Detection of Brain Tumor Using Machine Learning Approaches

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This Report Presented in Partial Fulfillment of the Requirements for the Degree of Bachelor of Science in Computer Science and Engineering

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APPROVAL

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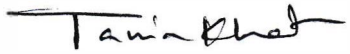

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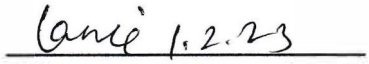

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We hereby declare that this project has been done by us under the supervision of **Al Amin Biswas, Senior Lecturer, Department of CSE**, Daffodil International University. We also declare that neither this project nor any part of this project has been submitted elsewhere for award of any degree or diploma.

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ABSTRACT

Brain tumor is a very panic issue because many people have died from this problem. Early detection of brain tumors can save many lives. Magnetic resonance imaging (MRI) is more effective than any other technique. In this study, we used an ensemble of machine learning algorithms to identify tumors in the brain at an early stage. We have done our task in several steps. At first, we collect data then analyze and filter the data by using and following tricks and techniques. Next, we use our covetable algorithms. At the end of our task, we found out about our algorithm. The average accuracy of our model is 99.80% and the highest accuracy is 99.20% which contains the XGBoost classifier algorithm.

Index Terms—Brain Tumor, Machine Learning, Ensemble, Feature Extraction, XGB, ADB,R

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CHAPTER 1
INTRODUCTION

1.1 Introduction

The human body is built with various kinds of organs. Brain is the central organ of the human body. All of the parts of the body are doing their activities by the commands of the brain. The activities of the body are obstructed when the brain faces any minor or major problem. Tumor is one kind of major brain problem. It is a serious disease for human beings. Our body and the parts of the body are built with billions of cells. These cells grow in a normal procedure. When the cells of the brain grow in an abnormal way then This is called brain tumor. Generally, there are two kinds of brain tumor, benign and malignant. Benign is an initial step of brain tumor. It is not harmful like a malignant tumor. Basically benign tumors are non-cancerous, very slowly they grow up and spread to other cells of the brain. In the elementary phase patients can't realize that he/she is bearing tumors. Malignant tumors are very much aggressive. These are like cancer. The growth of these cells are very high and attack the other normal cells. There are some common symptoms of malignant cancer. Headaches, seizures, feeling sick all the time, being sick, and drowsiness, mental or behavioral changes, such as changes in personality, weakness or paralysis, vision problems, or speech problems are the common symptoms of malignant cancer [13]. A brain tumor affects around 700,000 people in the United States today. In 2021, more than 84,000 people will be diagnosed with their first brain tumor. There are more than 120 different types of primary brain and central nervous system tumors. Only in the USA above 28,000 childs are fighting with brain tumors [1]. According to [14] brain and other central nervous system cancer is the 10th biggest cause of death, with a five-year survival rate of 34 percent for men and 36 percent for women for those with malignant brains. Furthermore, the World Health Organization (WHO) estimates that roughly 400,000 people worldwide are affected by brain tumors, with 120,000 people dying in recent years [15]. In all age categories, a brain tumor is the leading cause of mortality. The National Brain Tumor Foundation (NBTF) and the American Brain Tumor Associations (ABTA) both report that the number of people affected by brain tumors has increased dramatically in the recent decade [16]. There are many people in the world who are dying from this malignant disease. In the initial stage the disease has no major symptoms for this reason maximum people don't care about this. When a brain tumor becomes a serious stage then the patient of this disease becomes panicked and the

helping hand of doctors becomes feeble. For this reason, we have to find out this deadly disease in the primary stage. Brain is the most important part of our body but it is very sensitive and cells of the brain are very delicate for this reason diagnosis of brain tumor is very difficult. The World Health Organization (WHO) has graded brain tumors in four grades. The tumors of grade1 are less harmful tumors and combined with long-term survival. It seems normal to be viewed by microscope. In grade2, under a microscope, these tumors appear to be slow-growing and slightly aberrant. Some tumors can extend into neighboring normal tissue and resurface as a higher-grade tumor. In grade3, there isn't often a noticeable distinction between grade II and grade III tumors, they are all malignant. Grade III tumor's cells are actively creating aberrant cells that spread into normal brain tissue nearby. These tumors frequently return as grade IV cancers. The most dangerous tumors are grade4. They reproduce quickly, have an odd look under the microscope, and grow quickly into normal brain tissue. The constant production of new blood vessels by malignant tumors is what allows for their fast growth to continue. Brain tumor therapy is impacted by the patient's age, general health, tumor size, and location. There are important distinctions in the treatment plans and timetables for kids and grownups. Treatment options for brain tumors include surgery, radiation treatment, and chemotherapy.[17]. The basic risk factors of brain tumor are Age (child and old are more affected), Gender (specific types of brain tumors invade specific gender), Home and work exposures, Family history (5% tumor occur for inheritance), Exposure to infec-tions, viruses, and allergens, Electromagnetic fields, Race and ethnicity (in the USA blacks, are invaded by tumors less than whites), Ionizing radiation, Head injury and seizures and N-nitroso compounds [18].Many imaging techniques are assessed and the findings are obtained in the diagnosis of brain tumors, including neurological tests, X-ray MRI, CT scan, MRS, 3D imaging, and biopsy. Magnetic Resonance Imaging (MRI) is a technique that uses radio frequency pulses to measure the strong magnetic fields in the nuclei of hydrogen atoms in the body and the magnetic field vectors acquired [19]. All of the systems Magnetic Resonance Imaging (MRI) is the best system because it doesn't use ionized radiation unlike CT and X-ray imaging [20]. In our operation we have used numeric data of Magnetic Resonance Imaging based images. At first we analyzed this data then we applied some enriched and ensemble algorithms like Random Forest, AdaBoost classifier, XGBoost classifier etc. These algorithms worked very well to identify the brain tumor. The accuracy of our model is so favorable.

