# Integrating Feature Selection and Machine Learning Boosting for Accurate Breast Cancer Prediction

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Abstract: Breast cancer is a prevalent and devastating disease and remains a major contributor to cancer-related mortality among women worldwide. The increasing incidence and fatality rates are often associated with changes in lifestyle and the influence of environmental factors. In response to these alarming trends, the development and deployment of automated breast cancer diagnostic systems have become increasingly important in modern healthcare. This study investigates the performance of several boosting algorithms - CatBoost, LightGBM, XGBoost, AdaBoost, and Gradient Boosting - for breast cancer prediction using the Wisconsin Diagnostic Breast Cancer (WDBC) dataset. The dataset is publicly available on Kaggle and consists of 569 instances, including 357 benign and 212 malignant cases. The proposed framework encompasses data preprocessing, feature selection, and classification stages. Model performance was evaluated using multiple metrics to ensure robust analysis and objective assessment. The experimental results demonstrate that LightGBM outperformed the other models, highlighting the effectiveness of boosting-based approaches for breast cancer diagnosis and emphasizing the potential of these techniques for further advancements in oncology research.

## 1 INTRODUCTION

Breast cancer affects women more than any other malignancy [1], [2]. It ranks fifth in terms of overall cancer mortality worldwide [3] and is the second leading cause of cancer-related death among women [4]. Globally, breast cancer is the most prevalent malignancy in women, accounting for approximately one in four cancer diagnoses and one in six cancer-related deaths. It holds the highest incidence and mortality rates in 159 and 110 countries, respectively. Annually, over 2,000,000 new cases are reported, resulting in approximately 685,000 deaths worldwide [5], [6]. Hormonal imbalances, genetic predisposition, marital status, and reproductive history are considered contributory factors in the development of breast cancer [7].

Therefore, the implementation of automated methodologies for breast cancer screening and diagnosis is essential. Early and accurate detection plays a crucial role in improving patient outcomes and increasing survival rates. Previous studies have proposed various decision support systems for breast cancer prediction; however, many of them do not explicitly address time complexity or provide detailed criteria for training and evaluation.

Furthermore, understanding training and computational complexity is critical for assessing algorithm feasibility, particularly in healthcare systems with limited CPU and memory resources. For example, in 2021, study [1] applied a range of machine learning algorithms for breast cancer prediction, including CatBoost, XGBoost, Linear Regression (LR), K-Nearest Neighbors (KNN), Support Vector Machine (SVM), Naïve Bayes (NB), Decision Tree (DT), and Random Forest (RF). CatBoost achieved the highest performance, with an accuracy of 97.8% and an Area Under the ROC Curve (AUROC) of 0.983, outperforming the other algorithms.

In 2022, study [8] employed twelve machine learning techniques for breast cancer prediction. The

Perceptron and SVM demonstrated superior sensitivity and accuracy, while LR achieved the highest precision and F1-score. In contrast, DT exhibited lower sensitivity and accuracy, and KNN recorded reduced precision and F1-score. Overall, the Perceptron and SVM emerged as the most effective predictors, achieving an accuracy of 90% and showing consistent performance across multiple evaluation metrics.

In 2023, study [9] utilized several machine learning classifiers and ensemble techniques on a breast cancer dataset, reporting that DT and XGBoost achieved the highest accuracy of 97%.

In 2024, study [3] trained seven machine learning algorithms, including DT, SGD, RF, SVM, Logistic Regression, and AdaBoost. The AdaBoost–Logistic model achieved the highest accuracy of 99.12%, outperforming the other approaches.

In 2025, study [10] proposed a hybrid deep learning framework for predicting breast cancer recurrence by combining deep learning and traditional machine learning models, resulting in sixteen predictive models. The BCR-HDL framework not only predicted recurrence outcomes but also provided recurrence time estimation. The hybrid MLP+RF and Xception+RF models achieved an accuracy of 97% on the WDBC dataset, while the MLP+RF model reached 78% prognostic accuracy on the WPBC dataset. Additionally, the hybrid ResNet+SVM and ResNet+RF models demonstrated strong predictive performance, achieving an accuracy of 92%.

