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Breast Tumor Detection using Machine Learning Boosting Classifiers

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Abstract: Breast cancer is most commonly found in women and the second greatest cause of death worldwide. As breast cancer is detected early, the ratio of survival rate increases because better therapy may be provided. ML algorithms play a critical role in the early detection of breast cancer. In this study, we purposed a Novel method that increases the accuracy and performance using these three different classifiers: Gradient Boost (GB), Ada Boost (ABC), and Extreme Gradient Boost (XGB). On the Public dataset WBC, we evaluated and compared the classifiers' performance and accuracy. Because the chance of examples belonging to the majority of the class is relatively high, algorithms are far more likely to categorize new observations into the majority class in the classification phase. We address such a situation that True positive, false positive, precision, recall, F1 score, and accuracy are all used to evaluate the efficiency of each classifier. Experiments demonstrate that utilizing a boosting classifier improves the performance, with the Gradient Booster (GB) outperforming others in the WBC dataset.

Keywords: Breast Cancer; Brain Tumor; Deep Learning; Detection, Machine Learning.

1. Introduction

Cancer is a disease in which the cells of the body grow out of control and spread to other sections or tissues of the body. Cancer disease is a major cause of death around the world, accounting for approximately 10 million deaths in the previous year. Out of 10 million cases, the most common in terms of new cases of cancer were breast cancer cases approximately 2.26 million. Breast cancer is a type of cancer that starts in the breast. It starts when cells begin to grow uncontrollably in the breast. Today Breast Cancer is known as the 2nd most leading cause of mortality among women worldwide. Breast Cancer is mostly found in females but also occurs in men. The occurrence rate of breast cancer in men is 1 out of 100. In the case early detection of breast cancer is the greatest approach to maximize the chances of treatment and survival.

Data mining has grown increasingly, becoming more popular and is rapidly expanding in the field of knowledge discovery, without standing outcomes in fields such as medical, social science, marketing, and finance. Several data mining techniques have recently been used in medical data sets in order to conduct analyses on patients and their medical diagnoses. For example, evaluating the behavior of tumors in breast cancer patients using various ML algorithms.

The problem which we are dealing with is that in the training dataset there is a class imbalance. Since the risk of not getting this disease is greater than the risk of getting it. Previously Many different ML classifiers: Gradient Boosting, XG Boost, and Ada Boost have been used to achieve the best accuracy. In this paper, we introduced a novel technique with advanced preprocessing and ML techniques. This paper compares three distinct classifiers: Gradient Boosting, XG Boost, and Ada Boost regarding accuracy in term of Breast Cancer detection. All tasks were conducted, Jupiter Notebook.

A number of the author have as recognized Because of the large amount of data compatibility and availability of data type, the healthcare business is one of the most precise areas for data science application In hospitals, data flow would be an ongoing process that involves numerical quantities. With studies on data mining and ML approaches, healthcare is indeed an open development system. Multiple researches on different datasets of breast cancer dataset have been conducted, and the bulk of them have achieved adequate classification accuracy. These algorithms produce good classification results, which encourages many academics to use them to solve difficult problems. Breast cancer diagnostics using Artificial Intelligence (AI) techniques to increase classification accuracy and performance. Here we present some previous work done on the use of different machines and deep learning methodologies to solve the problem of a medical breast cancer diagnosis.

For breast cancer classification, Arpit B. and Aruna T. et al. presented a GONN (malignant and benign). By introducing novel mutation operators and crossover, they were able to enhance the neural network architecture. They employed WBCD to evaluate their work, comparing the classification, specificity, accuracy, confusion matrix, receiver operating characteristic (ROC) curves, AUC (area under ROC curves) and GONN sensitivity to the classical Backpropagation model as well as the classical model. This method provides high level of accuracy of categorization. Although, it might be improved by using a larger dataset than WBCD and extracting characteristics to make GONN more efficient for real-time breast cancer diagnosis.

A hybrid model based on AdaBoostM1 classifier, k-means clustering (KMC) based feature weighting and the crazy normalization was proposed by Kemal P. et al. There are three steps to detecting the existence of breast cancer: The dataset was first normalized using the MAD normalization approach in the first stage. In the second stage, the normalized data were weighted using KMC based on feature weighting. Finally, the weighted data set was classified using the AdaBoostM1 classifier. The Breast Cancer Coimbra dataset (BCC) was used, which was obtained from the UCI ML database. In terms of accuracy, this approach performs well. It is, however, a computationally intensive method.

On the WBC datasets, Hiba A. et al. compares the performance of these four classifiers: Support Vector Machine (SVM), Decision Tree (C4.5), k Nearest Neighbors (K-NN) and Naive Bayes (NB). Using a hybrid feature selection approach, Na L. et al. presented an intelligent classification algorithm for breast cancer detection based on again guided simulated data to eliminate duplicate and unnecessary features out from feature set with CSSVM learning algorithm. This method can enhance classification accuracy while lowering computing costs. The proposed approach is tested on WBC original and WBCD to ensure its efficacy. The proposed work performs well and reduces the calculation's complexity.

Dr. William H. Walberg from Wisconsin Hospital gave the dataset to Muhammed Fatih Ak. Et al. This dataset was subjected to data visualization and ML techniques such as support vector machine (SVM), k-nearest neighbors (K-NN), nave Bayes, logistic regression, random forest, decision tree, and rotation forest. These ML techniques and visualization were implemented using Python and R, Minitab. Each and every procedure was subjected to a comparative study. The model of logistic regression with all features achieved the greatest classification accuracy (98.1%), while the recommended technique improved inaccuracy.

Dana Bazazeh et al. compared three ML techniques: Support Vector Machine (SVM), Bayesian Networks (BN), and Random Forest (RF). As a training set, the Wisconsin original breast cancer data set was employed. The simulation results revealed that classification performance varied depending on the approach used. SVMs shows best performance in terms of precision, accuracy, and specificity according to the findings. RFs, on the other hand, have the best chance of correctly identifying tumors.

