BREAST TUMOR DETECTION USING EFFICIENT MACHINE LEARNING AND DEEP LEARNING TECHNIQUES

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ABSTRACT

Breast cancer tissues grow when cells in the breast expand and divide uncontrollably, resulting in a lump of tissue commonly called and named tumor. Breast cancer is the second most prevalent cancer among women, following skin cancer. While it is more commonly diagnosed in women aged 50 and above, it can affect individuals of any age. Although it is rare, men can also develop breast cancer, accounting for less than 1% of all cases, with approximately 2,600 cases reported annually in the United States. Early detection of breast tumors is crucial in reducing the risk of developing breast cancer. A publicly available dataset containing features of breast tumors was utilized to identify breast tumors using machine learning and deep learning techniques. Various prediction models were constructed, including logistic regression (LR), decision tree (DT), random forest (RF), support vector machine (SVM), Gradient Boosting (GB), Extreme Gradient Boosting (XGB), Light GBM, and a recurrent neural network (RNN) model. These models were trained to classify and predict breast tumor cases based on the provided features.

KEYWORDS

breast tumour, machine learning, deep learning, cancer, tumour detection

1. INTRODUCTION

Breast cancer is a serious health concern that affects a significant number of women worldwide. It is characterized by the growth of abnormal cells in the breast tissue and is the most commonly diagnosed cancer among women [1]. The prognosis of breast cancer refers to the likelihood or risk of the disease occurring based on various clinical and non-clinical factors. Prognosis is an essential aspect of breast cancer treatment and management. It helps patients and healthcare providers understand the potential outcomes of the disease, which can help guide treatment decisions and planning. Various factors can influence breast cancer prognosis, including the stage and subtype of cancer, the patient's age, overall health status, and other medical conditions. Breast cancer prognosis can be expressed in several ways, such as relapse-free survival (RFS) and overall survival (OS). The 5-year RFS rate indicates the percentage of patients who have not experienced a disease recurrence five years after treatment.

On the other hand, the 10-year OS rate reflects the percentage of patients still alive ten years after diagnosis, regardless of disease recurrence or progression. Accurately predicting breast cancer prognosis is crucial for patients, healthcare providers, researchers, and policymakers. It can help guide treatment decisions, evaluate the effectiveness of various therapies, and identify patients who may require more intensive monitoring or follow-up care. Several predictive models have been developed and tested in different contexts [2]. Prabira Kumar et al. proposed a classification

model utilizing fine-KNN, which incorporates a merger of deep learning features and handcrafted features extracted from H&E (Hematoxylin and Eosin) images. The aim is to automate classifying these images for various purposes. With ongoing research and innovation, breast cancer detection and treatment are continually improving, and survival rates are steadily increasing. Early detection, personalized treatment, and a better understanding of the disease are key to reducing the aftermath of breast cancer on women's health and well-being [3].

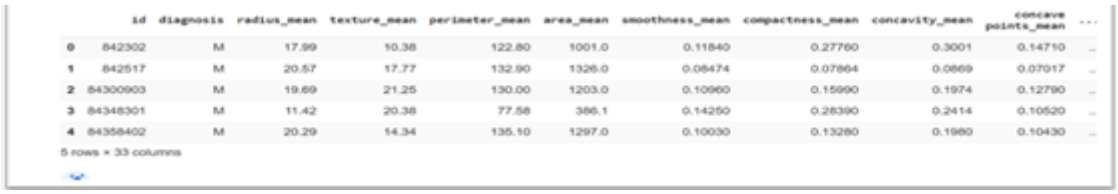
Turkki et al. argues that performing a prognostic evaluation for breast cancer without prior knowledge of its histology is possible. They propose a novel approach to breast cancer classification using five AI classification methods and a specialized CNN model. To assess their performance, the study evaluates several classification techniques, including logistic regression, random forests, support vector machine, voting classifier, decision tree, and a custom CNN model [4-7]. Mohammad Monirujjaman et al. also managed to test different approaches for breast cancer detection with a modified CNN network. According to a study, the new coronavirus illness (COVID-19) pandemic may have hindered advances in cancer care. The biggest hurdles were most likely delays and decreases in cancer screening, diagnosis, and treatment. Many models have been developed to predict breast cancer prognosis.