Despite these advancements, existing studies predominantly focus on classification accuracy while neglecting training time and prediction time, which are essential for identifying the most efficient algorithms from a practical perspective. Moreover, there remains a noticeable gap in the comprehensive application of boosting algorithms for breast cancer classification. Boosting techniques offer several advantages over conventional and deep learning approaches, particularly in handling data imbalance, missing values, and categorical features. By combining multiple weak learners, boosting algorithms enhance generalization capability and reduce the risk of overfitting. Although boosting methods have shown strong performance across various domains, their potential in breast cancer diagnosis has not been fully explored.

This study aims to develop predictive models for breast cancer using comprehensive datasets, advanced feature selection techniques, and five widely used boosting algorithms: CatBoost, LightGBM, XGBoost, AdaBoost, and Gradient Boosting (GB). The primary objective is to improve diagnostic accuracy and patient outcomes by rigorously evaluating these algorithms using multiple performance metrics. The evaluation criteria include accuracy, precision, recall, F1-score, confusion matrix, AUROC, as well as computational time for both training and prediction, ensuring a robust and comprehensive assessment.

# 2 THEORETICAL BACKGROUND

## 2.1 Theoretical Rationale for Boosting Algorithms in Medical Prediction

Boosting algorithms use ensemble learning with weak learners (often decision trees) to create a strong classifier. Boosting reduces bias and variance, improving predictive accuracy on unseen data. In medical datasets like breast cancer, boosting algorithms address class imbalance, noisy features, and complex relationships by focusing on misclassified instances. Boosting helps handle imbalanced data and prevents overfitting through adaptive weighting and regularization. The ensemble approach of boosting models improves generalization on new patient data for clinical deployment [11].

## 2.2 Theoretical Motivation for Feature Selection

Feature selection reduces dimensionality, eliminates irrelevant variables, and enhances model interpretability using statistical measures like Pearson correlation. This helps reduce overfitting, improve computational efficiency, and enhance interpretability for clinicians [12].

# 3 PRELIMINARY CONCEPTS

The subsequent subsections furnish a comprehensive background pertinent to the classification algorithms employed in the present study.

## 3.1 Categorical Boosting (CatBoost)

It is a formidable gradient-boosting library grounded in open-source principles. It is nonlinear, tree-based, and adept at handling intricate datasets. CatBoost consistently surpasses alternative boosting methodologies, demonstrating marked enhancements in both accuracy and performance. It achieves

optimal results with remarkable speed, which is invaluable for time-sensitive applications such as fraud detection. CatBoost streamlines data preparation by accommodating categorical features without necessitating preprocessing. Its sophisticated capabilities, user-friendly nature, and exceptional performance render it a premier choice for machine learning endeavors [13], [14].

### 3.2 Extreme Gradient Boosting (XGBoost)

It is a formidable machine learning algorithm elucidated in numerous scholarly articles for a myriad of applications. It has been employed for the detection of breast cancer with remarkable precision and recall rates. XGBoost distinguishes itself through its capacity to tackle intricate challenges, attain elevated predictive accuracy, and deliver efficiency across diverse domains [15], [16].

### 3.3 Light Gradiant Boosting Machine (LightGBM)

LightGBM stands out as a versatile and efficient tool in the machine learning toolbox, providing robust solutions for a wide range of predictive modeling tasks. Its speed, scalability, and accuracy make it popular among data scientists and machine learning practitioners [17], [18].

### 3.4 Adaptive Boosting (AdaBoost)

To improve predictive accuracy, AdaBoost combines multiple weak classifiers by placing greater emphasis on instances that are misclassified. After each iteration, the dataset is reweighted so that subsequent weak classifiers focus more on these difficult cases. When specific criteria are met, a new weak classifier is introduced, initially assigning equal weight to all input samples. The weights of misclassified instances are then increased, while the weights of correctly classified samples are decreased. This reweighted dataset is used to train the next weak classifier. Through this iterative process, all weak classifiers are combined to form a single, strong classifier [19], [20].

### 3.5 Gradient Boosting (GB)

Boosting algorithms amalgamate weak learners to construct a robust learner. Gradient Boosting (GB) serves as a prominent exemplar in regression tasks. It incrementally formulates a predictive model by optimizing a loss function. Overfitting presents a significant challenge when not adequately regularized. Consider GB for the estimation of housing prices; it commences with a rudimentary model that encapsulates the data trend. In each iteration, it rectifies the errors made by preceding models. Regularization techniques are imperative to mitigate overfitting. In the absence of such measures, the model may become excessively sensitive to the noise present in the training data, leading to suboptimal generalization to unseen datasets. Meticulous tuning of hyperparameters and regularization parameters is essential. Achieving a harmonious balance between model complexity and generalization is pivotal for GB in the realm of predictive modeling [21], [22].