Prashant Pathak et al. performed a comparison of ANN and SVM and combined multiple classifiers such as CNN, KNN, and Inception V3 for improved dataset processing. Because ANN was demonstrated to have a greater efficiency rate than SVM, the experimental findings and performance analyses concluded that ANN was a better classifier than SVM.

Teresa et al. utilize Convolutional Neural Networks (CNNs) to classify eosin- stained breast biopsy images and hematoxylin. They provide four types of medical relevance: benign lesion,

Normal tissue, aggressive carcinoma and in situ carcinoma. The suggested CNN architecture is intended to combine data from a number of histological scales. The model is validated using a set of uncompressed and high-resolution annotated images. Images were strained from breast histology classification challenge (Bio imaging 2015).

Meraryslan Meraliyev et al. studied breast cancer prediction difficulties and devised solutions using five modeling methods, including Greedy Search and K-fold cross-validation Neural Networks, Decision Tree Classifiers, Support Vector Machines (SVM), Logistic Regression and K-Nearest neighbor (KNN) were among the algorithms studied. The results of the modeling revealed that SVM and KNN are the best algorithms for predicting breast cancer.

In a review titled "Applications of ML in Cancer Prediction and Prognosis," Joseph A. et al. identified a number of trends in the types of training data integrated, the types of ML methods used, the types of cancers studied, the types of endpoint predictions made, and their overall efficacy in predicting cancer risk or prognosis. They concluded that if the quality of studies continues to increase, ML classifiers will likely become much more popular in many clinical and medical settings.

The rest of the paper is structured as follows. Section 2 discusses the Material and Methods. Section 3 illustrates the dataset. Section 4 describes the research methodology. Section 5 portrays the experimental result and Section 6 shows the conclusion.

2. Materials and Methods

The main purpose of our research is to find the most predictive and effective algorithm for breast cancer detection. To do so, we used ML classifiers such as Gradient Booster (GB), Extreme Gradient Boosting (XG Boost), Ada Boost Classifier (ADB), and Stochastic Gradient Boosting (SGB) on the Breast Cancer Wisconsin Diagnostics dataset was used, and the results were compared to evaluate which model had the greatest accuracy. Our procedure starts with data collection and then moves on to pre-processing, data correlation, ML classifiers, performance evaluation and result discussion as shown in Figure. 1.

ML algorithms are built using the prepared data to forecast breast cancer for a new set of measures. To test the algorithms' performance, we provide the model a fresh data with labels. This is commonly accomplished by using the Train and the test split technique is used to divide the labeled data we've collected into two halves.

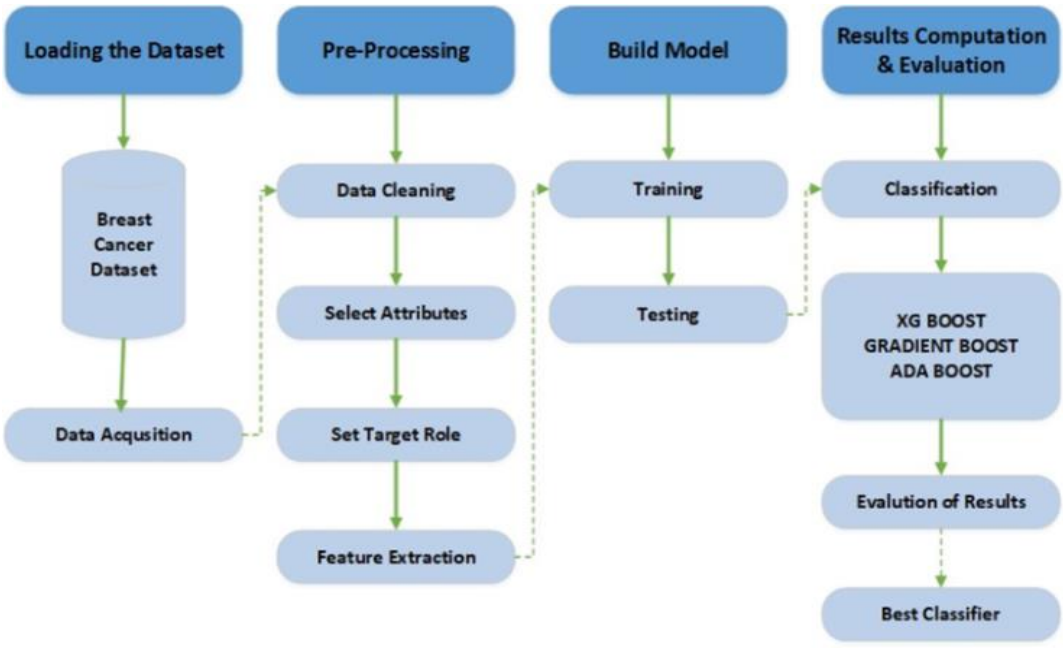

Figure 1. Flowchart of Research Methodology

2.1. Data acquisition

The dataset used in this research paper is available at UCI Repository. There are 569 instances and 11 attributes in the WBC dataset, with 357 benign and 212 cancerous cases as shown in Figure 2. As a result, data pretreatment is critical for this dataset, as it requires us to manage the unbalanced data.

The training data, also known as the training set, accounts for 70% of the data utilized to develop our ML model. Test data, or test set, is 30% of the data will be utilized to assess the model's performance. After evaluating the models, we compare the findings to determine which algorithm delivers the highest accuracy and which algorithm is the most predictive for breast cancer screening.

The dataset utilized in this study is susceptible to missing and imbalanced data; a significant portion of the work will be spent preparing the data in order to improve the classifier's performance. The missing values and imbalanced data will be managed during preprocessing. To control the missing attributes, all instances with incomplete values are deleted. Finally, comparison of each of the three classifiers is compared accomplished.