Along with it, the range of models has grown significantly, as have their emergence methods, predictive variables, results, demonstrations, and performance in various contexts [8-13]. Several studies have explored the practicality of AI and deep learning in healthcare to enhance the quality and assurance of treatments [14–17]. Bejnordi et al. employed a deep learning system to detect breast cancer and collate the results with diagnoses made by pathologists. The findings revealed that automated detection using a deep learning system surpassed human efforts in diagnosis [18-23]. Patra et al. researched to investigate the performance of advanced deep learning methods in detecting breast cancer by combining different features. Specifically, the study evaluates the efficacy of fusing the features of AlexNet, vgg16, and vgg19 in a two-layer fusion approach when applied to thermal images for breast cancer detection. Breast cancer identification at an early stage also results in lower treatment costs. Building devices for the visual assessment of the potential pleasing effects of Breast Conservative Treatment, with potential implications in reducing the number of secondary measures or in the indicative outcomes of additional therapies such as radiation therapy or systemic interventions. A method is proposed to augment the Kaggle breast tumor dataset with synthetic data and apply it via different ML and deep computing algorithms to compare its accuracy in detecting cancer [24].

2. MATERIALS AND METHODOLOGY

2.1. Dataset Description

The dataset is collected from Kaggle (breast tumor.csv) [25]. It has 568 samples, from which 357 samples indicated benign breast (Class:0) and 212 samples indicated Malignant breast tumors (class:1) [23]. As we observe in Figure 1 the dataset comprised 32 features: diagnosis, radius_mean, texture_mean, perimeter_mean, area_mean, smoothness_mean, compactness_mean, concativity_mean, symmetry_mean, etc.



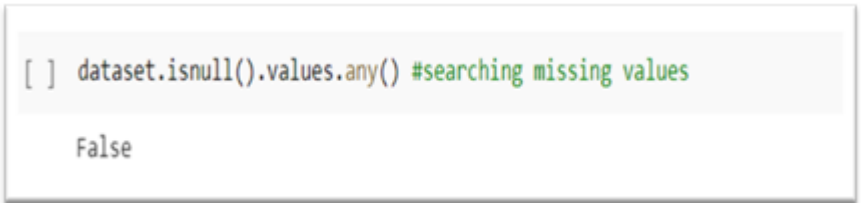
	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	...
0	842302	M	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.3001	0.14710	...
1	842517	M	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.0869	0.07017	...
2	84300903	M	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.1974	0.12790	...
3	84348301	M	11.42	20.38	77.58	386.1	0.14250	0.28390	0.2414	0.10520	...
4	84358402	M	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.1980	0.10430	...

5 rows × 33 columns

Figure 1. The First 5 Rows of the Dataset

2.2. Data Preprocessing

The breast tumor features dataset was utilized in this study. It has 568 rows and 32 breast tumor characteristics. 357 data points in the target column (class:0) represent benign healthy breasts, whereas 212 data points indicate malignant breast cancers. Before model improvement, data preprocessing is required to remove unwanted noise and anomalies in a dataset that may cause the model to deviate from the estimated preparation set. The model's evolution aims to remove any barriers to its creation and evaluation. After gathering the data, it should be cleaned up and prepared for model construction. Moving ahead, the dataset is examined for mistakes. Regardless, there are correct attributes in this dataset. After checking, there was no indication of missing data. Zero missing values according to the data presented in the Figure 2.



```
[ ] dataset.isnull().values.any() #searching missing values

    False
```

Figure 2. Zero Missing Values

2.2.1 Exploratory Data Analysis

Exploratory data analysis (EDA) has always been an excellent tool data scientists use to gain insights and knowledge from large and complex data sets. Understanding data and its hidden patterns is quite a task achieved through various statistical and visualization techniques, thus exploring the given data. In Figure 3 examination is done for the target column containing unique values.

The primary objective of EDA is to procure basic as well as an in-depth apprehension of the data sets and their properties, such as their distribution, skewness, kurtosis, outliers, and missing values. Data visualization is an essential aspect of EDA, as it enables data scientists to portray obscure data through a visual format, making it clearer and easier to interpret studies. Graphs, charts, and plots can provide valuable insights into the data, helping data scientists identify patterns, correlations, and anomalies that may not be immediately apparent from raw data. EDA techniques allow data scientists to identify data quality issues and perform data cleansing or transformation if necessary. In Figure 4 Count Plot of the target column is done and in the graph shown in Figure 5 is data distribution and outliers after plotting of Data.

```
[33] dataset.diagnosis.unique()

     array([1, 0])
```