## 4 PROPOSED MODEL

This model contains three stages: preprocessing, feature selection, and classification, as shown below.

### 4.1 The Dataset

The dataset utilized was the Wisconsin breast cancer dataset. It has 569 instances without missing values across thirty-two columns in a CSV file. 30 columns describe breast cancer physiological characteristics; one is for ID numbers, and one is for cancer categories. Features extracted from digital images of breast mass fine-needle aspiration delineate cell nuclei characteristics. Resource accessible online at no cost. The dataset includes cases of women aged 29 to 89, categorized as "B," denotes benign tumors, while "M" signifies malignant tumors.
Figure 1 illustrates a histogram depicting the distribution of diagnoses, comprising 212 malignant cases and 357 benign instances [3], [23].

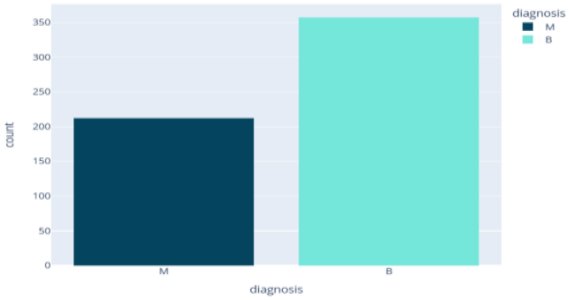


Figure 1: The histogram of diagnoses in the dataset.

## 4.2 Preprocessing Stage

Preprocessing is a critical component of the data science workflow, serving to meticulously prepare data for the construction of predictive models. Without it, prediction quality can suffer. Preprocessing is crucial for strong predictive models. Invest time and effort in preprocessing for robust and reliable models [24]. The preprocessing stage involved three key steps:

1) Categorical data, such as diagnostic classifications, was transmuted into numerical representations (0 denoting benign and 1 signifying malignant).
2) Eliminating Non-Essential Features. Attributes such as identification numbers were extricated to streamline the dataset and mitigate the risk of overfitting.
3) Balancing data prevents model bias toward the majority class, avoiding favoritism. Balanced models are less likely to suffer accuracy paradox. Figure 2 shows the histogram of diagnoses after 100% balancing using resampling from the sklearn library in Python. Both classes (benign and malignant) have 357 instances.

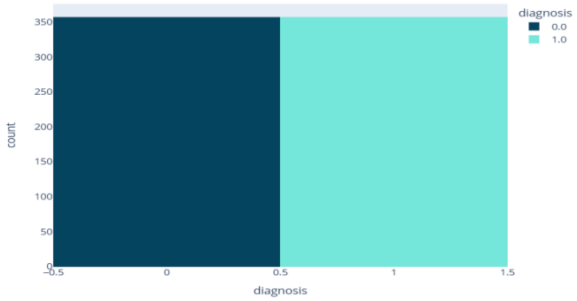


Figure 2: The histogram of diagnoses in the dataset after 100% balanceing.

## 4.3 Features Selection Stage

The myriad of diverse features complicate the accuracy of predictions. It is imperative to extract key features through a meticulous feature selection process prior to the implementation of a machine learning model. This approach not only mitigates the presence of irrelevant variables but also curtails associated costs and minimizes the risk of overfitting. The judicious selection of significant features is paramount for achieving successful predictive outcomes [25]. The correlation between features is ascertained through the application of Pearson correlation, facilitating the comprehension of relationships and elucidating attribute interdependence. Statistical indicators of variable variability and linear association are subsequently computed (1).

$$Px, y = Covx, \frac{y}{} \sigma x \sigma y, \quad (1)$$

where x and y are standard deviations of x[n] and y[n], while Covx,y represents the covariance. Correlation coefficients, x and y, range from -1 to +1. A value of zero signifies an absence of a linear relationship. A robust positive correlation approaches +1, whereas a pronounced negative correlation nears -1 [26], [27].
Figure 3 illustrates the heatmap depicting the correlation among various features.

The most important features for diagnosis were chosen according to their correlation values (≥0.5). This threshold was meticulously selected to preserve only the most pertinent features, mitigate extraneous noise, and enhance both the interpretability and efficacy of the model. 15 features were selected for prediction from the original features. Figure 4 shows the ranked features by Pearson correlation with the diagnosis.