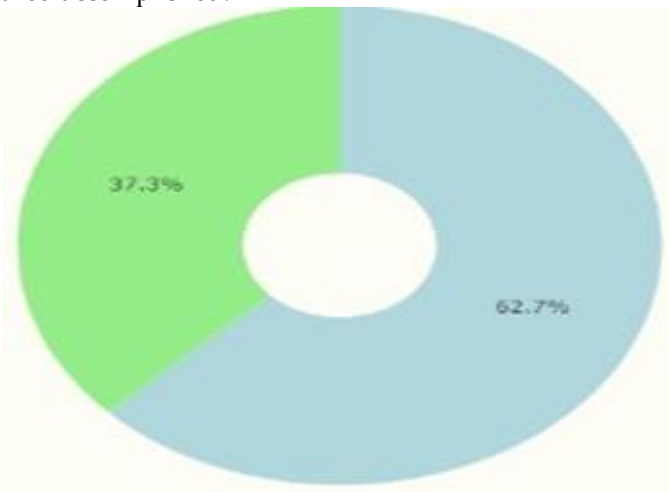

Figure 2. Distribution of Patients

2.2 Data Preprocessing

The data was first discretized using the discretized filter. Second, the discovered missing values were deleted in order to keep the subsample's class distribution and bias it toward a uniform distribution.

The following stages were used in the data preprocessing technique: discretization, instances resampling, and missing value removal as shown in Figure. 3.

Data Discretization: is a technique for transforming a large number of data values into smaller ones, making data interpretation and management easier. To put it another way, data discretization is a technique for turning continuous data's attribute values into a finite collection of intervals with little data loss.

Missing Values: These values aren't recorded in a dataset. They can range from a single value missing in a single cell to an entire observation being lost (row). Missing data can arise in both continuous and categorical variables. The prepared datasets were then used to test three classifiers. We must train the data in such a way that it can forecast whether the cells are M (malign) or B (beneficial) and (Benign).

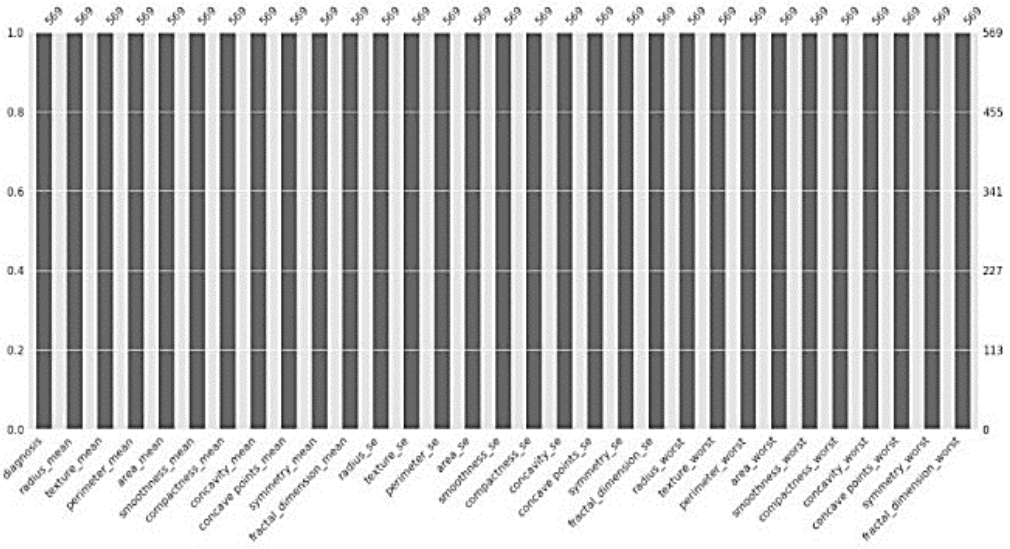

Figure 3. Visualizing the Data after Dropping the Null Values

2.3. Data Correlation

The degree to which changes in the value of one variable anticipate changes in the value of another is measured by the correlation coefficient. When the value of one variable changes, when one variable dependably predicts a comparable fluctuation in another, there's a temptation to believe that the change in one causes the change in the other. However, correlation does not imply causation that there is a link between the two. When it comes to determining the difference between correlation and causation, it's important to know the difference.

Positive Correlation: A positive correlation is a relationship between 2 variables where both variables move in the same similar direction. This happens when one variable rises while the other falls or vice versa.

Negative Correlation: When two variables tend to move in opposite sizes and directions from one another, such as when one grows, the other decreases, and vice versa, this is referred to as a negative or inverse correlation..

The following figures will illustrate the correlation of the data and attributes. The SE Features and Diagnosis difference is shown in Figure.4, the Mean Features and Diagnosis is shown in Figure.5, and the Worse Features and Diagnosis difference is depicted in Figure.6. The heatmap with respect to various features is illustrated in Figure 7.

