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Enhancing Breast Cancer Diagnosis: A Comparative Evaluation of Machine Learning Algorithms Using the Wisconsin Dataset

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ABSTRACT

Breast cancer remains a leading cause of morbidity, particularly among women, underscoring the critical importance of early detection. In recent years, highly accurate machine learning algorithms have revolutionized breast cancer identification, significantly improving early diagnosis by analyzing tumor attributes to aid in detection and treatment decisions. This study evaluates seven machine learning algorithms using the Wisconsin breast cancer dataset, revealing that the Support Vector Machines (SVM) algorithm outperforms all others with an exceptional accuracy of 97.66%. These findings highlight the transformative potential of machine learning in clinical practice, offering healthcare professionals a powerful tool to enhance diagnostic precision, improve patient outcomes, and advance progress in oncology.

1. Introduction

The most common cancer among women around the world is the result of the abnormal proliferation of the breast tissue, constituting tumors in the breast. The cancer usually manifests as a palpable mass in the breast; however, early-stage breast cancer sometimes shows no obvious symptoms[1]. There are many risk factors related to how breast cancer develops, such as genes, family history, age, hormone replacement therapies, and lifestyle-related factors. Besides that, changes observed in the BRCA1 and BRCA2 genes significantly increase the likelihood of developing this disease[2]. Timely identification of breast cancer is crucial in the effective management of this neoplasm. Hence, the screening should include never skipping mammogram checks and self-exams coupled with low-fat dietary choices. These include a nutritionally balanced diet with the maintenance of weight within a reasonable range to reduce the risk of cancer. A variety of treatment approaches would depend on the stage and type of breast cancer and may involve surgery, chemotherapy, radiotherapy, hormonal therapy, and targeted agents. [3]

This means that the advancement in research in medicine and greater awareness, as well as appropriate treatment programs, has allowed researchers to not only detect disease at an earlier

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stage but also initiate more effective treatment. Furthermore, the adoption of salutary lifestyle habits like food balance, active living, and limited alcohol have proven to decrease the probability of disease manifestation [4]. Increased interest in research and public health information has brought more understanding and better management of breast cancer. Its incidence has increased notably in recent years, with various modalities posing challenges to human health. Cancer remains a worldwide issue affecting about one in every six inhabitants of our planet [5]. Skin cancer is thought of as the most common variant worldwide, while breast cancer is viewed as the leading cause of cancer-related mortality in women. Such trends lay bare the important need for continued research and public health intervention to help stem what has turned into a widely rampant and deadly disease [6]. The sooner a diagnosis is made, the greater the probability of positive treatment outcomes. Early diagnosis requires both extensive profiling and prompt detection of the variance witnessed in the symptoms of the patients. [7]

Traditional methods of breast cancer detection can both be inefficient and expensive. This makes the treatment process all the more difficult. Artificial intelligence algorithms are widely used in medical data processing and cancer detection [8,9]. In addition, with the advent of big data and ML-based technologies, the focus has shifted toward quality rather than quantity [10,11]. Due to their flexibility and ability to perform various functions-disease prediction, diagnosis, medication, cost reduction, and real-time decision-making-the algorithms of ML are applied widely in the healthcare sector. In this regard, evaluating seven classification algorithms-Support Vector Machines (SVM), Decision Tree (DT), Random Forest (RF), K-Nearest Neighbors (KNN), Categorical Boosting (CatBoost), Gradient Boosting (GB), and Extreme Gradient Boosting (XGBoost)-highlights the importance of investing in cancer research and treatment initiatives. The assimilations of ANN-based systems will increase the workability and efficiency of information and communication technologies that are to be aligned with improving health and treatment outcomes in oncology [12]. The capability of AI to analyze vast amounts of patient data and to detect patterns that may go unnoticed by doctors may increase the efficacy of cancer detection and treatment, with a final benefit to the provision of more precise and personalized patient care. [13]