1.2 Motivation

The overall goal of this research is to assist the medical community in quickly and accurately identifying brain tumors in their early stages. I hope that everyone will benefit greatly from our research.

1.3 Rationale of the Study

Three ensemble machine learning methods for brain tumor identification were compared via the use of ML, Random Forest, Adaboost, and XGBoost, among other data analysis and processing approaches.

1.4 Research Questions

1. What are the most effective algorithms for brain tumor identification using machine learning?

2. What are the most common features or metrics used to train models for brain tumor identification?

3. What methods can be used to evaluate the accuracy of machine learning models for brain tumor identification?

4. How can the results of machine learning models for brain tumor identification be interpreted?

5. What challenges are associated with using machine learning for brain tumor identification?

1.5 Scope of the Problem

To reliably detect brain cancers from scans or other medical pictures is the goal of the machine learning issue of brain tumor identification. This model should be able to distinguish between benign and malignant tumors and should be able to provide accurate classification results. Additionally, the model should be able to accurately distinguish between different types of tumors, such as gliomas and meningiomas. The model should also be able to provide accurate prognostic information about the tumor, such as its size or grade. Furthermore, the model should be able to provide useful information about the treatment options available for the tumor, such as surgical or radiation therapy. Finally, the model should be able to provide valuable insights into the underlying biology of the tumor and its potential to spread or recur.

1.6 Challenges

1. Limited availability of data: Brain tumor datasets are limited in size due to the difficulty in obtaining MRI scans of patients with brain tumors. This makes it difficult for machine learning algorithms to learn from the data and accurately identify brain tumors.

2. Low accuracy: Machine learning algorithms can suffer from low accuracy rates when identifying brain tumors due to the complexity of the task. This is because the features used to identify brain tumors can vary from patient to patient, making it difficult for the algorithm to accurately distinguish between healthy and abnormal brain scans.

3. Overfitting: Overfitting is a common problem in machine learning. This is when the algorithm learns from the data too well, leading to poor generalization on unseen data. This can lead to inaccurate predictions when identifying brain tumors, as the algorithm may not be able to identify patterns in the data that are not present in the training dataset.

4. Compute time: Brain tumor identification is a computationally intensive task due to the complexity of the algorithms used. This can lead to long commute times, which can be a barrier to using machine learning in real-time applications.

1.5 Output

In this project we use the Ensemble Method. The average accuracy of our model is 99.80% and the highest accuracy is 99.20% which contains the XGBoost classifier algorithm.

1.7 Report Layout

The following are the contents of this research paper:

I. In the first chapter, we talk about goals, reasonable study, and motivation.

II. In the second chapter, we go over the research summary and related activities.

III. Research technique, data preparation and collection, research subject, and instrumentation are covered, and Chapter 3 discusses the used model.

IV. Chapter 4 discusses the study's numerical results and experimental evaluation.

V. In the last section of the dissertation, the speaker draws conclusions and discusses the implications of the study for future studies.

CHAPTER 2

BACKGROUND

2.1 Related Works

Komal Sharma [2] proposed supervised machine learning algorithms named Multilayer perceptron(MLP) and Naive Bayes for detecting tumors of the brain. In the initial stage complete Preprocessing part then use Feature Extraction and in the finishing part use Multilayer perceptron and Naive Bayes algorithms and checking accuracy. MLP takes more time to build and give more accurate results on the other hand Naive Bayes take less time to build and give less accurate results. Here the maximum accuracy rates are 98.6% and 91.6%.

G.Hemanth [3] used some machine learning (ML) algorithms and data mining. At first preprocess and average filter brain images then segmented the images. As machine learning algorithms G.Hemanth used Conditional Random Field (CRF), Support Vector Machine, Genetic Algorithm and convolutional Neural Network (CNN). Here minimum accuracy (83.64%) contained Genetic Algorithm and maximum accuracy (91%) contained CNN algorithm.

Dr. K Meena [4] proposed some machine learning and segmentation methods and algorithms. First used Watershed, Patch-Based method, Bayesian with HMM, SVM, K-Means, Fuzzy Clustering, Neural Network Based algorithm and Support Vector Machine (SVM) as segmentation.Then used the Artificial Networks algorithm, Bayesian, Na¨ıve Bayes, Hidden Markov Models, Deep belief networks, Case Based Reasoning, Decision Tree, Random Forest, Monte Carlo Method as a machine learning algorithm.

With the use of six classic classifiers and a Convolutional Neural Network, Tonmoy Hossain [5] was able to (CNN). Support Vector Machine (SVM), K-Nearest Neighbor (KNN), Multilayer Perceptron (MLP), Logistic Regression, Naive Bayes, and Random Forest are some of the common classifiers used today. A similar five-layer convolutional neural network was

employed for this identification. SVM, the classic classifier with the best accuracy, achieved 92.42%, while CNN achieved 97.87%.

In [6] first use image Preprocessing and Segmentation then use Features Extraction techniques. After that they used classification algorithms which are The multi-layer perceptron (MLP) and the C4.5 decision tree algorithms. Their C4.5 decision tree gained 91% precision and MLP gained 95% precision.

Chirodip Lodh Choudhury [7] applied a 3-layered Convolutional Neural Network (CNN) Architecture model. The model is based on Keras, using TensorFlow, a basic Python machine learning API, at the backend. Rectified linear units (ReLU), Hyperbolic Tangent function(Tanh), Sigmoid Activation function are the activation functions of that model. The accuracy of that model was 97.47

The noise in [8] was pre-processed using an adaptive median filter. The Mixture Model was used to locate the relevant area (GMM). The characteristics were extracted using a Grey Level Co-occurrence Matrix (GLCM). Finally, Neural Networks (NN) were used to evaluate whether or not the tumor was malignant. That model has a sensitivity of 93.33%, a specificity of 96.6%, a precision of 93.33%, and an accuracy of 93.33%.