Figure 3. The target column containing unique values

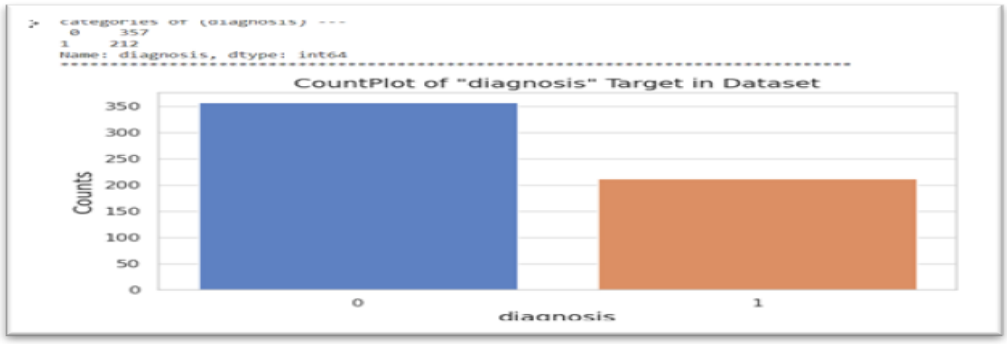


Figure 4. Count Plot of the target column

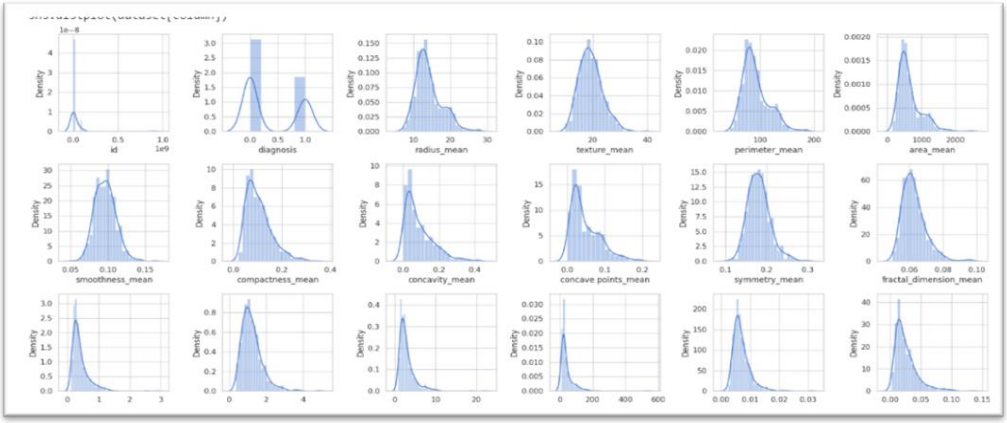


Figure 5. Data distribution and outliers

2.2.2. Feature Selection

We have used a correlation map to check the correlation among different features. After analyzing the map properly, we got all the negatively and positively correlated features. And thus selected the ones which are needed and positively related to the target column, diagnosis. Of them, 23 features were further selected for modeling in different algorithms. Feature Correlation Map of all 32 features is seen in Figure 6 and in Figure 7 feature correlation map of selected 23 features are observed.

