MRI-based brain tumor classification. This paper encompasses several notable contributions, which are outlined as follows (MRI-Based Brain Tumor).

- Introducing a cropping process aimed at eliminating unnecessary background elements from the original MRI images to enhance image composition and elevate the outcomes of the classification technique.
- Suggesting an image preprocessing step to ensure high-quality images, thereby facilitating the extraction of Precise characteristics extracted from the MRI images.
- Proposing a feature extractor for each image and feeding the feature to the optimization method.

- Proposing ant colony optimization algorithm (ACO) to reduce the unimportant features extracted from the extractor to find the best representation of the image, which in turn will help the Neural Network (NN) in classification.
- Proposing a Neural Network (NN) method as a classifier to classify of the vector that comes from the optimization method.
- Integrating all the aforementioned procedures into a cohesive pipeline to precisely forecast the category based on MRI images.

Previous Research

This section presents a short review of previous work related to Sub Brain tumor classification from an MRI image through both Image classification and Ant Colony Optimization methods (Liao et al., 2013).

Brain Tumor Classification

Rajagopal (2019) devised a method for classifying Glioma brain cancer from MRI images, employing a random forest classifier. This technique involved training the classifier to categorize a range of features and subsequently using the optimal feature set to classify brain MRI images as either containing glioma or not. Furthermore, tumor areas were segmented using an energy-based segmentation algorithm applied to the classified glioma images. Gopa asserts achieving a diagnostic accuracy of 98.01%, with sensitivity at 97.7% and specificity at 96.5%, in detecting glioma brain tumors (Devkota et al., 2018).

Abdelbar & Salama, (2019) They proposed access to the active modification of the ACO algorithm are checked arguments and the centered width argument was made available in 2019. The charismatic winner is determined by the selection rate of previous replies provided by the ACO who have adopted that charisma. As a result, they evaluate the recommendations by employing 65 benchmark datasets and taking them from the University of California Irvine repository to train feedforward NN for classification and optimize different democratic synthetic benchmark uninterrupted-domain offices.

Gong et al., (2020) They provided a multistep approach for detecting the brain cancer region in 2019. Once image preprocessing and feature extraction are completed, NN is utilized to control the tumor area in the picture. They modified version of the whale "optimization algorithm" for select feature and classification weight optimization. The new method's simulation solutions are compared to opposite approaches and applied to the FLAIR, T1, and T2 datasets. In this work, an algorithm was used that was hard to train, didn't work well, and didn't give the results that were promised.

Kulkarni & Sundari, (2020) They upgraded the cuckoo search approach with morphological reconstruction filters in 2019 to segment the MR brain tumor. They also gathered the BRATS 2013 and objective datasets to see how efficient the algorithm was. PSO, GA, and ACO are all less accurate than their solution, which achieves 97 percent accuracy of the cancer part of MR brain images taken at least 4 seconds. Although the complexity time is greater, the precision, recall, and accuracy values of their proposed technique are much better than PSO and GA algorithms.

Nayak & Dash, (2016) have asserted and demonstrated significant advancements in solving optimization problems through enhancing ACO-based image edge detection. Their improvements in ACO have effectively addressed issues related to detecting damaged edges, outperforming traditional methods such as Canny, Sobel, and Prewitt (also known as Robert edge detectors) in 2016. The research experienced early convergence, leading to output stagnation.

Hussain et al., (2020) They proposed a five-step process for segmenting and classifying brain tumors. And the curve approach is used to increase tumor visibility, which is afterward segmented using ACO and the threshold method. Mixtures of texture and form characteristics were also minimized using the PCArS. They were calculated using all fused features, the top 70% priority boasts, and 50% priority boasts. When compared to other companies, their categorized accuracy of the top 50% is the best. As a result of the findings, it was determined that greater tumor segmentation provides valuable characteristics, resulting in improved accuracy. Furthermore, the removal of 50% of characteristics provides for improved truth, while on 70% of features, the results are logical for all datasets. In this search, high performance but optimal power flow and the full cost.