K-nearest neighbor algorithm (KNN), introduced by Gokalp Cinarer and Bulent Gursel Emiroglu [9], is simple to implement, whereas Linear Discriminant Analysis (LDA) is used to shrink classes into smaller groups, and Support Vector Machine (SVM) and Random Forest (Rf) algorithm are ensemble methods. In this case, the maximum accuracy was achieved by using a support vector machine, which was 90%.

Suhib Irsheidat and Rehab Duwairi [10] applied Artificial Convolutional Neural Networks architecture.In their task they augmented their data 14 times larger. In their model they used Input layer, Convolutional block, Convolutional layer 2D, Maxpool layer, Loss function, Optimizer function and Activation function. The model gave 96.7% on validation data and 88.25% accuracy on test data.

In [11] first used pre-processing, decision making, post-processing, Evaluation criteria. Then used some ensemble algorithms. Random forest (RF) classifiers, adaboost classifiers, artificial neural networks (ANN) and binary decision trees (BDT) were used here.The size of the ensemble varied in four steps, using values of 5, 25, 125, and 255. Average accuracy of ANN was 97.48%, Adaboost was 97.65%, RF was 97.65% and BDT was 97.51%.

When performed regularly, a pap smear may help find cervical cancer early. The MASO technique, which uses mutations to improve search results, is used to fine-tune the DenseNet 121 framework. Chitra [20] used a variety of DenseNet-121's built-in augmentation methods. The performance of the MASO-optimized DenseNet 121 architecture for cervical cancer detection was evaluated using a wide range of performance measures and confusion matrices.

Omar Sedqi Kareem [12] proposed some segmentation techniques such as thresholding for segmentation,region growing method for serial segmentation, edge-based techniques to assess object information with intensity detection (grayscale) and watershed techniques. Then applied K-Nearestneighbour, Support vector machine, Random forests, Artificial neural network as supervised Learning method. Here also used some unsupervised Learning techniques/algorithms and they are Clustering techniques, Active contour models (deformable models). After that the authors of the paper used hybrid techniques.

2.2 Comparative Analysis and Summary

Brain is the most important part of the human body and can be infected by a tumor, which turns it into a useless object. These algorithms are highly accurate with maximum accuracy rates of 98.6% and 91.6%. G.Hemanth used some machine learning (ML) algorithms and data mining. In [6] and [7] they applied a 3-layered neural network model which is based on Keras, using TensorFlow, a basic machine learning API, at the backend. The accuracy of that model was 97.47%, specificity 96.6% and precision 93.33%.

In [8] they used adaptive filtering for pre-processing to remove noise and then used the Mixture Model (GMM) to find the region of interest. Their C4.5 decision tree gained 91% precision and MLP gained 95% precision.

CHAPTER 3

Research Methodology

3.1 Research Subject and Instrumentation

This study intends to employ an automated computerized ensemble model that is useful for brain tumor prediction that helps doctors and patients in the medical sector. The use of several machine learning algorithms on the data set and dataset analysis are explored in this research study to achieve the goal. This research also shows which model contributes more than others to the prediction of higher precision. This could save money by avoiding the cost of multiple trials for a patient, as all of the models may not play a significant role in predicting the outcome. In this study, a model to detect tumors in MR images using extracted features are proposed as shown in figure 1.

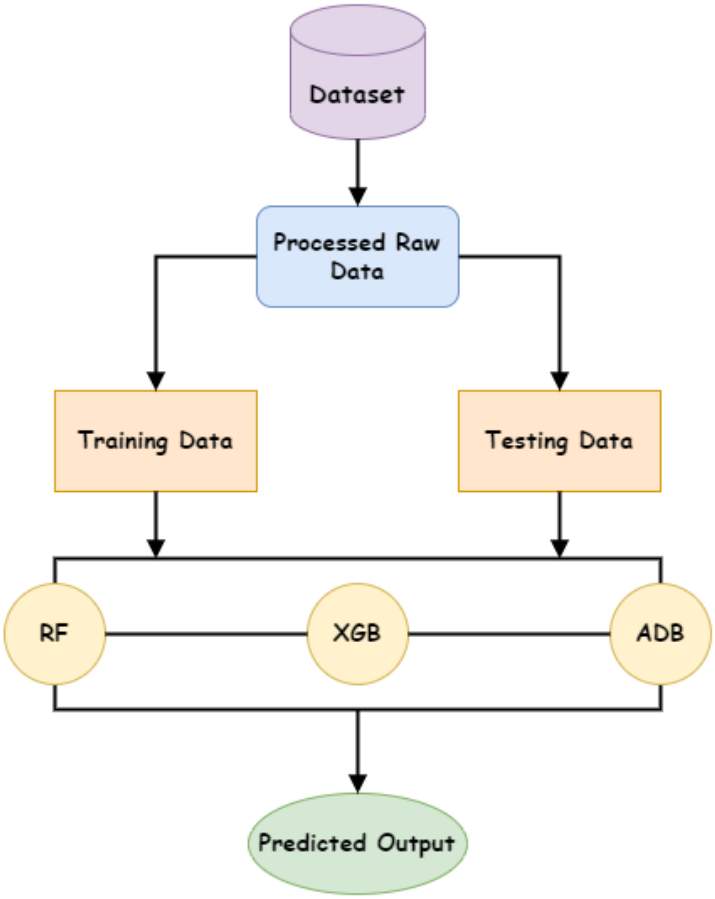


Fig. 1. Process of the proposed model

3.2 Dataset Description

In this study, we used a brain tumor dataset to create our anticipated model. The brain tumor dataset was retrieved from the Kaggle [21]. There are MRI-predicted 3762 image datasets and 3767 feature extracted texture data. The image dataset example is depicted in figure 2. And the texture dataset contains two types of features one is first order and another one is second order. There are 15 features in this dataset mainly divided into first order and second order. The details of all features are depicted in Table 1.