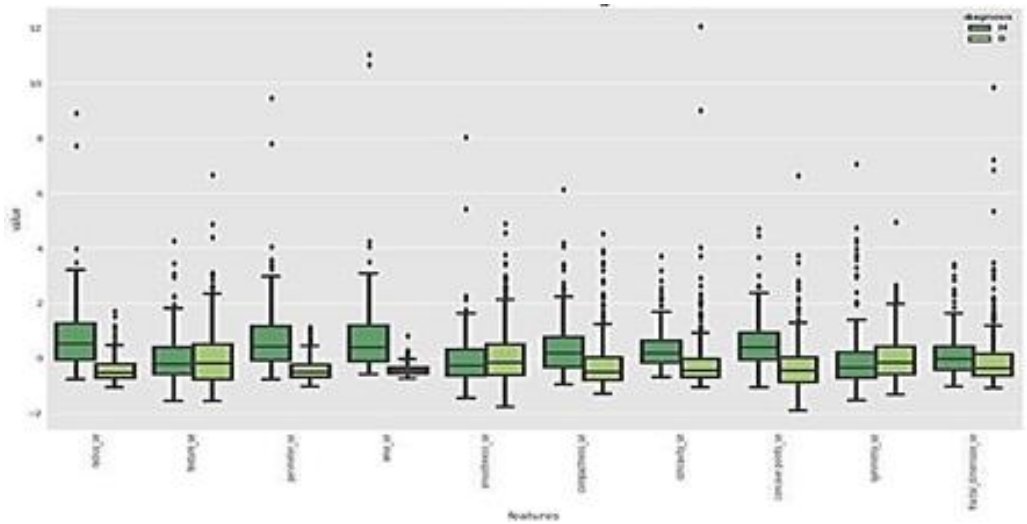

Figure 4. SE Features Vs Diagnosis

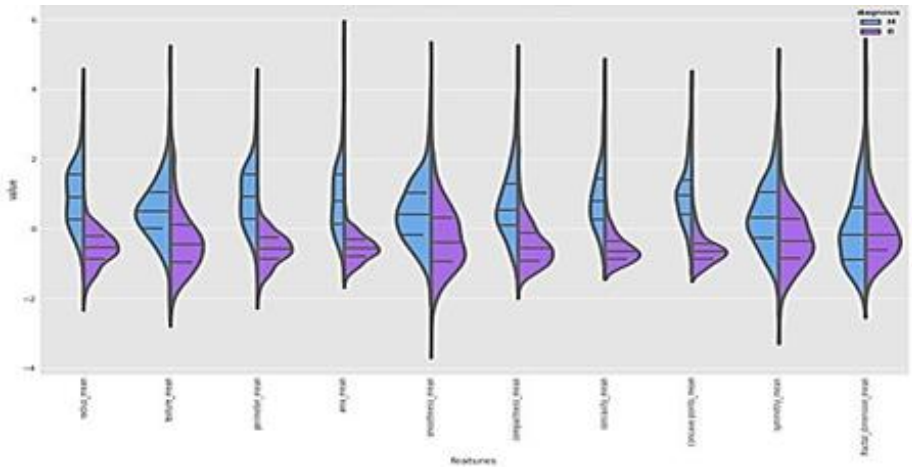

Figure 5. Mean Features Vs Diagnosis

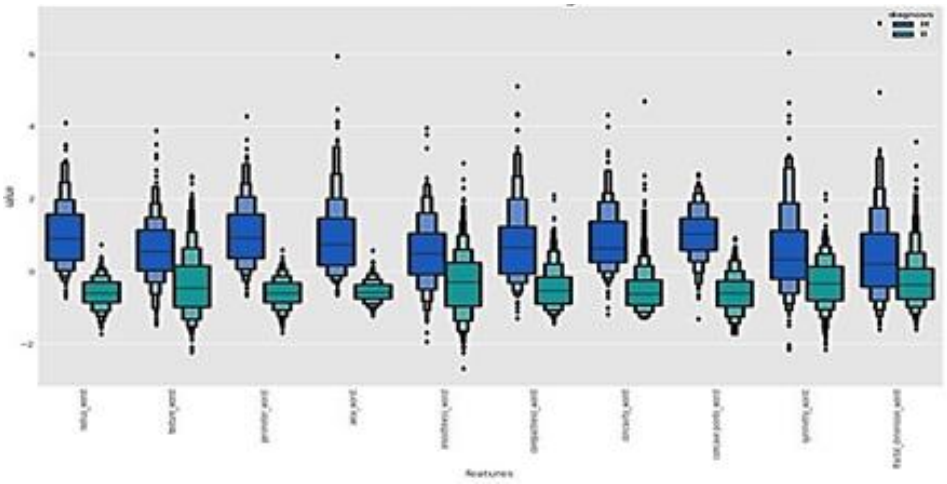

Figure 6. Worse Features Vs Diagnosis

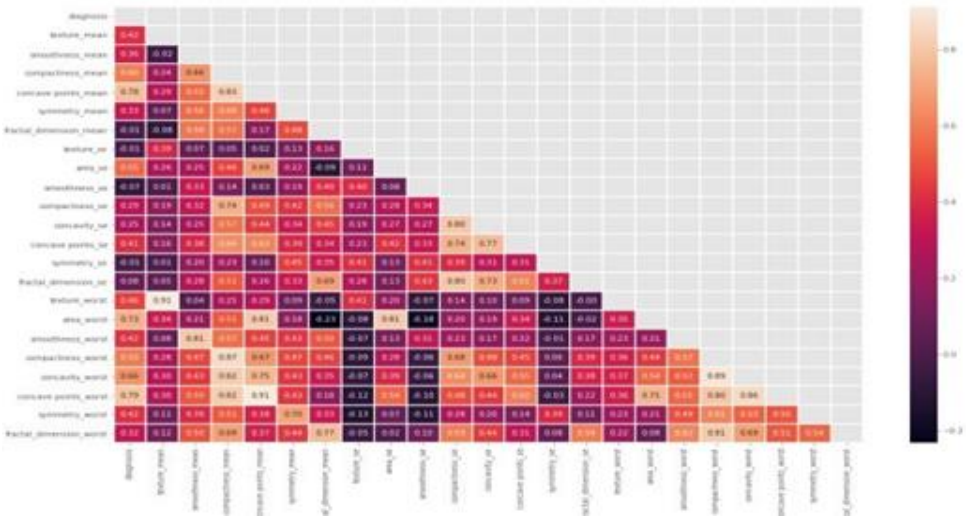

Figure 7. Heatmap Features

Density Plot: A density plot is a visual representation of a numeric variable's distribution. It shows the probability density function of the variable using a kernel density estimate. The distribution of one or a few variables is studied using density plots. The very first thing you must do when you get a new dataset is examine the distribution of our variables one at a time. It contains a considerable quantity of information as shown in Figure.8.