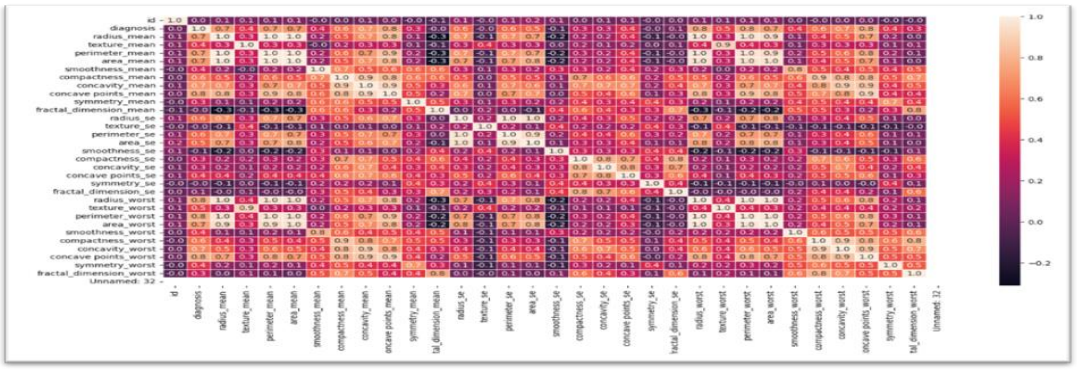


Figure 6. Feature Correlation Map of all 32 features

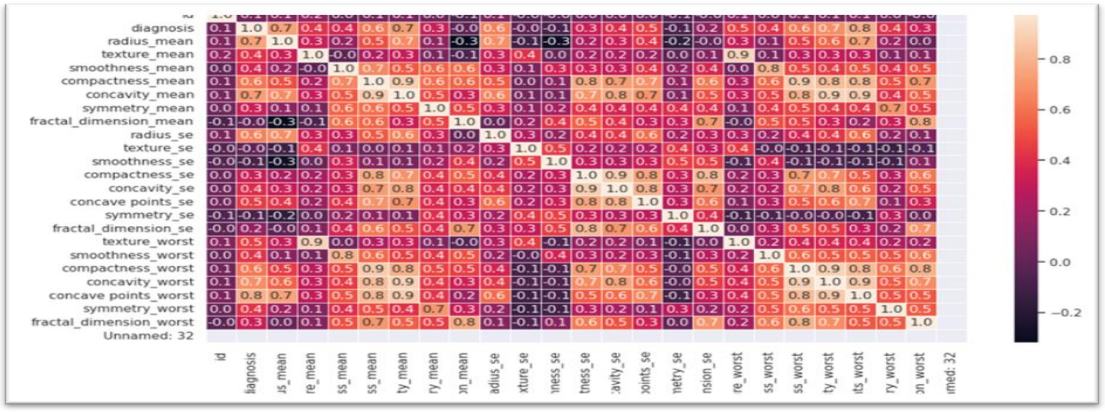


Figure 7. Feature correlation map of selected 23 features

2.3. Proposed Methodology

The architecture of the prospective methodology is shown in Figure 5. The given dataset was properly examined and available for model development. A preliminary processed dataset and machine and deep learning algorithms are vital for model building. Among the techniques employed are "Logistic Regression," "Decision Tree classification," "Random Forest classification," and "SVM classifier." The accuracy metrics are the accuracy score, precision score, recall score, and F1 score. They are used to assess five distinct machine learning models and a deep learning model once built. As illustrated in the Figure 8, proposed architecture for breast cancer prediction.

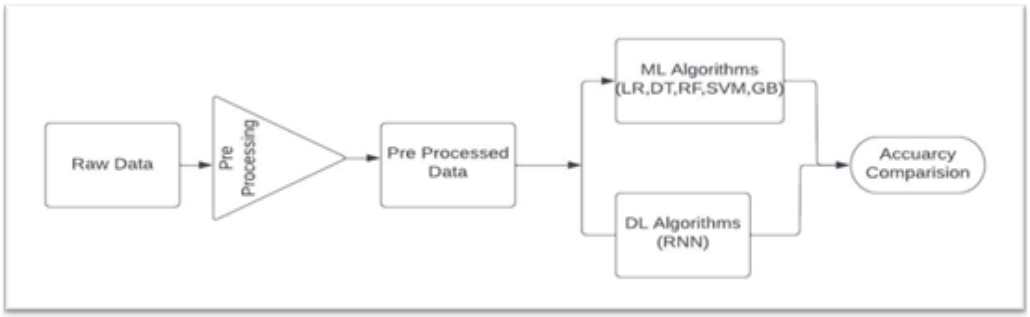


Figure 8. Proposed Architecture for Breast Cancer Prediction

2.3.1. Logistic Regression

Logistic regression is a less complex and more efficient solution for discrete and continuous classification problems, which, unlike its name utilized much more efficiently for categorization. This paradigm is easy to construct and works well with linearly independent classes. It is a popular corporate categorizing strategy. The LR model is an approach to statistics used in binary classification, although it is also used in multiclass classification. Scikit-learn provides an extremely efficient logistic regression execution. Logistic regression uses the logistic function below to describe a binary output variable.

$$\text{Logistic Function} = \frac{1}{1+e^{-x}}$$

2.3.2. Decision Tree

Decision tree learning utilizes a divide-and-conquer strategy to find optimal split positions within a tree. After classifying information under unique labels, the recursive splitting procedure occurs from top to bottom. Subgroups are formed by testing attributes, known as "recursive partitioning." The process continues until further splits do not enhance predictions or subsets with identical target variable numbers. When predicting a record's class label, the comparison starts at the root, choosing the route based on attribute values.

2.3.3. Random Forest

Random Forest is an extension of bagging that adds randomness and creates a network of decision trees. The random subspace strategy, or feature bagging, ensures little correlation among trees by randomly selecting features. Unlike decision trees, random forests evaluate only a subset of feature splits. It is a powerful and widely used method that handles categorical, continuous, and binary data.

2.3.4. Support Vector Machine

Support Vector Machine (SVM) is popular due to its high accuracy and minimal resource consumption. It solves regression and classification problems by identifying a hyperplane that separates data points based on attributes. The hyperplane's size and placement depend on the number of features. Support vectors close to the hyperplane impact its orientation and margin. Utilizing these vectors increases the classifier's margin while removing them shifts the hyperplane.

2.3.5. Recurrent Neural Network

Recurrent Neural Network (RNN) processes sequential or time series input, incorporating previous information to influence the current input and output. Unlike conventional networks, RNNs have memory and produce outputs based on previous sequence elements. Although they cannot predict future events, they excel in determining the output order.

2.3.6. Ensemble Learning

Ensemble learning is a machine learning method that combines predictions from many models to improve and enhance the accuracy and robustness of the final forecast. The core idea behind ensemble learning is to reduce every possible mistake or bias in individual models by using the aggregate intelligence of numerous models, resulting in a more exact prediction.