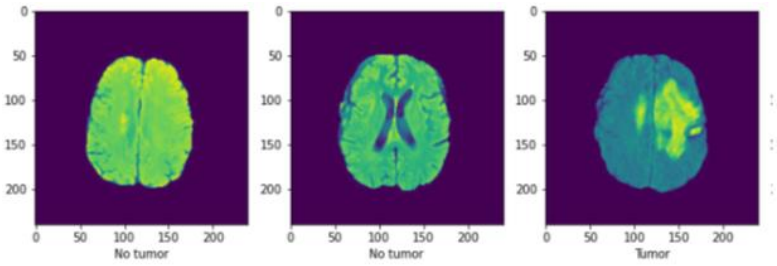


Fig. 2. Sample of image dataset

The dataset contains several extracted features from MRI images. The dataset contains 3767 patient records where 55% of patients were normal and 45% of patients detected tumors. And the image dataset mainly used extracted texture features from the images and texture data describe the tumor texture and description and this data is mainly used to employ our model.

3.3 Dataset Prepossessing

It contains 3767 brain tumor patients' data from MRI predicted extracted features, comprising 15 parameters. We can see that the column 'Class' has a strong relationship with all of the other columns, with the exception of the 'Image- no' column, which has no meaning and should be eliminated. As a result, the 'Image-no' parameter was removed from the data set. When we ran the analysis, the accuracy was harmed if the 'Image-no' column was not eliminated. This dataset has no missing data. However, there don't exist null values, but the dataset has some outliers. Some major outliers given in Figure 3.

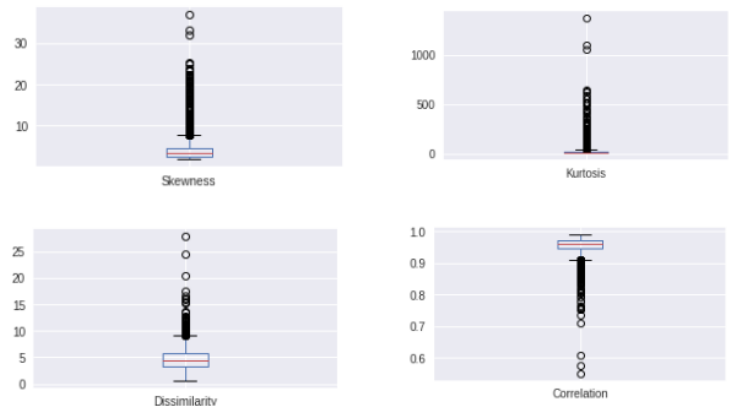


Fig. 3. Some impactful outliers feature

To get rid of the outlier values, we used a function to clean outliers. We used interquartile range (IQR) technique to clean outliers from the dataset [22]. The IQR is the difference between q3 (75th percentile) and q1 (25th percentile). To find outliers, the IQR technique calculates the lower and upper bounds that are given below.

$$\text{LowerBound} = q1 - 1.5 \times IQR \quad (1)$$

$$\text{UpperBound} = q3 + 1.5 \times IQR \quad (2)$$

TABLE I

DATASET FEATURE DESCRIPTION

First Order Feature		
Feature	Type	Description
Image-no	Numerical	Feature extracted image number
Class	Tumor Or Not Tumor	Classification result
Mean	Numerical	The mean is the average or most common value among a set of numbers.
Variance	Numerical	The variance is a statistical measure of the dispersion between individual values in a dataset.
Standard Deviation	Numerical	The standard deviation is a statistic that calculates the square root of the variance and measures the dis-pereion of a dataset relative to its mean.
Skewness	Numerical	The degree to which the probability distribution of a random variable deviates from the normal distribution is measured.

Kurtosis	Numerical	Kurtosis determines if a distribution's tails contain extreme values.
Second Order Feature		
Contrast	Numerical	It provides an overall evaluation of the difference in brightness between two adjacent pixels in the picture.
Energy	Numerical	It provides a metric for textural consistency, or the number of pixel pairs repeats.
ASM (Angular second moment)	Numerical	The uniformity of gray level distribution in the image is represented by the Angular Second Moment (ASM).
Entropy	Numerical	By determining the outcome of a random trial entropy assesses the expected (average) quantity of information delivered.
Homogeneity	Numerical	It indicates how near the distribution of elements in GLCM (Gray Level Co-occurrence matrices) is to the GLCM diagonal.

Dissimilarity	Numerical	The Pairwise differentia-ton between M items is described by the dissimilarity matrix (also known as the distance matrix).
Correlation	Numerical	It quantifies the degree to which one image pixel is connected to all of the other pixels in the picture.
Coarseness	Numerical	When one observes not the exact value of the data but simply some set(a subset of the sample space) that contains the precise value, the data is defined as Coarse.