Gopal & Karnan, (2010) introduced a technique for diagnosing brain tumors from MRI images, integrating image processing aggregation algorithms like Fuzzy C Means with intelligent optimization tools like Genetic Algorithm (GA) and Particle Swarm Optimization (PSO). The tumor detection process consists of two stages: the initial stage encompasses pretreatment and optimization, while the subsequent stage involves segmentation and classification.

Al-Dawoodi & Mahmuddin, (2017) Performed an empirical investigation that analyzed the efficacy of the Double-Bridge Search Move technique in the process of Subset Feature Selection Search within the framework of the Bees Algorithm. This study aimed to address the computational time and accuracy limitations observed in the Bees Algorithm applied to wrapper feature selection (BAFS). The proposed Double-Bridge Search Move sought to improve accuracy and decrease computational time. Key findings indicated that the introduced technique successfully enhanced both accuracy and computational efficiency compared to conventional BAFS. By extending the search neighborhood, the new approach surpassed the performance of the original BAFS method. The study highlighted the identified weaknesses of BAFS, particularly its heavy computational load, and proposed the Double-Bridge Search Move as a solution. Overall, the research demonstrated the potential of this novel approach to significantly enhance subset feature selection within the Bees Algorithm framework.

Ant Colony Optimization Method

When considering the overall enhancement of pheromone, the ant colony system holds utmost significance due to the presence of two distinct forms of updates: local and global (Pellegrini et al., 2012), as the pheromone of all elements from the graph that may be part of the good solutions, that may be generated during the current iteration, ACO can be decreased (evaporation) and then a new pheromone is added, which may be equal to the first way that the quantity of pheromone in the graph elements has it will not be lower than the initial pheromone. In the local regeneration of the pheromone, only the features of the best solution receive a pheromone compared to the cost from the objective function. With the global update of the pheromone, diversification from research. **Figure 1**, we show the basic structure of the Ant Colony.



Figure 1: The Basic Structure of the Ant Colony

The pheromone value may be close to zero (Stützle et al., 2012). ACO is prevented and some areas of the collection are left with uncharted solutions. The local updating of the pheromone enhances its value around the best existing solutions and focuses the search near him. Metaheuristic approaches like the one used by the ant algorithm are powerful tools for optimization. Metaheuristics is a high-level process that seeks, creates, or selects a low-level process that can guarantee to find sufficiently a decent solution to an optimization issue, even when the knowledge is partial or computational resources are few. (Al-Ani et al., 2005) The original ACO algorithm was designed to determine the best route across a graph, taking inspiration from the way ant colonies locate food. Since then, several scholars have built upon and refined Dorigo's initial concept so that it may be used in a broader range of activities. Different scholars have refined and broadened Dorigo's initial notion to make it applicable to a broader range of activities since then (Liu et al., 2006). All the aforementioned methods concern extracting only the contents and structure features of the images that yield blurring of the predicted classes. Therefore, we need to benefit from optimization method to reduce the unimportant features extracted from the extractor and keeps the accurate features from the MRI images to find the best representation of the image, which in turn will help the Neural Network (NN) in classification. Thus, in this work, we introduce a system that use optimization method to predict the Brain tumors classification form MRI images (Arora, 2024).

2 Methodology

This excerpt explains the key steps of the suggested methodology, as well as the utilized tools and resources in this investigation. It also presents a suggested framework for categorizing Brain tumors using MRI images. An overview of the suggested framework is shown in Figure 2, which comprises key elements including cropping processing, image preprocessing, feature extraction, optimization method, and neural network classification. Initially, we employ cropping to remove the black background from the MRI image. Subsequently, image preprocessing is applied to the MRI image obtained from the first step. Following this, features are extracted from the preprocessed image. Subsequently, an optimization technique is introduced for the features obtained in the third step. By this approach, the attributes obtained from the process of optimizing are fed into a Neural Network classifier to categorize the MRI image into four distinct classes: normal, glioma tumor, meningioma tumor, and pituitary tumor. We present the problem formulation in subsection A and proceed to elaborate on the proposed methodology in the following subsections, providing a comprehensive explanation (Gyamfi et al., 2022).