A range of ML techniques could be employed to diagnose and predict the breast cancer. Studies show that early diagnosis is very helpful for effective treatment. There is a need to improve the accuracy and efficiency of testing for breast cancer. One of the high technologies in detecting and classifying cancer is ML [14]. These methods have a fantastic potential to diagnose diseases, especially those of cancer [15]. A major benefit of these models is their performance in learning from big data and noticing the minute changes that are not usually reported in conventional ways, thus being able to facilitate quick diagnosis and lessening risks of complications. Present advancements in cancer detection have aided in easing the early treatment, preventing the disease from spreading and avoiding invasive medical treatments. AI and ML are now important treatment procedures due to personalized treatment and improved cancer solutions providing better care, this indeed serves as pressing and important global health matters. [16]

This research studies various ML algorithms for breast cancer detection and stresses in the introduction the fact that the early diagnosis improves the prognosis [17]. Each model was systematically evaluated against seven machine learning models on breast cancer dataset. The method was about complete preprocessing of the data, followed then by training and testing in order to choose the most accurate model. The results showed the positive role of ML in succeeding better in preventive diagnosis of breast cancer. It will help clinicians to reach an early diagnosis of breast cancer, offer less invasive treatment, and contribute to up-to-date development in the field of oncology. The results emphasize the tremendous potential of integration of artificial intelligence and ML into clinical practice, approaching more personalized and effective healthcare [18].

1.1 Literature Review

Akhil et al. state that breast cancer (BC) incidence is increasing. Limited diagnostic tools like dynamic MRI and X-rays can delay detection. Early diagnosis extends survival, as advanced medical technologies remain insufficient for treatment. While WNBC, AR+NN, and AdaBoost ELM aid detection, bootstrapped random networks struggle with class imbalance, data preprocessing, and poor feature selection [19]. Law et al. define feature selection (FS) as a key strategy for improving machine learning (ML) systems. Metaheuristic FS algorithms, including Gravitational Search Optimization (GSA), Emperor Penguin Optimization (EPO), and their hybrid, hGSAEPO, are proposed in this study. BC, chosen for its high mortality rate, benefits from early detection to improve survival and reduce unnecessary interventions. The approach combines GSA, EPO, and hGSAEPO to eliminate irrelevant features, reducing complexity and improving classification. Nine classifiers applied FS to WDBC, achieving 98.31% accuracy, 0.9800 precision, 0.9700 sensitivity, 0.9887 specificity, 0.9539 F1-score, and AUC above 0.998. The study highlights challenges in developing reliable breast cancer prediction systems [20]. Timothy et al. state that breast cancer is the most common cancer in women, affecting about 93%, with its incidence rising. Despite an 84% 10-year survival rate, early detection is crucial, especially for women with dense breast tissue, where 41% of cases go undetected. This study explores feature selection and enhancement methods using various ML approaches for breast cancer classification. Analysis on the Wisconsin Diagnostic Breast Cancer dataset found LDA to perform well across key binary metrics, including Accuracy, Precision, Recall, and F1-Score [21]. Aman et al. classify breast cancer as a condition of uncontrolled cell growth in the breast, with various types determined by malignancy cells. Predominantly affecting women, it draws interest from AI-focused clinical researchers for improved diagnosis and prediction. This study uses the Wisconsin Breast Cancer Dataset (WBCD) from the UCI archive, containing 30 features, including mean, standard error, and worst values, selected for their role in classification. The proposed classifier is a stacked ensemble model combining Decision Tree, AdaBoost, Gaussian Naive Bayes, and Multi-layer Perceptron. Performance is evaluated using ROC curve, AUC, specificity, F1-score, sensitivity, and accuracy. Experiments show the model achieves 97.66% accuracy, surpassing previous studies, emphasizing AI-based ML approaches in breast cancer prediction and diagnosis to enhance clinical decision-making and patient outcomes [22].