## 4.4 Classification Stage and Performance Evaluation

The total number of features used in this study is 15. Five boosting algorithms - CatBoost, XGBoost, LightGBM, AdaBoost, and Gradient Boosting - were employed for breast cancer prediction. All models were implemented using the Python programming language. The dataset was randomly divided into two subsets, with 80% of the data used for training and 20% reserved for testing, ensuring that model performance was evaluated on previously unseen samples.

The classification performance was assessed using several widely adopted evaluation metrics, including precision, recall, accuracy, and F1-score [28]. Precision reflects the proportion of correctly identified positive cases among all predicted positives, while recall measures the model's ability to correctly identify actual positive cases. Accuracy indicates the overall correctness of the classification results, and the F1-score provides a balanced measure by combining precision and recall.

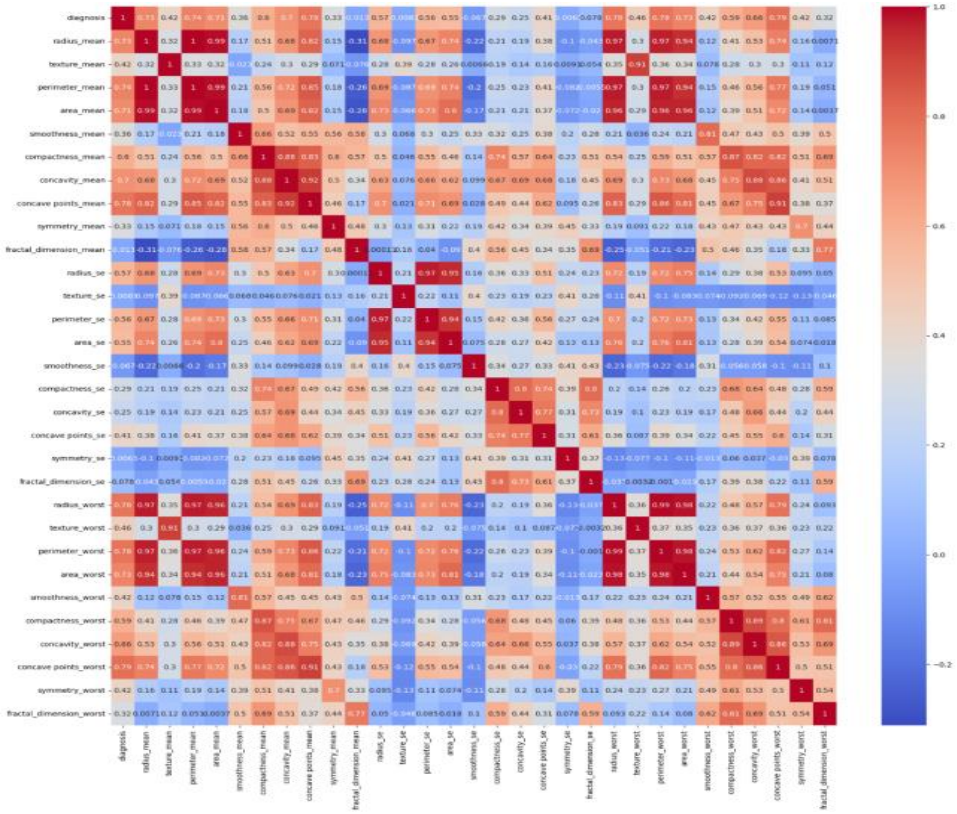

Figure 3: The correlation between features.