The primary sources of error in learning models are noise, variation, and bias. Machine learning ensemble techniques aim to mitigate these error-inducing factors, ensuring the robustness and longevity of machine learning (ML) computations. By harnessing the power of diverse models and combining their predictions, ensemble approaches effectively reduce the impact of noise, mitigate the effects of variation, and mitigate bias. This collective wisdom of multiple models leads to improved accuracy, generalization, and overall performance in ML tasks.

2.3.7. Bagging and Boosting

Ensemble learning can be classified into two types: bagging and boosting. The primary difference between these methods is how weak learners are trained. Bagging trains weak learners in parallel, whereas boosting trains them sequentially. In boosting, a series of models are created, and the weights of incorrectly classified data in the previous model are increased with each successive iteration. This redistribution of weights aids the algorithm in identifying which parameters it should focus on to enhance its performance.

AdaBoost is among the most well-known boosting algorithms, and it was one of the earliest algorithms of its kind. Other examples of boosting algorithms include XGBoost, Gradient Boost, and Brown Boost.

2.2.7.1. Bagging

Bagging, also known as Bootstrap Aggregation, is an ensemble learning strategy that aids ML models' performance and accuracy. It mostly aids in overcoming the overfitting problem in categorization. This procedure takes random subsets of a dataset and replaces them in a classifier or regressor. Predictions for each subgroup are then determined using either a majority vote for classification or averaging for regression, boosting prediction accuracy.

It should be noted that the random forest technique expands the bagging approach, employing both bagging and attribute unpredictability to construct a forest without the correlation of decision trees.

2.2.7.2. Boosting

Boosting is a widely used ensemble modeling strategy that aims to combine multiple weak classifiers to form a single strong classifier. The primary goal of boosting is to boost and refine the accuracy and generalizability of the model by iteratively learning from the mistakes made by the previous models.

The boosting algorithm works by sequentially training a series of weak models on the same training dataset, where each model attempts to correct the general mistakes made by the previously existing model. During training, the algorithm assigns a higher weight to misclassified samples, which are then used to train the next weak model. This way, the boosting algorithm focuses on the most challenging examples, gradually reducing the overall error rate and improving the model's performance.

2.2.7.2.1. Gradient Boosting

Gradient Boosting is a boosting algorithm that creates a strong learner from multiple weak learners by training each new model to mitigate the loss function of the previous model using gradient descent. The algorithm calculates the changing slope of the loss curve concerning the current ensemble's predictions in each iteration and then trains a new weak model to minimize

this gradient. The new model's predictions are then combined with the group, and the process is repeated until a stopping criterion is met. Loss functions used in gradient boosting can include mean squared error or cross-entropy. Overall, gradient boosting is a powerful and effective algorithm for creating strong learners from weak ones.

2.2.7.2.2. XG Boost

XGBoost is an optimized networked gradient boosting framework for efficient and flexible machine learning model training. It is an ensemble learning approach that integrates the predictions of numerous weak models to obtain a stronger prediction. Because of its capacity to handle massive data sets and achieve state-of-the-art efficiency for numerous machine learning operations such as regression and categorization, XGBoost has grown and expanded to become one of the most prevalent as well as extensively utilized machine learning algorithms.

Among the numerous benefits of XGBoost, one peculiar asset is its ability to handle missing data efficiently, eliminating the need for extensive preprocessing and enabling it to work with incomplete real-life datasets. Additionally, XGBoost's parallel processing capabilities make it feasible to train models on large datasets in a reasonable amount of time. Its flexibility is noteworthy, as it allows for fine-tuning various model parameters to enhance overall performance.

3. RESULTS AND ANALYSIS

The dataset, after being passed through different algorithms, both Machine Learning (Logistic Regression, Decision Tree, Random Forest, SVM) and Deep Learning (CNN, RNN), the results of their accuracy in determining whether it is a healthy breast or otherwise was noted and analyzed. Following is the report obtained:

3.1. Logistic Regression

The Test Accuracy acquired is 97.6%, while the Train Accuracy remains 98.9%. Figure 9 shows the Precision, Recall, f1-score, and Logistic regression support. In Figure 9, 0 denotes benign tumor, and 1 denotes malignant tumor data. The f1-score of benign tumors is calculated to be 98%, whereas, for malignant tumors, it is 97%.

```
y_pred = logreg.predict(X_test)
print(classification_report(Y_test, y_pred))
```

	precision	recall	f1-score	support
0	0.97	0.99	0.98	108
1	0.98	0.95	0.97	63
accuracy			0.98	171
macro avg	0.98	0.97	0.97	171
weighted avg	0.98	0.98	0.98	171

Figure 9. Logistic Regression Result

3.2. DECISION TREE

The Test Accuracy acquired is 97.4%, while the Train Accuracy remains 98.4%. Figure 10 shows the Precision, Recall, f1-score, and support of the Decision Tree.