Figure 2: Overview of the Proposed Model

1. Problem Formulation

Let's denote an input image as $a \in A$. The task of predicting its label class can be formally defined as a function $f: A \to R^4$, where the function takes the input image and predicts four possible values: Normal, Glioma tumor, Meningioma tumor, and Pituitary tumor. To address this problem, we introduce a Neural Network model along with an optimization method. The subsequent subsections provide a comprehensive explanation of our model's architecture and the training procedure (Akin et al., 2022).

2. Model Architecture

As depicted in Figure 2, the complete model consists of five sequential steps: cropping, preprocessing, feature extraction, optimization method, and neural network classification. In the following subsection, we provide a detailed description of each step involved in transforming the input MRI image into predicting its class (Jelena & Srdan, 2023).

a) Cropping Processing

To eliminate unnecessary background elements from the original MRI images, we present **Algorithm 1**, which has been specially designed to extract MRI images that are free of background interferences. This method is seamlessly integrated into our system to effectively filter out undesired objects or irrelevant noise from the image edges, improve overall composition, and enhance the classification method's performance.

ALGOR	ITHM 1: IMPLEMENTATION OF THE CROP FUNCTION FOR THE MRI BRAIN IMAGE					
	Input: original image					
	Output:crop image					
1	Read the Image.					
2	Obtain the weight and height of the image.					
3	Initialize x_{\min} , y_{\min} , x_{\max} , $y_{\max} \leftarrow -1$					
4	for $i \leftarrow l$ to wight do:					
5	for $\underline{j} \leftarrow l$ to height do:					
6	$x \leftarrow Image\ (i,j)$					
7	<i>if</i> $x > 128$ <i>then:</i>					
8	<i>if</i> $min_y = -1$ <i>then:</i> $x_{min} \leftarrow j$, $y_{min} \leftarrow i$					
9	<i>if</i> $x_{min} > j$ <i>then</i> $x_{min} \leftarrow j$					
10	<i>if</i> $x_{max} < j$ <i>then</i> $x_{max} \leftarrow j$					
11	if $y_{max} < I$ then $y_{max} \leftarrow i$					
12	$Out Image = in crop(Image, [x_{min} y_{min} (x_{max} - x_{min}) (y_{max} - y_{min})])$					
13	return Out image.					

b) Image Preprocessing

Image preprocessing is crucial for obtaining high-quality images devoid of noise, as noise can significantly impair image quality and affect the accuracy of subsequent analysis. Various types of noise, such as Rician noise, can degrade image quality. Therefore, ensuring good image quality is essential for

obtaining accurate results in specific applications. In our model, we employed preprocessing techniques to enhance the input image, including the use of a median filter. The median filter is a straightforward method that effectively reduces noise while preserving brightness differences and minimizing blurring at regional boundaries. It also preserves border positions in the image, making this method useful for visual inspection and measurement.

c) Feature Extraction

The process of feature extraction entails transforming unprocessed data into numerical features while preserving the dataset's original information for further analysis. This method often yields better results compared to directly applying machine learning algorithms to raw data. In our model, we employed HOG and LBP feature extraction techniques for every image acquired during the initial step of image preprocessing. Subsequently, these extracted features are inputted into the optimization method to identify and choose the most significant features. The function for extracting features can be defined as follows:

F = f(I)

Where the letter F denotes the sources of the features obtained from the method used for extracting features, that is extracted from image I. Feature F we will feed to the optimization method to select the best features.

d) Optimization Method

The ant colony optimization algorithm (ACO) is a probabilistic approach employed to solve computational problems that require the identification of the most efficient routes within graphs. In this work, we used it to reduce the unimportant features extracted from the HOG extractor to find the best representation of the image, which in turn will help the Neural Network (NN) in classification. The Optimization method function can be defined in the following manner:

$F_{(m \times 1)} = ACO(F_{(n \times 1)})$

Where the $F_{(m \times 1)}$ means the features come from the optimization method *ACO* that is optimized from the input features for the image $F_{(n \times 1)}$. The feature $F_{(m \times 1)}$ we will feed to the Neural Network classifier (Gustavo et al., 2024).

e) Neural Network Classifier

A neural network consists of neurons organized into layers, processing input vectors to generate output. Each neuron receives input, applies a non-linear function, and transmits the result to the subsequent layer. Neural network classifiers, being supervised machine learning algorithms, are employed for data classification (Gaikwad & Joshi, 2015). Neural networks operate on the principle of identifying the optimal decision boundary, often referred to as the "super plane," based on the neural architecture of the brain (Nadweh, 2023). They are essentially simplified electrical networks of neurons, where learning occurs by iteratively comparing the network's classification of data records with their actual classifications. Errors from the initial categorization of records are fed back into the network, facilitating adjustments to the algorithm for subsequent iterations (Billah & Javed, 2022). In our system, we employed a neural network (NN) as a supervised machine learning algorithm to classify vectors derived from the optimization method, thereby diagnosing sub-brain tumors into four classes: glioma, meningioma, normal, and pituitary.

3. Training

To evaluate the effectiveness of optimizing the network training, we experimented with different loss functions to compare the input class A_i to the predicted class P_i. One of the tested loss functions is called "L_mse," which stands for Mean Squared Error (MSE). MSE is frequently utilized in regression tasks and calculates the mean of the squared differences between true and predicted values, MSE is defined as follows:

$$L_mse = \frac{1}{n} \sum_{i=1}^n (A_i - P_i)^2$$

Where the A_i means the input class, P_i means the predicted class that comes from the Neural Network classifier model. *n* Means the number of samples.

The second loss function, Mean Absolute Error (Lmae), calculates the average discrepancy between the true and predicted values across all data points. This discrepancy is determined by comparing the input class A_i to the predicted class P_i generated by the Neural Network classifier model. Mathematically, it is expressed as the mean of the absolute differences between these values, and it can be defined as:

$$L_mae = \frac{1}{n} \sum_{i=1}^n |A_i - P_i|$$

The third loss function is cross-entropy "L_ce". CE is depending on the input class A_i to the predicted class P_i class that comes from the Neural Network classifier model. CE is defined as follows:

$$L_{ce} = -\sum_{i=1}^{n} A_i \cdot \log\left(P_i\right)$$

Algorithm 2 provides a detailed depiction of how our proposed MRI brain detection method is carried out. It covers the entirety of our system, including both the training and testing stages.



3 Experiments and Results

In this segment, we will elucidate the experiments conducted to assess the suggested model and analyze the evaluation metrics employed for these experiments.

1. Dataset

This study encompasses a wide range of experiments aimed at validating the performance of the proposed model using the publicly available BT-large-4c dataset. This dataset offers both images and corresponding labels extracted from MRI scans, all at a resolution of 512×512 pixels (Barbara, 2023). The dataset comprises a total of 3,264 raw MRI images, which are utilized for both training and testing purposes. As part of the preprocessing steps, all images are resized from 512×512 to 256×256 pixels before being fed into the model. Figure 3 presents various examples from the dataset.



Figure 3: Samples from the BT-large-4c Dataset. For each image, showing (column 1) glioma images, (column 2) meningioma images, (column 3) normal images and (column 4) pituitary images.

2. Data Augmentation

In this research, we employed data augmentation methods to address the need for extensive and balanced datasets during neural network training, aiming to mitigate overfitting. This involved enhancing the training images to expand the available samples for training across various conditions. Figure 4 depicts the transformations applied to each input image, including techniques like random uniform rotation and flipping. Specifically, these augmentation methods were applied to the training instances of the smaller classes until their size matched that of the largest class, thereby achieving a balanced training dataset. Initially, the training data comprised four categories: glioma (826 images), meningioma (822 images), normal (395 images), and pituitary (827 images). Post-augmentation, the number of images in the normal class increased to 790, resulting in a total of 3,265 images available for training across all classes (glioma, meningioma, normal, and pituitary).