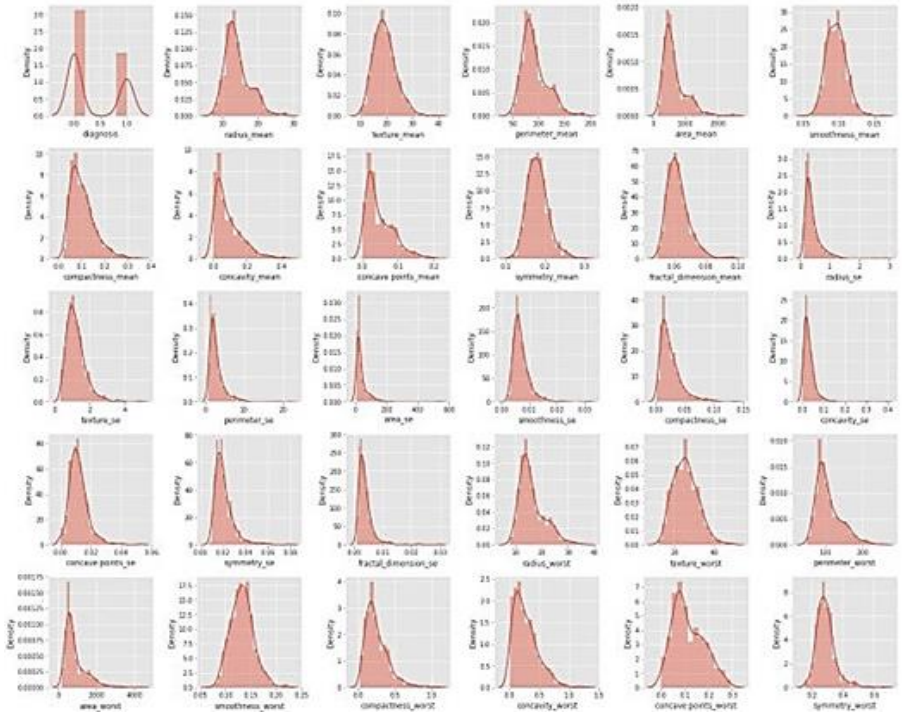

Figure 8. Density Plot of Breast Cancer

2.4 ML Algorithms

2.4.1 Gradient Boost

Gradient boost classifier is a collection of ML algorithms that combine several Weak learning models are used to develop a powerful prediction model. Decision trees are frequently used in gradient boosting. Gradient boosting models become more popular due to their ability to categorize tough data, the flowchart of GB boost shown in Figure.9.

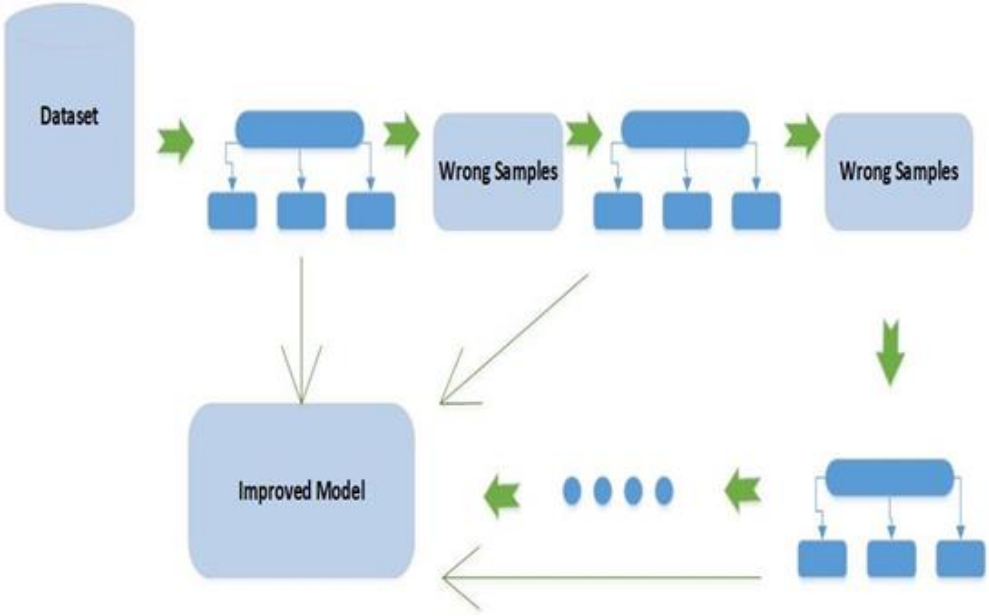

Figure. 9. Flowchart of Gradient Boost

Loss function: The loss function's goal is to determine how efficient the model would be at making a prediction based on the data provided. This might alter depending on the situation at hand.

For example, if we're attempting to estimate a person's weight based on a set of input factors (a regression problem), the loss function will assist us in determining the difference between the predicted and observed weights. If, on the other hand, we're trying to predict whether or not a person

would enjoy a particular film based on their personality, we'll need a loss function to figure out how good our model is at classifying people who did or didn't enjoy various films.

Weak Learner: A Week or poor learner is one who attempts to classify our data but fails miserably, achieving no better results than random guessing. To put this another way, it makes a lot of errors. Typically, these are often decision trees, (sometimes known as decision stumps, since they are less intricate than conventional decision trees).

Additive Model: This is a sequential and iterative strategy of gradually increasing the trees (weak learners). We must be closer towards our final model with each cycle. In other words, with each repetition, the value of the loss function should be reduced.

2.4.2. XGBoost

It is a fine-tuned and customized version of a gradient-boosting decision tree system designed for speed and performance. XG Boost stands for "Extreme Gradient Boosting," and it alludes to the fact that the algorithms and methodologies have been tweaked to push the envelope of what gradient boosting algorithms can achieve. XG Boost is a parallel tree boosting (also known as GBDT, GBM) algorithm that solves a variety of data science problems quickly and accurately. The same code can solve problems with billions of examples in a distributed environment (Hadoop, SGE, and MPI), the flowchart of XG boost shown in Figure 10.