In Figure 10, 0 denotes benign tumor, and 1 denotes malignant tumor data. The f1-score was calculated to be 96 % for benign tumors, whereas, for malignant tumors, it is 93%.

```
print(classification_report(Y_test, predTree))
```

	precision	recall	f1-score	support
0	0.98	0.94	0.96	108
1	0.90	0.97	0.93	63
accuracy			0.95	171
macro avg	0.94	0.95	0.94	171
weighted avg	0.95	0.95	0.95	171

Figure 10. Decision Tree Result

3.3. XG Boost

The Test Accuracy acquired is 97%, while the Train Accuracy remains 98%. Figure 11 and figure 12 show the Precision, Recall, f1-score, and support of the XG Boost with its confusion matrix. In Figure 11, 0 denotes benign tumor, and 1 denotes malignant tumor data. The f1-score was calculated to be 98 % for benign tumors, whereas, for malignant tumors, it is 96%.

```
**************************************************
```

	precision	recall	f1-score	support
0.0	0.97	0.98	0.98	108
1.0	0.97	0.95	0.96	63
accuracy			0.97	171
macro avg	0.97	0.97	0.97	171
weighted avg	0.97	0.97	0.97	171

Figure 11. XG Boost Result

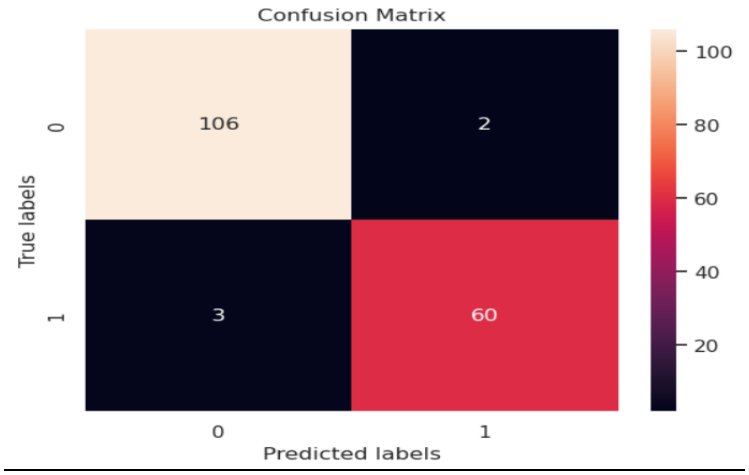


Figure 12. XG Boost Confusion Matrix

3.4. Random Forest

The Test Accuracy acquired is 95.9%, while the Train Accuracy remains 98%. Figure 13 shows the Precision, Recall, f1-score, and support of the Random Forest. In Figure 13, 0 denotes benign tumor, and 1 denotes malignant tumor data. The f1-score was calculated to be 97 % for benign tumors, whereas, for malignant tumors, it is 94%.

```
from sklearn.metrics import classification_report

print(classification_report(Y_test, y_pred))
```

	precision	recall	f1-score	support
0	0.97	0.96	0.97	108
1	0.94	0.95	0.94	63
accuracy			0.96	171
macro avg	0.95	0.96	0.96	171
weighted avg	0.96	0.96	0.96	171

Figure 13. Random Forest Result

3.5. Support Vector Machine

The Test Accuracy acquired is 98%, while the Train Accuracy remains 97.2%. Figure 14 shows the Precision, Recall, f1-score, and support of the Support Vector Machine. In Figure 14, 0 denotes benign tumor, and 1 denotes malignant tumor data. The f1-score was calculated to be 98 % for benign tumors, whereas, for malignant tumors, it is 97%.

```
y_pred=svm.predict(X_test)
print(classification_report(Y_test, y_pred))
```

	precision	recall	f1-score	support
0	0.97	0.99	0.98	108
1	0.98	0.95	0.97	63
accuracy			0.98	171
macro avg	0.98	0.97	0.97	171
weighted avg	0.98	0.98	0.98	171

Figure 14. SVM Result

3.6. Gradient Boosting

The Test Accuracy acquired is 95.6%, while the Train Accuracy remains 100%. Figure 15 and figure 16 show the Precision, Recall, f1-score, and support with the confusion matrix of the Gradient Boosting.

```
**************************************************
```

	precision	recall	f1-score	support
0	0.96	0.98	0.97	108
1	0.97	0.94	0.95	63
accuracy			0.96	171
macro avg	0.97	0.96	0.96	171
weighted avg	0.96	0.96	0.96	171