Figure 4: Samples from the BT-large-4c Dataset Augmentations. Applying the transformations for each image. We show (column 1 and column 3) the original input images, (column 2) random uniform rotation, and (column 4) random flipping

3. Parameter Settings

To train our networks, we utilized the Adam optimizer (MRI), with a gamma value set to 0.1 and an initial learning rate of 0.001, implementing early stopping after 5 epochs. Through experimentation, we determined that a batch size of 1 and 300 epochs yielded the most optimal results. All experiments were conducted on a system equipped with a 64-bit Core I7-6700 CPU running at 3.40GHz and 8GB of memory, paired with an NVIDIA GTX 1080 GPU, operating on Ubuntu 20.04 within the MATLAB. During the training phase, our proposed method typically requires approximately 10 minutes and 12 seconds per epoch with a batch size of 1. Subsequently, during the testing phase, our model demonstrates a performance of approximately 0.015 seconds per image.

4. Evaluation Measures

In this research, we assess the effectiveness of the proposed system using the Accuracy metric, which evaluates the correctness of predictions by dividing the number of accurate predictions by the total number of predictions made, computed as:

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

In this particular situation, TP denotes the tally of accurate positive samples, TN symbolizes the tally of accurate negative samples, FP signifies the tally of inaccurate positive samples, and FN denotes the tally of inaccurate negative samples.

4 Results and Discussion

a) Ablation Study

In the beginning, we conducted an ablation study on our proposed system using the BT-large-4c dataset to showcase the effects of various enhancements. This study was carried out without any data augmentations. This study investigated the effects of different loss functions (Mean Absolute Error - MAE, Mean Square Error - MSE, and Cross Entropy - CE) as well as various feature extractors (Histogram of Oriented Gradients - HOG and Local Binary Patterns - LBP):

- Baseline: the model without optimization method.
- Baseline with optimization method: the baseline model optimization method.

Tables 1 and 2 present the quantitative outcomes of the ablation study conducted on the BT-large-4c dataset, conducted without data augmentations. Our proposed model incorporating the optimization method outperformed the baseline model lacking this optimization technique. Specifically, our model achieved a 2.1% improvement in accuracy compared to the baseline model. Additionally, when comparing our model with data augmentations to the baseline model, our proposed model demonstrated a slight improvement in accuracy by 0.04%.

Furthermore, when evaluating different loss functions, the accuracy with Mean Square Error (MSE) loss showed a marginal improvement of 0.02% compared to the other loss functions (Mean Absolute Error - MAE and Cross Entropy - CE) without data augmentations. Moreover, employing Cross Entropy (CE) loss resulted in a notable accuracy improvement of 1.6% compared to the other loss functions (MAE and CE) without data augmentations.

	Types of Extractors	Without optimizationTypes of Loss function			With optimization		
Types of					Types of Loss function		
Stages		MAE	MSE	Cross	MAE	MSE	Cross entrony
				chuopy			chuopy
Training	HOG	0.819%	0.989%	0.992%	0.985%	0.971%	0.981%
Training	LBP	0.822%	0.94%	0.969%	0.941%	0.994%	0.975%
Validation	HOG	0.736%	0.81%	0.834%	0.804%	0.739%	0.863%
v anuation	LBP	0.727%	0.785%	0.819%	0.804%	0.85%	0.801%
Testing	HOG	0.715%	0.815%	0.83%	0.815%	0.81%	0.851%
resung	LBP	0.732%	0.773%	0.83%	0.787%	0.838%	0.836%

Table 1: Summarizes the Quantitative Findings of the Ablation Study Performed on the BT-large-4c
Dataset without Employing Augmentations