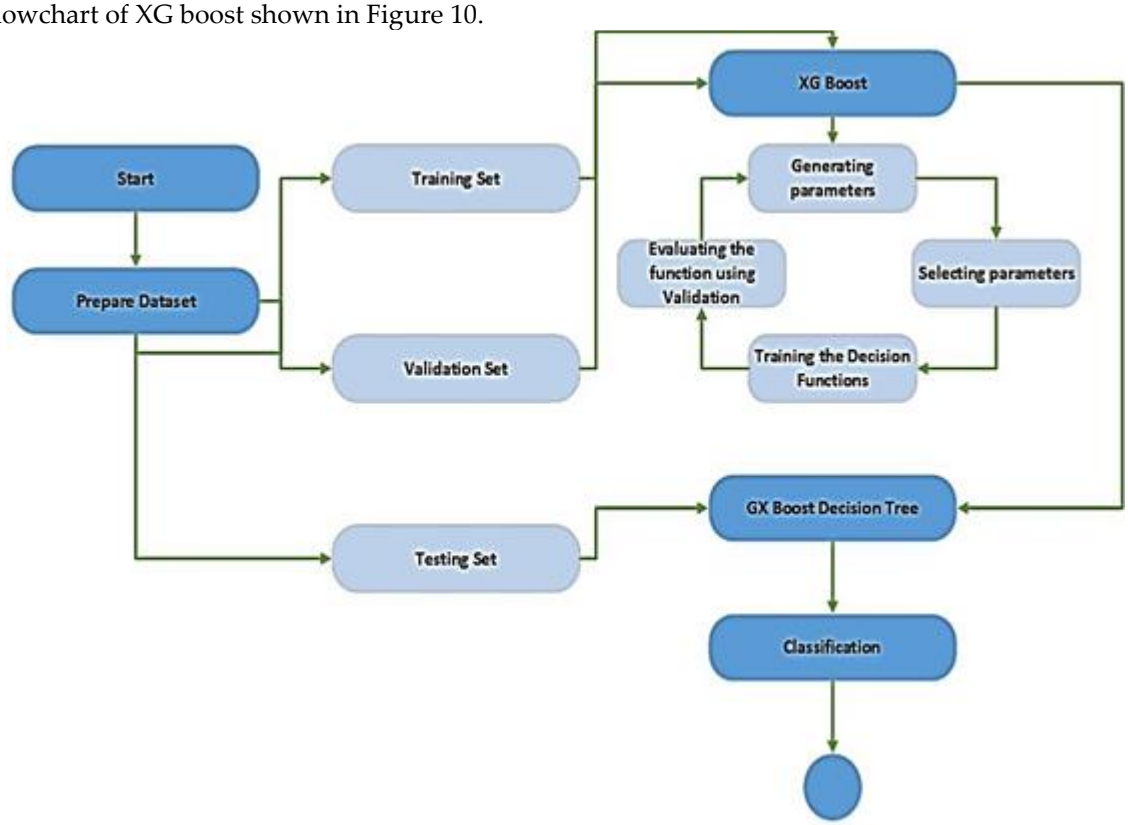

Figure 10. Flowchart of XG Boost

2.4.3. AdaBoost

An Ada Boost classifier is a meta-estimator that starts by fitting a classifier on the original dataset, then fits further copies of the classifier on the same dataset, but adjusts the weights of poorly classified instances so that future classifiers focus more on difficult cases. It can be combined with a variety of other learning algorithms to boost performance.

Other learning algorithms' output ('weak learners') are blended into a weighted total that represents the boosted classifier's final output. Ada Boost is an adaptive in the sense that it adjusts successive weak learners to prefer examples misclassified by previous classifiers. In some instances, it might be less prone to over fitting than other learning methods. Individual learners could be ineffective, as long as learners' performance is somewhat more efficient than random guessing overall final model will merge to a powerful learner, the flowchart of ADA boost shown in Figure 11.

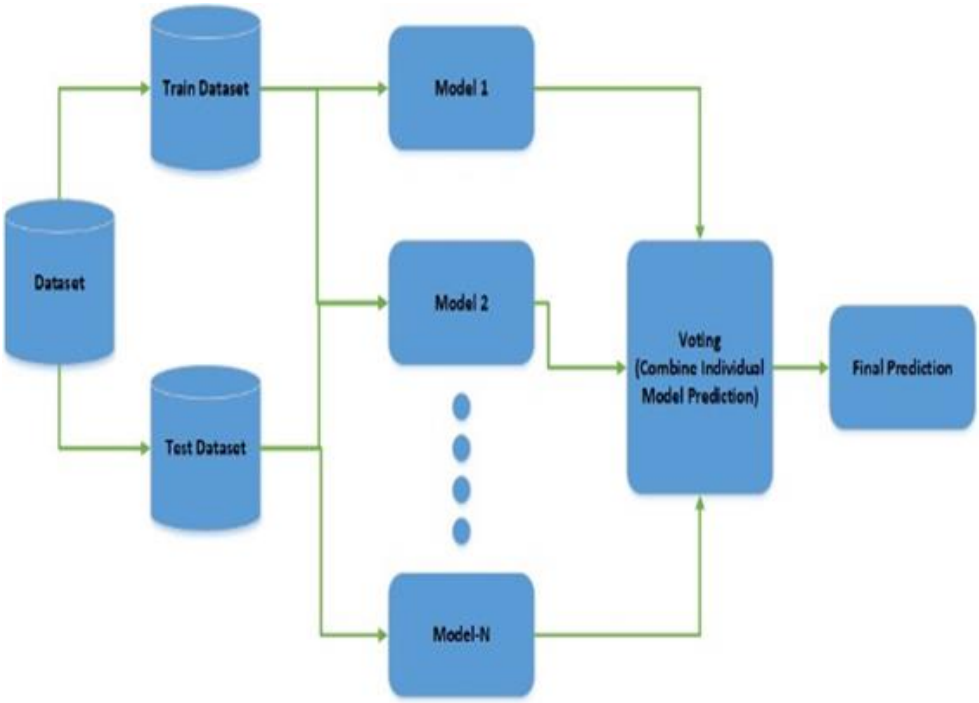

Figure 11. Flowchart of ADA Boost

2.4.4. Performance Evaluation

To assess the suggested work, we conducted a summary comparison based on the following criteria: algorithm utilized performance measurements precision, recall, f1-score, support, and accuracy.