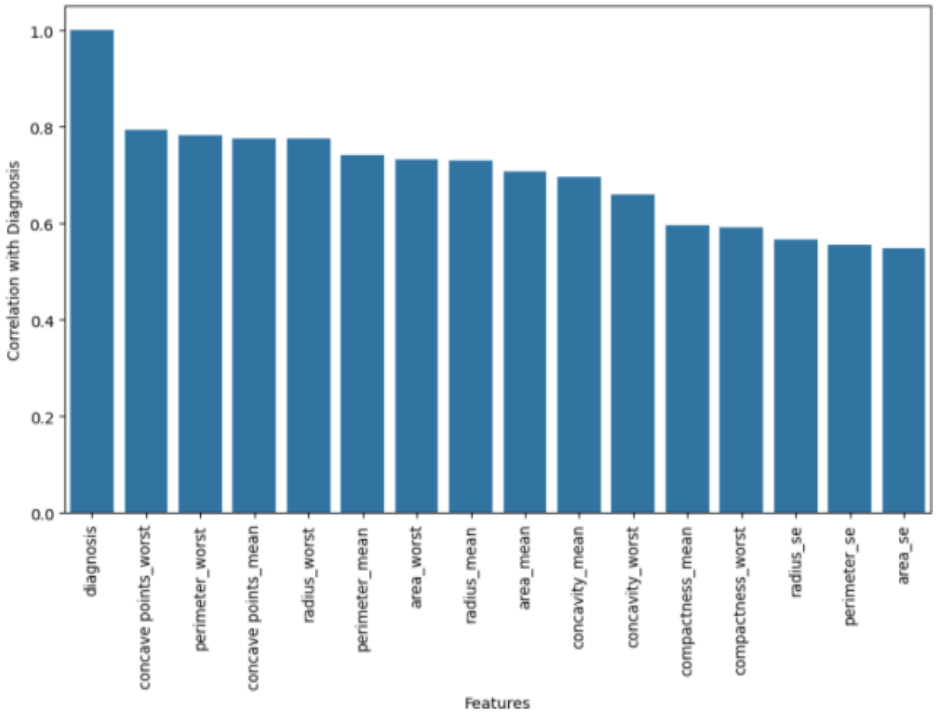


Figure 4: Ranked features by Pearson correlation with diagnosis.

In addition, a confusion matrix was utilized to summarize the classification results by presenting the counts of true positives, true negatives, false positives, and false negatives in a structured manner. This representation facilitates a clearer understanding of model performance across different classes, as illustrated in Table 1.

Table 1: Classification report for the algorithms used.

| Boosting algorithm | Presition | Recall | F1-score | Class Label |
|---|---|---|---|---|
| CatBoost | 0.95 | 0.97 | 0.96 | Bengin |
| | 0.95 | 0.90 | 0.93 | Malignant |
| | | | 0.95 | Accuracy |
| XGBoost | 0.96 | 0.97 | 0.97 | Bengin |
| | 0.95 | 0.93 | 0.94 | Malignant |
| | | | 0.96 | Accuracy |
| LightGBM | 0.97 | 0.97 | 0.97 | Bengin |
| | 0.95 | 0.95 | 0.95 | Malignant |
| | | | 0.97 | Accuracy |
| AdaBoost | 0.96 | 0.97 | 0.97 | Bengin |
| | 0.95 | 0.93 | 0.94 | Malignant |
| | | | 0.96 | Accuracy |
| GB | 0.96 | 0.97 | 0.97 | Bengin |
| | 0.95 | 0.93 | 0.94 | Malignant |
| | | | 0.96 | Accuracy |

Figures 5, 6, 7, 8, and 9 illustrate the confusion matrices for Catboost, XGBoost, LightGBM, AdaBoost, and Gradient Boosting, respectively.

Figure 10 shows AUROC for all the five boosting algorithms used.

Figure 11 shows a training times between the five algorithms used in this work.

Figure 12 shows the prediction times between the five algorithms used in this work.

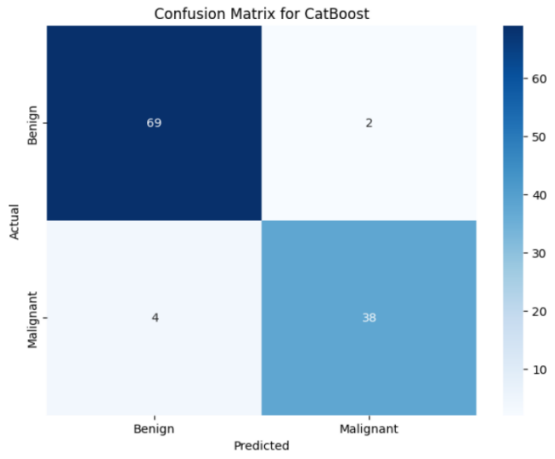


Figure 5: CatBoost. Model Confusion Matrix

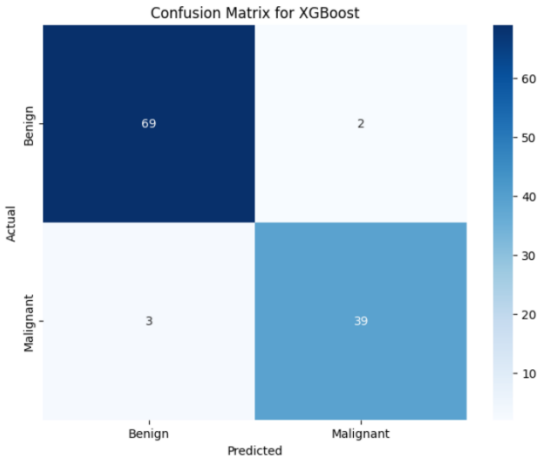


Figure 6: XGBoost Model Confusion matrix.