 Table 2: Illustrates the Quantitative Findings from the Ablation Study Carried out on the BT-large-4c

 Dataset with Augmentations

	Types of Extractors	Without optimization			With optimization		
Types of		Types of Loss function			Types of Loss function		
Stages		MAE	MSE	Cross	MAE	MSE	Cross
				entropy			entropy
Training	HOG	0.982%	0.978%	0.997%	0.999%	0.99%	0.997%
Training	LBP	0.954%	0.981%	0.986%	0.974%	0.998%	0.994%
Validation	HOG	0.85%	0.784%	0.852%	0.847%	0.831%	0.858%
vanuation	LBP	0.874%	0.863%	0.877%	0.811%	0.858%	0.869%
Testing	HOG	0.861%	0.85%	0.873%	0.872%	0.852%	0.877%
resting	LBP	0.84%	0.851%	0.857%	0.847%	0.861%	0.877%

b) Analyzing Performance

In addition, we performed an analytical comparison between our suggested system and four cutting-edge models. Table 3 showcases the assessment measurements on the BT-large-4c dataset for these models, as well as our suggested model. Our model exhibited superior accuracy compared to all four tested models. Specifically, our accuracy demonstrated a 3.17% enhancement over the SVM (Linear) classifier, 1.22% improvement over the Random Forest (RF) model, 17.88% advancement over AdaBoost, and 19.19% increase over Gaussian NB.

 Table 3: The Assessment Metrics for the BT-large-4c Data Set, Comparing the Proposed Model with the Current Cutting-edge Models

Methods	Accuracy
Gaussian NB (Kingma & Ba, 2014)	0.6851%
AdaBoost (Kingma & Ba, 2014)	0.6982%
Random Forest (RF) (Kingma & Ba, 2014)	0.8648%
SVM (Linear) (Kingma & Ba, 2014)	0.8453%
Our model	0.877%

In order to evaluate the efficiency of our system, we conducted an analysis of the confusion matrix and calculated the overall classification accuracy. This assessment was performed using the test set obtained from the BT-large-4c dataset, which includes four distinct classes: glioma, meningioma, normal, and pituitary. The confusion matrix offers a comprehensive evaluation beyond simple classification rates. Figure 4 depicts the confusion matrix generated from our system's output utilizing the BT-large-4c dataset with three distinct filters. It showcases the true positives (TPs) and true negatives (TNs) of our model, both with and without data augmentation.



Figure 4: Analysis of the Confusion Matrix Including the Overall Classification Accuracy Achieved on the BT-large-4c Test Set, Comparing Results with and without the Implementation of Data Augmentation

Figure 5 presents the ROC curve, which showcases the equilibrium between sensitivity (also known as the true positive rate, TPR) and specificity (calculated as 1 minus the false positive rate, FPR). Classifiers that exhibit curves situated near the top-left corner exhibit superior performance. The illustration reveals that our model displays the most desirable ROC curve, whether with or without the incorporation of data augmentation.



Figure 5: ROC Curve Illustrating Sensitivity-Specificity Trade-off on BT-large-4c Test Set with and without Data Augmentation

5 Conclusion

We have presented a robust approach for detecting sub-brain tumors utilizing an ant colony algorithm in conjunction with a neural network applied to MRI input images. Our NN model is constructed based on the principles of the ant colony algorithm, which effectively reduces irrelevant features extracted from the feature extractor to identify the most optimal image representation. This refined representation aids the Neural Network (NN) in its classification task. Additionally, the model integrates a neural network that is fed with the most optimal features selected through optimization techniques to classify MRI images into four distinct classes: normal, glioma, meningioma, and pituitary. This innovative approach holds promise for garnering increased attention from the biomedical community, thereby enhancing diagnostic performance in critical applications such as automated disease diagnosis. Subsequent endeavors will focus on leveraging this model to classify tumor types across various forms of cancer, aiming for broader generalization.

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