2.4.4.1 Accuracy

The ratio of true positives and true negatives to all positive and negative observations is defined as model accuracy, a ML model performance statistic. In other words, accuracy indicates the likelihood that our ML model would accurately anticipate an outcome based on the total number of predictions it has made.

Consider the following scenario: You were testing your ML model using a dataset of 100 records, and your ML model successfully predicted 90 of those occurrences. In this situation, the accuracy measure would be (90/100) = 90%. The accuracy rate is excellent, but it tells us nothing about the faults our ML models make when dealing with new data. It is the ratio of the total of true positive and true negative predictions in mathematics and it is represented as follows in equation (1).

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

2.4.4.2 Precision

The model's ability to correctly forecast the positives out of all the positive predictions it produced is measured by its precision score. When the classes are extremely imbalanced, the accuracy score is a good indicator of prediction success. It shows the ratio of true positives to the sum of true positives and false positives in mathematics, as shown in equation (2).

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

2.4.4.3 Recall

The model's ability to correctly forecast positives out of real positives is measured by the model recall score. This differs from precision, which counts how many positive predictions a model makes out of all positive predictions.

For example, if your ML model is attempting to detect positive reviews, the recall score would be the percentage of positive reviews that your model correctly predicted as positive. In other words, it assesses how well our ML model recognizes all true positives among all possible positives in a dataset.

The better the ML model is in identifying both positive and negative samples, the higher the recall score. When the classes are very imbalanced, recall score is a good indicator of prediction

success. It is the ratio of true positive to the sum of a truly positive and false negative in mathematics represented as in equation (3).

$$Recall = \frac{TN}{TN\#FP} \quad (3)$$

2.4.4.4 F1- Score

The model score as a function of precision and recall is represented by the model F1 score. F-score is a ML model performance statistic that weighs Precision and Recall equally when evaluating the accuracy, making it a viable alternative to accuracy metrics (it does not require us to know the total number of observations), mathematics represented as in equation (4).

$$Recall = \frac{2*(Precision*Recall)}{Precision+Recall} \quad (4)$$

It's frequently utilized as a single value that conveys high-level information regarding the output quality of the model. This is a valuable model measure in situations where one tries to optimize either precision or recall score and the model performance suffers as a result. The aspects that was relevant to concerns with optimizing either precision or recall score are listed below.

Optimizing for recall helps to reduce the chances of missing a malignant malignancy. However, this comes at the cost of being able to anticipate malignant tumors in patients who are otherwise healthy (a high number of FP).

If the patient has a malignant malignancy, Optimize for Precision can aid with accuracy. However, this comes at the risk of more commonly missing aggressive cancer (a high number of FN).

2.4.4.5 Support

The number of actual occurrences of the class in the provided dataset is known as support. Imbalanced support in the training data could reveal fundamental problems in the classifiers reported scores, necessitating stratified sampling or rebalancing. Support does not alter depending on the model; instead, it diagnoses the evaluation process.

2.5. Proposed Approach

We apply a variety of ML algorithms to predict breast cancer in this paper. In this study, we describe a strategy that uses three different classifiers to improve accuracy and performance: Gradient Boost (GB), Ada Boost (ABC), and Extreme Gradient Boost (EGB) or (Xg boost). We construct such a situation using the dataset WBC. Precision, recall, F1 score, and accuracy are all utilized to measure the efficiency of each classification illustrated in Figure 12.

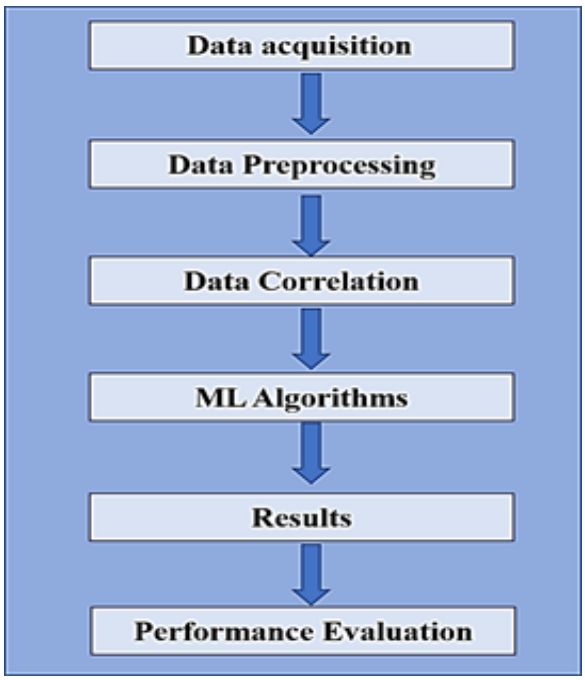

Figure 12. Flowchart of proposed approach

3. Results and Discussion

In this Section, the tests that we conducted to evaluate the performance of XG Boost, Gradient Booster, and Ada Boost in the job of breast cancer detection are presented. ML Algorithms were used to analyze the Breast Cancer Wisconsin dataset. To deeply analyzed and contrast the models in order to discover the best breast cancer algorithm as shown in Figure. 14, we used Confusion Matrix, F1 score, Accuracy, Support, and Precision as performance indicators.

The Confusion Matrix is a method of evaluating the performance of a classification task with two or more types of output. A confusion matrix is a table having two dimensions:" Predicted" and" Actual," as well as" True Negative (TN)"," True Positive (TP)"," False Negatives (FN)", and" False Positive (FP)" on both dimensions. The most common performance measures for classification algorithms are accuracy. It is defined as the proportion of correct forecasts to all predictions made. The confusion matrix of optimal Gradient Boost algorithms is shown in Figure.13.