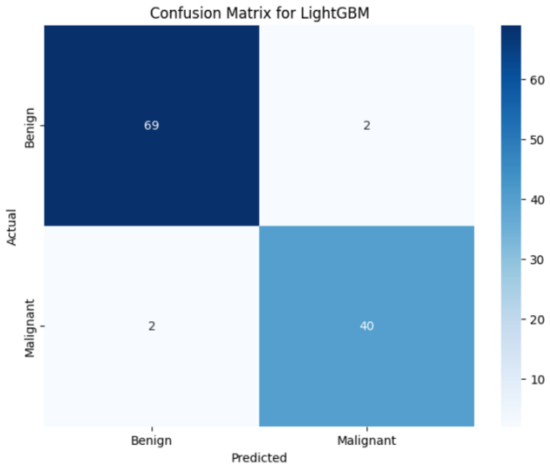


Figure 7: LightGBM Model Confusion matrix

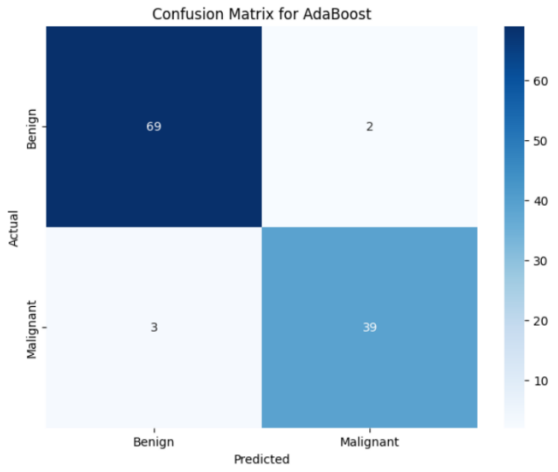


Figure 8: AdaBoost Model Confusion matrix

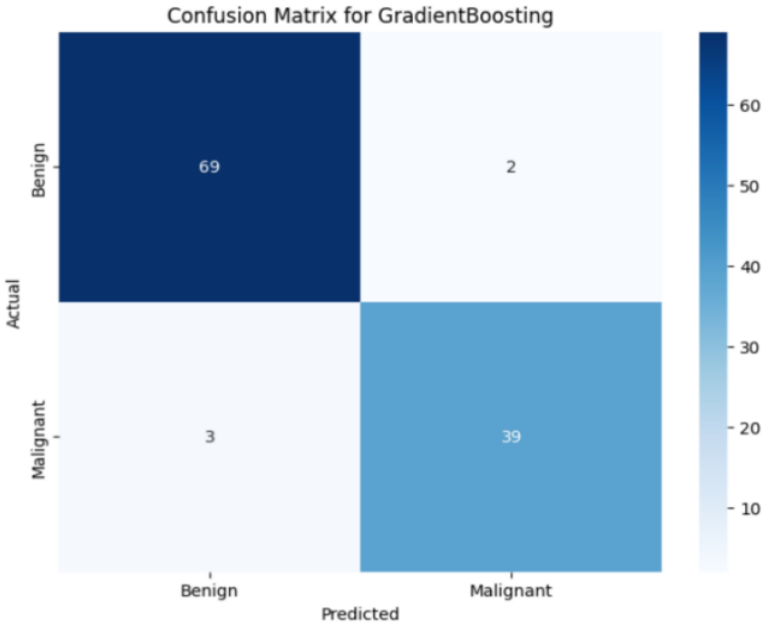