Figure 15. Gradient Boosting Result

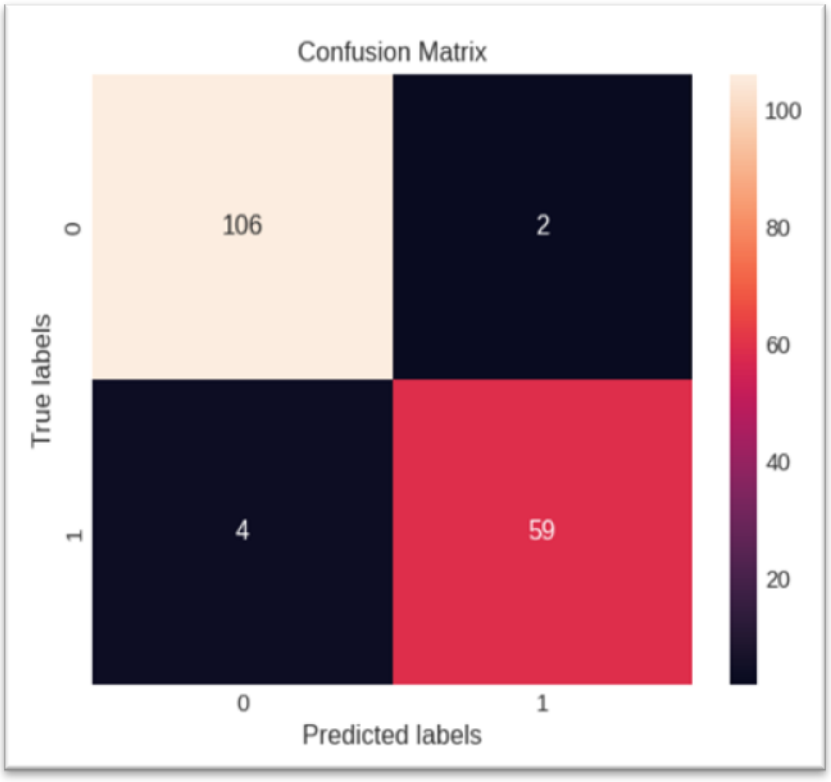


Figure 16. Confusion Matrix of Gradient Boosting

3.7. Light GBM

The Test Accuracy acquired is 98.2 %, while the Train Accuracy remains 100 %. Figure 17,18,19 shows the result of the accuracy of Light GBM.

```
y_train accuracy: 1.0
y_test accuracy: 0.9824561403508771
```

Figure 17. Accuracy Result of Light GBM

	precision	recall	f1-score	support
0	0.98	0.99	0.99	108
1	0.98	0.97	0.98	63
accuracy			0.98	171
macro avg	0.98	0.98	0.98	171
weighted avg	0.98	0.98	0.98	171

Figure 18. Result for Light GBM

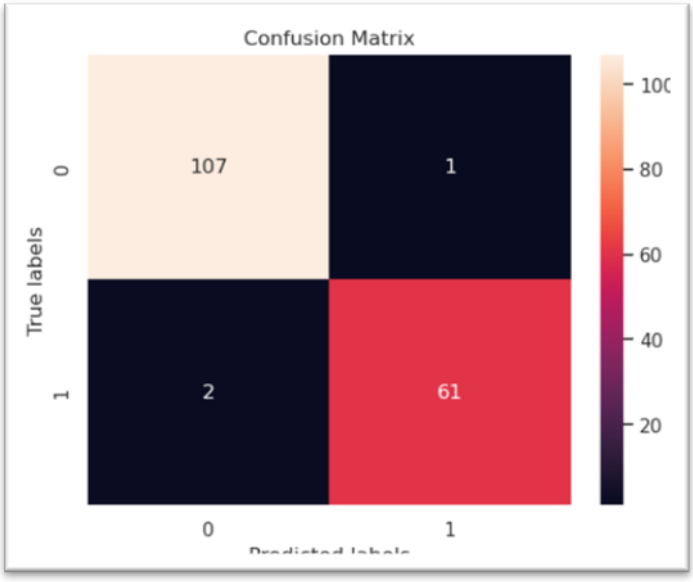


Figure 19. Confusion Matrix of Light GBM

3.8. RNN

The Test Accuracy acquired is 97%, while the Train Accuracy remains 98.7%. Figure 20 shows the result of the accuracy of RNN. It has been depicted in the graph of Model Loss in Figure 21.

```
print ('Train accuracy is: ' + str(train_acc))
print ('Test accuracy is: ' + str(test_acc))

Train accuracy is: 0.9874371859296482
Test accuracy is: 0.9707602339181286
```