We have 3594 entries after cleaning the datasets, including 14 parameters. As a result, no irrelevant columns were found in this brain tumor dataset (figure 4 shows dataset correlation). After cleaning all outliers from the dataset we perform feature scaling using standard scalar to smooth the dataset [23]. The following is the standardization technique

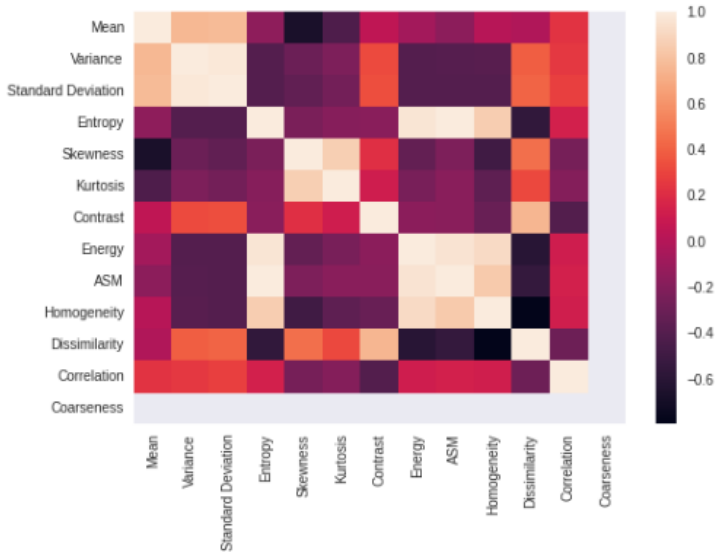


Fig. 4. Correlation all features of dataset

Standardization (z):

$$z = \frac{x - \mu}{\sigma} \tag{3}$$

where, x is the data point, μ is the mean and σ is the standard

deviation. Following shows mean (μ):

$$\mu = \frac{1}{N}\sum_{i=1}^{N}(x_i) \tag{4}$$

And standard deviation (σ):

$$\sigma = \sqrt{\frac{1}{N}\sum_{i=1}^{N}(x_i - \mu)^2} \tag{5}$$

3.4 Performance Measure Parameter

The effectiveness of machine learning algorithms is assessed using a set of performance metrics. To evaluate the parameters, a confusion matrix including TP, FP, TN, and FN for actual data and predict data is created. The following is the implication of the terms(Table II):

TABLE II

PERFORMANCE METRICS TERMS

Actual/Predictive	Actual Positive	Actual Negative
Predictive Positive	True Positive(TPs)	False Positive(FPs)
Predictive Negative	False Negatives(FNs)	True Negatives(TNs)

The following factors are heavily employed in our study to evaluate specific terms by their corresponding law to evaluate our study's performance. There are several characteristics like these that explain various relationships that can be used to measure a system's performance. The following formulas are used to evaluate the comparison study's performance: Accuracy(Acc)The ratio of correctly identified samples to total samples

$$Accuracy(Acc) = \frac{(TP+TN)}{(TP+TN+FP+FN)} \quad (6)$$

Sensitivity(Sen)Recall is another term for sensitivity. The ratio of perceived positive cases to total positive cases is as follows:

$$Sensitivity(Sen) = \frac{TP}{TP+FN} \quad (7)$$

Specificity(Spec)Specificity is a measure of how successfully your classifier detects negative cases by the proportion of actually negative cases that were categorized as negative. The true negative rate is another name for it.

$$Specificity(Spec) = \frac{TN}{TN+FP} \quad (8)$$

Precision (Prec)The division of the examples that are truly positive among all the examples that we anticipated positive is known as precision:

$$Precision = \frac{TP}{TP+FP} \quad (9)$$

Negative predictive value(NPV)The proportion of negatively classified instances that stayed truly negative is known as the negative predictive value (NPV):

$$NegativePredictiveValue(NPV) = \frac{TN}{TN+FN} \quad (10)$$

False-positive rate(FPR)The number of false-positive predictions divided by the total number of negatives is the false positive rate. The legitimate false-positive rate ranges from 0.0 to 1.0, with 0.0 being the lowest and 1.0 being the highest:

$$FalsePositiveRate(FPR) = \frac{FP}{FP+TN} \quad (11)$$

False-negative rate(FNR)The rate of negative test results leads to people who have the quality or illness for which they are being tested:

$$FalsePositiveRate(FNR) = \frac{FN}{FN+TP} \quad (12)$$

F1-Score The harmonic mean of precision and sensitivity is defined as the F1 score:

$$F1Score = \frac{2TP}{2TP + FP + FN} \quad (13)$$

Matthews correlation coefficient(MCC) MCC is used for binary categorization. The range is + 1 to 1 in this case. The best performance is exhibited when the value is + 1, and the worst performance is shown when the value is – 1. It's written like this:

$$MCC = \frac{(TP \times TN) - (FP \times FN)}{\sqrt{(TP + TP)(TP + FN)(TN + FP)(TN + FN)}} \quad (14)$$

3.5 Applied Algorithm

Ensemble Technique: Ensemble learning is a technique that combines multiple base models to do the same goal. The weak learner is a term used to describe these foundation models [24]. Ensemble learning is based on the idea that when a poor learner is left alone, it would make poor predictions. When coupled with other weak learners, however, they become powerful learners. The strong learner outperforms the weaker learners by a wide margin.

Random Forests (RF): A strong supervised classification algorithm is the random forest classifier. The RF classification is a type of nearest neighbor predictor that may be explored as an ensemble method. Many decision trees make up RF. Each decision tree provides a vote that indicates the object's class decision. Tin Kam HO of Bell Labs proposed the random forest item for the first time in 1995. The RF approach combines bagging with random feature

selection. Instead of generating a single classification tree, RF creates a forest of classification trees from a given dataset. For a given collection of qualities, each of these trees generates a categorization. The workflow of the RF classifier is given below.

i. K data points were chosen at random from the training set.

ii. Create decision trees based on these K data points.

iii. Choose the number of N-trees from the created trees and repeat steps (i) and (ii).

iv. For each new data point, create an N-tree that forecasts the category to which the data points belong, and assign the new data point to the category with the highest likelihood.