Figure 9: GB. Model Confusion Matrix

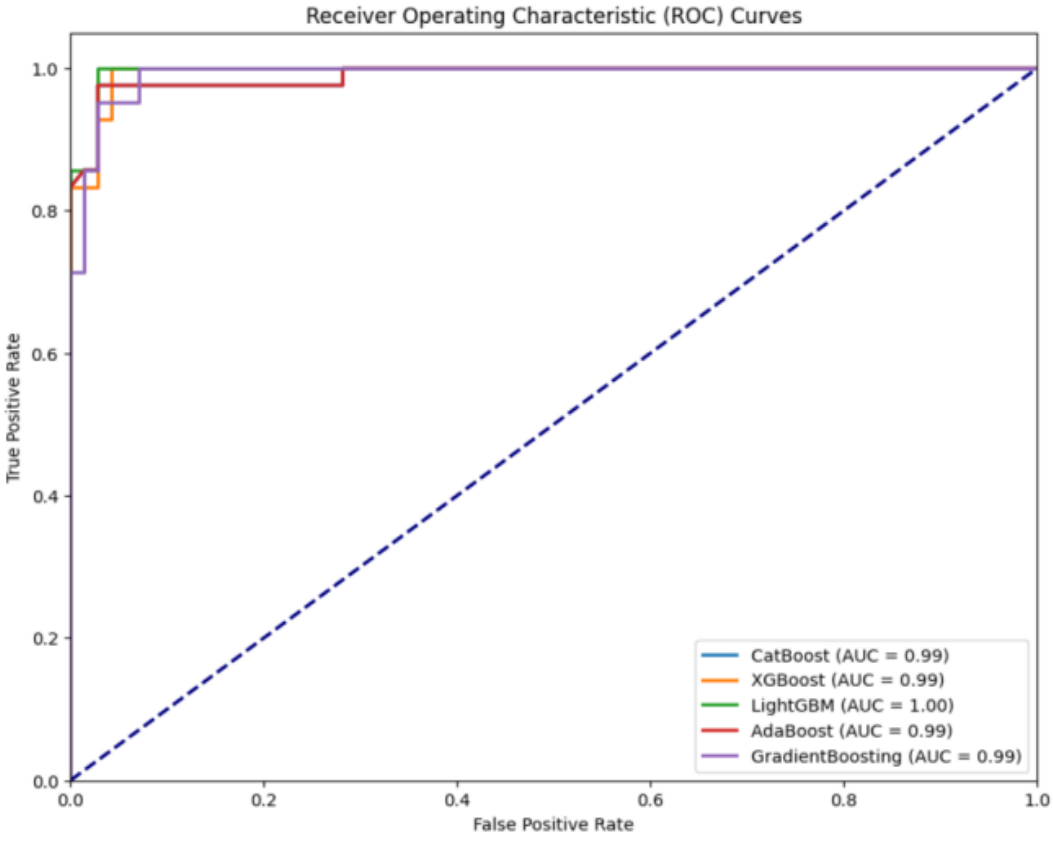


Figure 10: The AUROC for the boosting algorithms used.

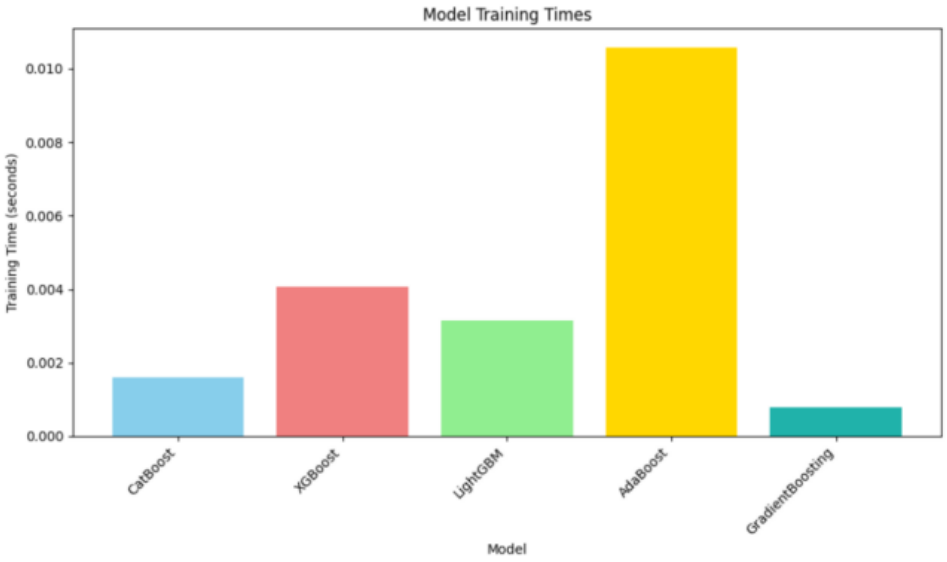


Figure 11: The comparison of training times.