Figure 20. Result of RNN

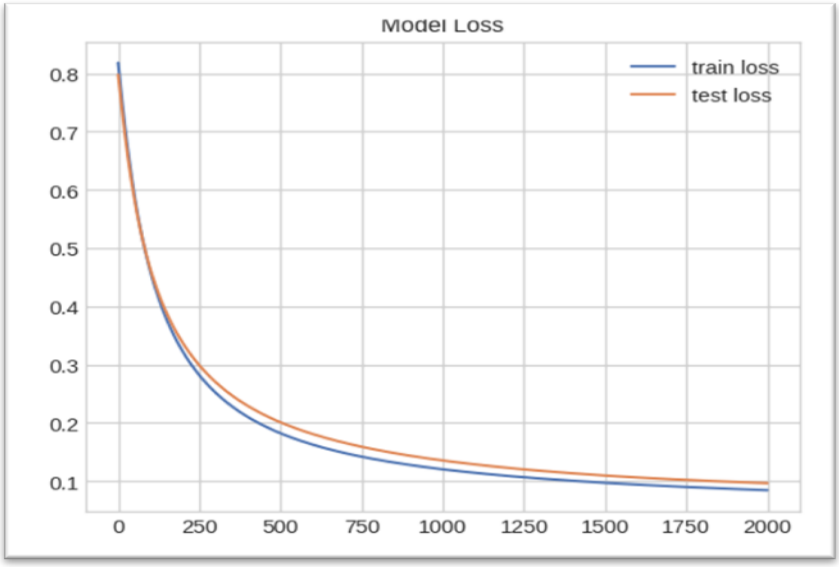


Figure 21. Model Loss

3.9. Performance Analysis of Models

Table 1. Performance Analysis of Models for Breast Tumor Prediction

Models	F1 score		precision		recall		accuracy
	0	1	0	1	0	1	
LR	0.98	0.97	0.97	0.98	0.99	0.95	0.98
DT	0.96	0.93	0.98	0.90	0.94	0.97	0.95
RF	0.97	0.94	0.97	0.94	0.96	0.95	0.96
SVM	0.98	0.97	0.97	0.98	0.99	0.95	0.98
GB	0.97	0.95	0.96	0.97	0.98	0.94	0.96
XGB	0.98	0.96	0.97	0.97	0.98	0.95	0.97
RNN	0.95	0.96	0.97	0.98	0.96	0.98	0.97
LGBM	0.99	0.98	0.98	0.98	0.99	0.97	0.982

We evaluated the performance of different machine learning and deep learning algorithms using metrics such as F1 score, precision, recall, and accuracy. Our analysis determined that the Light GBM algorithm achieved the highest accuracy of 98.2%, followed closely by the Support Vector Machine and Logistic Regression, which achieved an accuracy of 98%. The RNN deep learning algorithm yielded the third-highest accuracy, i.e., 97%. Decision Tree, on the other hand, had the lowest accuracy at 95%.

Additionally, the F1 scores for Logistic Regression, Support Vector Machine, and Xtreme Gradient Boosting were all the same and the highest among the evaluated algorithms. The Logistic Regression had an accuracy of 98% compared to [4] with 96%. The SVM Classifier used here also gives higher and more efficient results than other previously used models, with an accuracy of 98%; [4] compared to it has submitted 97% accuracy with the same approach.

This model has presented a model with more algorithms, such as RNN and Gradient Boosting. Thus, the average accuracy rate of the proposed model is higher, with Light GBM having the highest accuracy rate of 98.2%.

4. CONCLUSION

Breast cancer presents a unique environment for medical diagnosis by taking the patient's condition and treatment response into account. Machine learning has offered much for the detection of breast cancer. Despite technological advancements, there are still challenges in achieving reliable breast cancer screening and monitoring. It is essential to incorporate biological, social, and demographic data to improve prediction models. In this study, we worked towards evaluating the effectiveness of several machine learning and deep learning approaches for classification.

We investigated the performance of four commonly used classifiers: logistic regression, random forest, decision tree, and support vector machine with sequential minimum optimization. Additionally, we explored ensemble methods, such as the voting classifier, and deep learning techniques, specifically the Recurrent Neural Network (RNN).

To assess the performance of these seven classifiers, we utilized various peculiar performance measures, including accuracy, precision, recall, and F1 score. These metrics provide insights into the models' predictive capabilities, capturing aspects such as overall correctness, the precision of positive predictions, the ability to identify true positives, and the balance between precision and recall.

By evaluating these classifiers and their performance measures, we aimed to contribute to developing improved breast cancer prediction models, considering both machine learning and deep learning techniques.

In this study, Light GBM achieved 98.2% accuracy. On the other hand, LR, DT, RF, SVM, GB, RNN, and XGB got accuracy 98%, 95%,96%,98%, 96%, 97%, 97%, and 97%, respectively. We can use the fine-tuning of the parameters to boost the accuracy and score of the model.

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