Adaboost Classifier(ADB): Freund and Schapire proposed AdaBoost, which is the most widely used boosting method for binary classification [25]. It accepts as input a training set S of m examples S = (x_1 , y_1), ...,($x_{m,}y_m$), where each instance (example) xi is a vector of attribute values belonging to a domain or instance space X, and each label , y_i is the class label associated with x_i belonging to a finite label space Y = −1, +1 for binary classification puzzles. For binary classification issues, Adaboost method generalized the version process given below.

Given: Sequence of m instance S = (x_1 y_1), ..., ((x_m y_m) where ($x_i \in$ X with labels yi ∈ Y = {−1, +1} weak learning algorithm Weak Learn, T(Number of iteration)).

Firstly Initialize $D_1(i) = \frac{1}{m}$ for all i = 1, ..., m Then start iterate κ = 1 to K

First step of iteration, Call Weak Learn Distribution D_k Then, get a weak classifier(hypothesis) h_κ : X{−1, +1} with its error(ϵ_κ):

$$\epsilon_\kappa = \sum_{i=h_\kappa(xi \neq yi)} D_k(i) \tag{15}$$

After that, Set (α_κ)

$$\alpha_\kappa = \frac{1}{2} ln \frac{1-\epsilon_k}{\epsilon_k} \tag{16}$$

Lastly, Update distribution (D_κ)

$$D_\kappa : D_\kappa + 1(i) = \frac{D_\kappa \exp\left(-\alpha_k y_k h_k(x_k)\right)}{z_k} \tag{17}$$

After end all iteration,The algorithm provide the Output(H_x)

$$Output: H_x = sign\left(\sum_{k=1}^{k} \alpha_k h_k(x)\right) \quad (18)$$

In each iteration k, Adaboost weights the training samples using the probability distribution $D_\kappa\ (x)$ (weight function over the training examples).The learning method (WeakLearn) is then used to create a classifier h_k on the training examples with an error rate of k (k was used to alter the probability distribution $D_\kappa\ (x)$. The adjustment in weights has the con-sequence of putting more weight on training instances that were incorrectly classified by h_k and less weight on examples that were correctly classified in the final stage. As a result, Adaboost tends to design increasingly challenging learning problems in succeeding iterations. This process is repeated for k rounds, culminating in the construction of the final classifier, H, from a weighted vote of the distinct weak classifiers h_1, h_2, ..., h_k. Every classifier is given a weight based on the accuracy of the distribution D_t on which it was trained [25]. The classification and regression tree (CART) method, introduced by Breiman et al. [26], was employed as the weak Learn to AdaBoost algorithm in this study.

XGBoost Classifier (XGB): Chen and Guestrin [27] intro-duced XGBoost, a unique gradient tree boosting approach.It uses a set of Classification and Regression Trees (also known as CART) as weak learners, then improves the trees performance by combining them into an ensemble that reduce a regularized objective function. The algorithm combined methods of gradient tree boosting with concepts such as sparsity- aware split finding in every tree, cache friendly inferential algorithms to determine splitting points, and effective out-of-core calculation to create an algorithm with too much fast computational speed and excellent prediction power.

The ensemble $F_0(x)$ first contains a weak learner $F_0(x)$ that learns from the original dataset, given a dataset D, y , and p CARTs $f(x)$as weak learners. The ensemble method then sequentially adds weak learners who learn from the prior ensemble's residual. The ensemble $F_t(x)$at the t-th boosting round is if t > 0, $t\epsilon$N is the t-th boosting round.

$$F_t(\mathrm{x}) = \sum_{i=0}^{t} f_i(\mathrm{x}) \quad (19)$$

where $f_t(x)$learns from remaining $F_{t-1}(x)$ and is the learner who greedily reduces an objective function L^t, where.

$$L^t(x) = \sum_{i=0}^{n} l\left(y_{i,} F_{t-1}(x_i) + f_t(x_i)\right) + \Omega(f_i) \tag{20}$$

$$\Omega(f_t) = \gamma T \frac{\lambda \parallel \omega \parallel^2}{2} \tag{21}$$

where l is a differentiable complicated loss function between the i-th output $y_{i,}$ and the (t − 1)-th ensemble's predicted i-th output $F_{t-1}(x_i)$, and $\Omega(f_t)$ is a function that penalizes tree complexity, and T, ω are the quantity of leaves and amount of all leaf weights gradually, and,γ, λ are the regularization and minimal loss hyperparameters of XGBoost.

XGBoost, like gradient tree boosting machine learning methods, can determine the relevance of variables in a dataset (locally, in a specific ensemble). In a CART, given a variable V, the improvement $I(V)$ of a variable that splits a parent node P into child nodes $L, R$of which q is the fraction of pathways that pass-through L is defined as,

$$I(V) = E(P) - (qE(L) - 1(1-q)E(R)) \tag{22}$$

where E(K) is the node K′s weighted squared errors. In an ensemble, the gravity of a variable is defined as the average development of that variable over all trees in the ensemble.