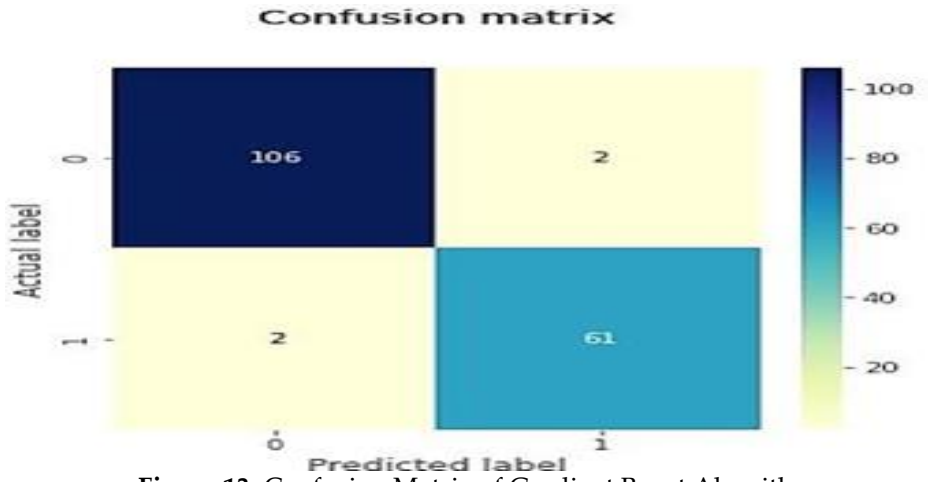

Figure 13. Confusion Matrix of Gradient Boost Algorithm

Accuracy, precision, F1-Score, and recall are the performance measures employed. To calculate accuracy, we employed the training and testing split approach, then applied three ML boost classifiers and compared their results in Table 1, and visualize them in Figure 15.

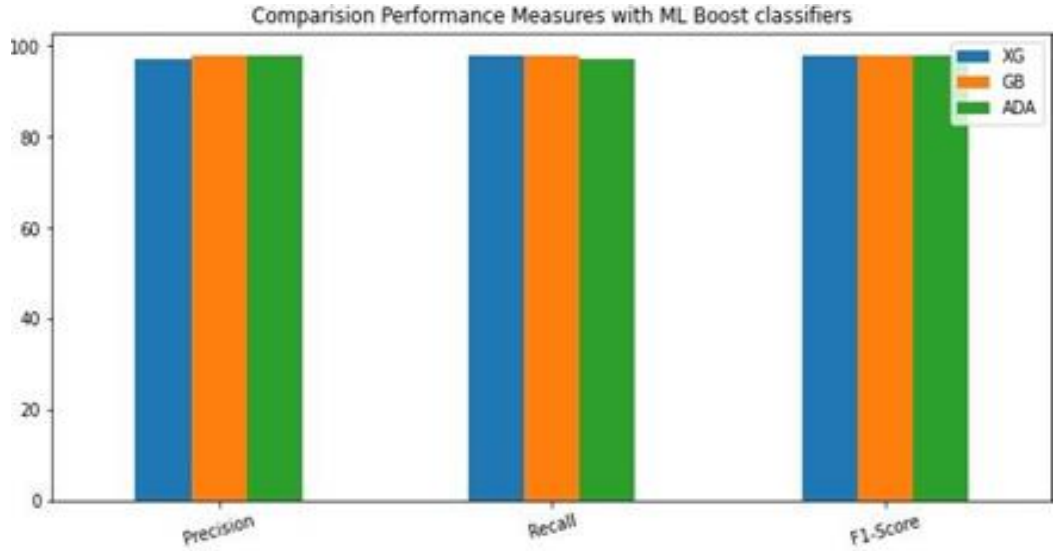

Figure 14.Comparison Results with ML Boost classifiers

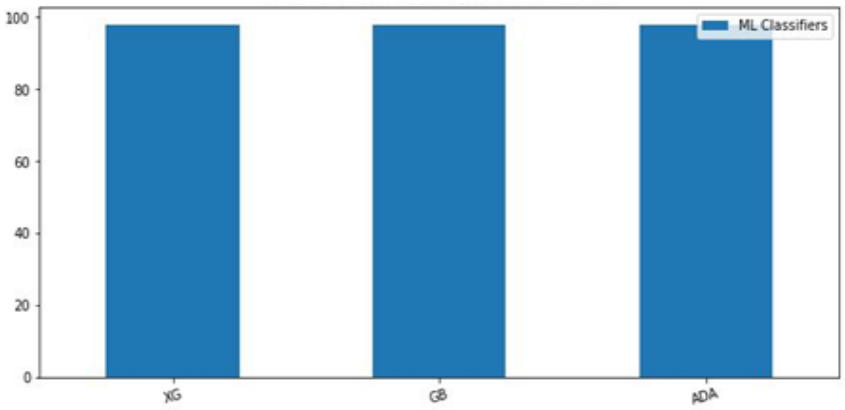

Figure 15. Comparison Performance Measures with ML Boost classifiers

Table 1. Performance Evaluation of ML Boost Classifiers.

ML Boost Classifiers	Accuracy (%)	Precision	Recall	F1-Score	Support
ADA Boost	97.66	0.98	0.97	0.98	171
XG Boost	98.24	0.97	0.98	0.98	171
GB Boost	98.83	0.97	0.98	0.98	171

4. Conclusions

We addressed the most recent studies that used ML algorithms to diagnose breast cancer. The majority of them were created in the last few years and focus on constructing prediction models that use ML and classification algorithms to anticipate accurate sickness outcomes. The proposed study with Gradient Boost Algorithm 98.83% accuracy and outperformed all other techniques. In the future, it is proposed that a big and a standardized public dataset be utilized in conjunction with multiple feature extraction and classification methods to give effective and robust interpretation tools in the cancer domain. These results provide a compelling reason to be applied for other diseases.

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