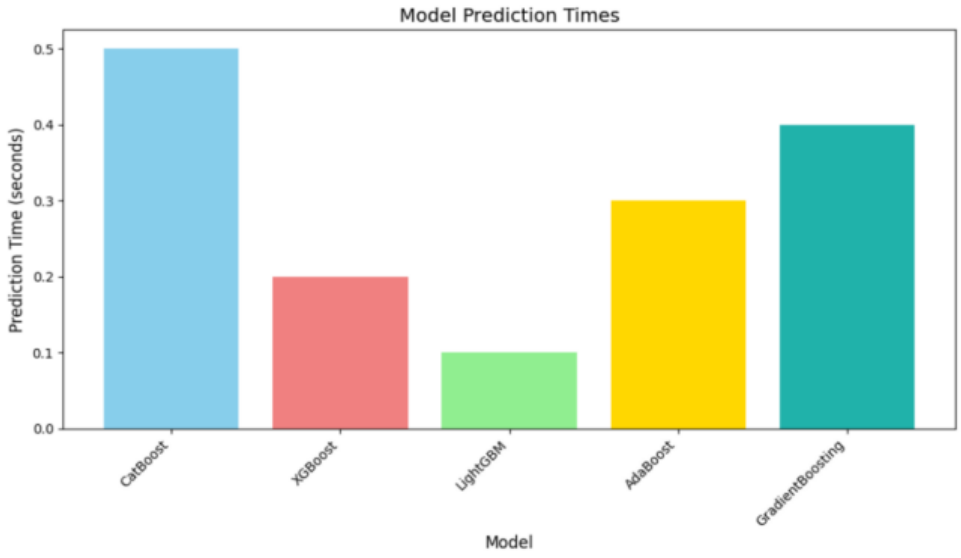


Figure 12: The comparison of prediction times.

# 5 DISCUSSIONS

Breast cancer is a significant health issue and a top cause of death in women. Early detection remains a key focus in medical research. This study elucidates the considerable potential of boosting algorithms in the realm of breast cancer prediction, with all five examined algorithms (CatBoost, XGBoost, LightGBM, AdaBoost, and Gradient Boosting) attaining exceptional performance metrics. The final AUC scores surpassed 99% across all models. Notably, LightGBM distinguished itself as the most proficient, owing to its innovative leaf-wise tree growth strategy, which facilitates enhanced accuracy and expedited convergence. Superior scalability and lower memory usage make it suitable for large datasets and real-time applications. It achieves remarkable performance, minimal prediction durations, and a substantial reduction in false negatives. This accomplishment is particularly consequential in the clinical realm of breast cancer diagnosis, where false negatives can precipitate delayed treatment and potentially exacerbate patient outcomes. By prioritizing recall metrics in conjunction with conventional accuracy assessments, our approach addresses a critical deficiency in

numerous prior studies that predominantly emphasized overall accuracy. Our research combines five boosting algorithms for breast cancer prediction, advancing the field significantly. The high accuracy, AUC, and low false negative rates of boosting algorithms (especially LightGBM) suggest they can improve automated diagnostic systems for breast cancer.

These models can aid clinicians in rendering more precise and timely diagnoses, thereby mitigating the risk of misdiagnosis and facilitating enhanced patient management.

# 6 CONCLUSIONS

This study identifies LightGBM as the top-performing boosting algorithm for accurate breast cancer prediction, highlighting its potential for integration into clinical decision-support systems. By leveraging its speed, scalability, and high accuracy, LightGBM demonstrates how advanced machine learning can contribute to earlier and more reliable breast cancer detection. The findings advance the understanding of boosting algorithms in medical machine learning and provide valuable insights for healthcare practitioners aiming to improve diagnostic workflows. Moreover, the research highlights the role of such models in facilitating timely interventions, which can be crucial for patient outcomes. For future work, employing multi-institutional datasets would improve the robustness and generalizability of the proposed models, ensuring their applicability across diverse populations and healthcare settings. Additionally, integrating the predictive framework with multimodal data sources such as mammographic, ultrasound, and MRI attributes could significantly enhance predictive power, providing a more comprehensive and precise diagnostic tool for clinicians and ultimately contributing to improved patient care and treatment planning.

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