3.6 Implementation Requirements

To perform the complete job, we need a high-end PC with high GPU, processor and RAM. As we mount our task on Google Collab, it will provide some extra RAM and Space. So, an average PC can perform our task with the help of Google Collab. All required tools are given below:

3.6.1 Hardware & Accessories

- Intel Core i3 8th gen or higher
- 8 GB (+4GB by Collab) RAM or Higher
- 512 GB HDD
- High-Speed Internet connection

3.6.2 Software, Language & Tools

- Windows 11
- Python 3.9
- Google Collab
- Browser (Edge/Chrome)

Chapter 4

Experimental Results and Discussion

4.1 Experimental Setup

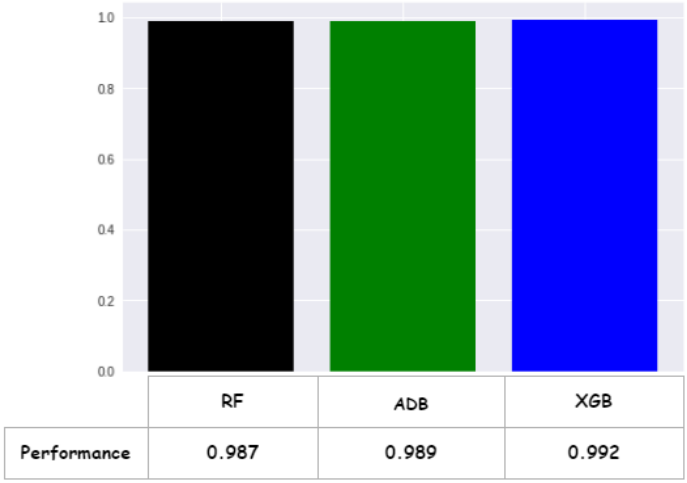
The proposed methodology was used as the reference to set up the experiment. Data collection, data preprocessing, feature selection, Machine Learning models for classification, all steps were completed.

For this task, we have used a personal computer which is built with Intel(R) Core (TM) i5-8265U CPU @ 1.60GHz 1.80 GHz, 12 GB RAM, 1 TB storage, 1 GB integrated GPU and Windows 11 Pro 64-bit operating system.

4.2 Experimental Results & Analysis

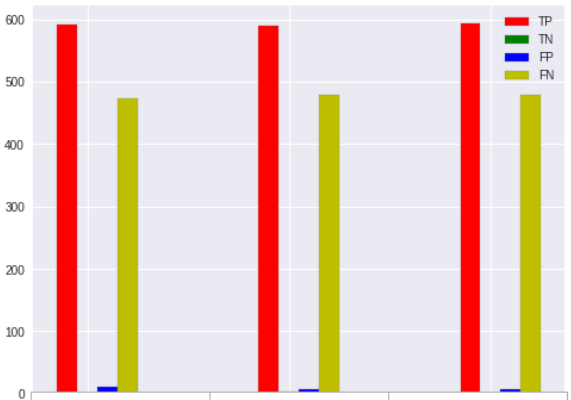
We will cover the general analytical procedure of the work in this section, which gives an analysis of brain tumor detection. Several measurement experiments have been used to test our models. The models' performance will then be presented, along with comparisons to other classifiers. I've been a part of multiple studies looking into three machine learning-based supervised ensemble strategies for brain tumor diagnosis and prediction. Three machine learning ensemble classifiers for brain tumor prediction were compared and their performance was measured. Figure 5 depicts the performance of the chosen ML classifiers. The XGBoost classifier had the best results, with a prediction accuracy of 99.2 %, while the Adaboost classifiers came in second, respectively (i.e., 98.9%). Furthermore, Random Forest classifiers achieve 98.7 % accuracy, which is nearly identical. The confusion matrix of forecast results for" Random Forest, XGBoost,Adaboost ensemble methods" was shown in fig 6. Three classification strategies are depicted in figure 7 based on performance metrics. The results clearly reveal that the XGB and RF have attained the highest level of precision (1.000 and 0.995). The highest sensitivity(recall) was attained by XGB and ADB, which is 0.983. In addition, ADB had the lowest specificity (99.30%) and highest specificity achieved XGB (1.00). Lowest false positive rate (FPR) achieved XGB (0.000) also XGB and ADB both had lowest false negative rate which is 0.013. And lowest negative predictive value (NPV) had RF

(0.975) on the other hand XGB and ADB both had the same 0.983.Highest Matthews correlation coefficient (MCC) had 0.985 performed by XGB and lowest had 0.973 performed by RF. In terms of the f1 metric, all of the classifiers have above good performance, which is above 98.00%.



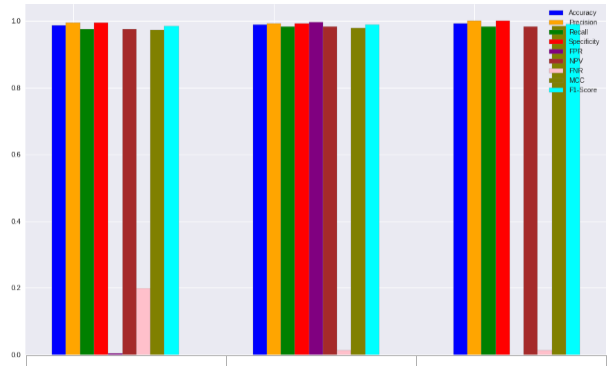
	RF	ADB	XGB
Performance	0.987	0.989	0.992

Fig. 5. Performance Ensemble Method (Brain Tumor)



	RF	ADB	XGB
TP	591	590	593
TN	2	3	0
FP	12	8	8
FN	474	478	478

Fig. 6. Confusion Matrix Analysis



	RF	ADB	XGB
Accuracy	0.987	0.989	0.992
Precision	0.995	0.993	1.000
Recall	0.975	0.983	0.983
Specificity	0.995	0.993	1.000
FPR	0.004	0.006	0.000
NPV	0.975	0.983	0.983
FNR	0.199	0.013	0.013
MCC	0.973	0.979	0.985
F1-Score	0.985	0.988	0.991

Fig. 7. Performance Measurements

The major appliance of the Receiver Operating Characteristics(ROC) curve is analytical test estimation. ROC curve mainly, the true positive rate(sensitivity) is plotted against the false positive rate(1-Specificity) at several thresholds. The ROC Brain tumor detection is illustrated in Figure 8. The Precision-Recall (PR) curve is mainly precision plotted against the recall. The PR-Curve shows the relation Precision and Recall. Precision is actual positive value is divided by anticipated positive value. Recall is the ratio of perceived positive cases to total positive cases. The PR-AUC curve for brain tumor prediction is Illustrated in Figure 9. Three classification strategies are depicted in figure 6 based on performance metrics. The results clearly reveal that the XGB and ADA have attained the highest level of precision (97%). The highest sensitivity was attained by RF, which is 100 percent. In addition, NB had the lowest specificity (92%). In terms of the f1 metric, all of the classifiers have the same performance, which is above 95%.

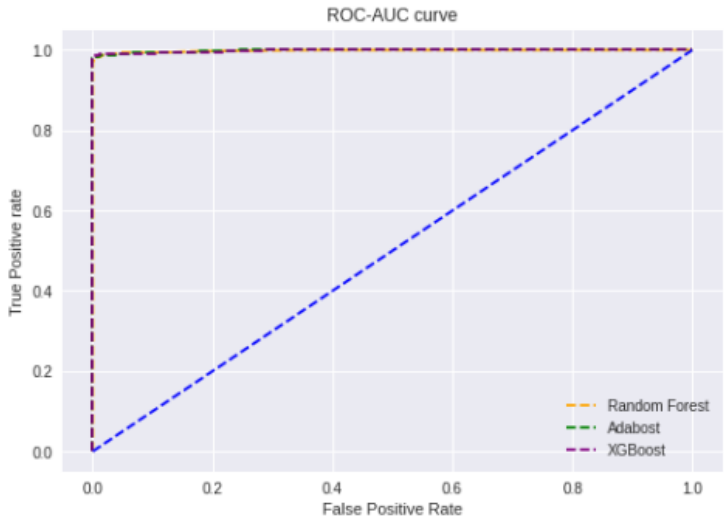


Fig. 8. Receiver Operating Characteristics(ROC) curve

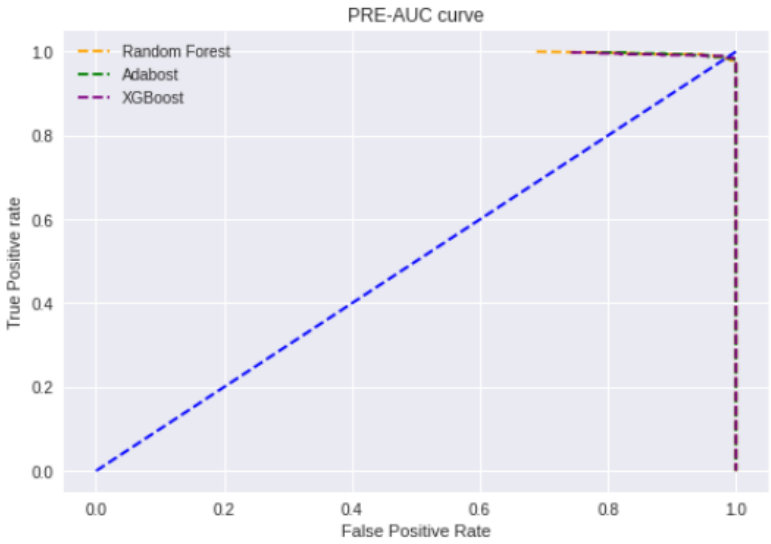


Fig. 9. Precision-Recall(PRE) curve for Brain Tumor Dataset

4.3 Discussion

Important and novel in the battle against brain tumors is the use of machine learning ensemble approaches for detection. Ensemble techniques combine the results of many machine learning algorithms into a single prediction. For the diagnosis of brain cancer, where conventional approaches like MRI images may be difficult to interpret and require substantial manual labor, this is a huge boon. The accuracy of the detection may be greatly enhanced by merging the results of many algorithms. The most popular ensemble approaches for detecting brain tumors include merging the results of several algorithms. These algorithms may range from simple support-vector machines to complex neural networks and deep learning models. An improved prediction of whether a tumor is benign or malignant, for instance, may be generated by combining the results of many algorithms. In theory, this might cut down on both overdiagnosis and underdiagnosis. Additionally, ensemble approaches may be used to enhance the precision of available therapeutic choices for patients. The most effective therapy for a given tumor may be determined more rapidly and correctly by combining the results of many algorithms.

CHAPTER 5

Conclusion and Implication for Future Research

5.1 Summary of the Study

This article discusses the use of machine learning ensemble methods for the detection of brain tumors. The ensemble method combines the results of different machine learning algorithms to get more accurate results. The study used a dataset of brain MRI images augmented with a variety of techniques, including contrast enhancement and data augmentation. The study showed that the ensemble method was able to achieve higher accuracy, precision, and recall than the individual algorithms. It was also able to reduce false positives and false negatives. The results of the study suggest that ensemble methods can be used effectively for brain tumor detection.

5.2 Conclusions

This research compared Random forest, Adaboost, and XGBoost to identify brain tumors. Essential elements and working concepts of each ensemble machine learning approach were shown. XGB had 99.2% accuracy, ADA 98.9%, and RF 98.7%. Diagnosing is expensive and time-consuming in medicine. The approach shows machine learning may be used to identify brain tumors, which will be helpful for new doctors in the case of a mistake. The XGBoost model is more consistent than any other and might change brain tumor prediction. Machine learning can identify tumors automatically and accurately, according to the study.

5.3 Implication for Further Study

Our intention is to gather a massive amount of high-quality, real-time data sets in the near future. To implement more time periods beyond the current one, we will provide high-end performance machine support.

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Appendix A

Dataset Link:

https://www.kaggle.com/datasets/jakeshbohaju/brain-tumor

Code Link:

https://colab.research.google.com/drive/1qzOPKJLJVXfPGQl7SaaD8ADh4sKoZu02?usp=sharing

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