Iman et al. emphasize the growing role of ML and data mining in breast cancer (BC) diagnosis, though many methods suffer from poor statistical evaluation or unsuitable assessment metrics. This study introduces the Extreme Learning Machine (ELM) as an efficient classification approach, preventing overfitting with binary and multi-class classification and performance comparable to kernel-based SVMs. To evaluate performance, WBCD and WDBC datasets were used. Results show ELM achieves 92.06% accuracy on WBCD and 94.52% on WDBC, with high precision, recall, F-measure, G-mean, MCC, and specificity. These findings establish ELM as a reliable BC classifier with potential for broader healthcare applications [23]. Mohammad et al. examine AI's role in enhancing early BC diagnosis, treatment optimization, and patient care. The study reviews 310 studies using 30 datasets and their evaluations. RNNs achieved the highest accuracy at 98.58%, maintaining over 96% in Genetic Principles, Transfer Learning, and ANNs. Basic ML models surpassed 90% accuracy, but deep learning performed better. WBCD analysis found logistic regression and SVM to be the most reliable, while decision trees overfitted. Ultrasound image processing emphasized preprocessing, whereas histopathological image classification showed strong accuracy. Findings suggest ML and DL could revolutionize BC diagnosis and detection technology [24]. Serhat et al. emphasize the importance of early breast cancer diagnosis and treatment. This study evaluates ML models on clinical and genomic data for improved classification. Findings show classification accuracy varies, highlighting the value of advanced analytics. LightGBM (LGBM) performed best individually, with a 99.2% F1-score and 98.9% accuracy. Ensemble models combining AdaBoost, GBM, and RGF outperformed individual models, achieving 99.5% accuracy. Key classification features included worst texture, worst concave points, mean concave points, and mean texture. Validation methods like K-fold and stratified shuffle split cross-validation provided deeper insights for distinguishing malignant from benign cases [25]. Musatafa et al. explore data mining (DM) and machine learning (ML) for breast cancer (BC) diagnosis with improved statistical validation. They introduce Online Sequential Extreme Learning Machine (OSELM) as a promising classifier. OSELM handles both binary and multi-class classification, performing comparably to kernel-based SVMs while risking overfitting. The study evaluates WDBC and WBCD datasets, showing OSELM achieves 96.13% accuracy on WDBC and 97.89% on WBCD. Precision, recall, specificity, and F-measure confirm its reliability. The authors suggest OSELM as a valuable BC diagnosis tool with potential applications in healthcare to support oncologists in data-driven decisions [26]. Shazzad et al. highlight the rising incidence of breast cancer and stress early detection's role in reducing mortality and improving treatment. This study explores ML models for breast cancer classification to determine the best feature selection method using a merged dataset. Five classical models and two meta-models were evaluated with LASSO and SHAP. Results show models performed significantly better with SHAP, with three classical and two meta-classifiers achieving 99.82% accuracy. The study underscores the importance of feature selection in enhancing diagnosis accuracy, emphasizing its relevance in modern medical advancements [27]. This study conducted by Gani et al. attempts optimization approaches in improving breast cancer detection through dimensionality reduction techniques. They used the Wisconsin breast cancer dataset, implemented PCA and LDA, and showed that incorporation of PCA on detection models provided a significant improvement in accuracy and performance [28].

2. Methodology

2.1 Dataset and Preprocessing

2.1.1 Wisconsin Breast Cancer Dataset

The research applies a breast cancer dataset from the University of Wisconsin Hospital, which has 569 samples and 31 attributes. Each sample provides details regarding the tumor characteristics of a patient. The aim is to classify these tumors as benign (0) or malignant (1). Out of these cases, 357 are benign and 212 are malignant. Singh and his team introduced three feature selection techniques by metaheuristic algorithms: the GSA, EPO, and a hybridization of both. Though classic feature selection approaches have been used in a number of machine learning applications, their actual efficacy in classifying breast cancers has not been explored much. This study addresses this gap by using these strategies in breast cancer classification. The reason why the researchers have decided to work in breast cancer is that it is the second most important cause of mortality in women. Early diagnosis is crucial, as it boosts treatment efficiency and reduces undue medical interventions [29]. The distinction between benign and malignant data in our dataset is presented in Figure 1, both as percentages and numerical values.

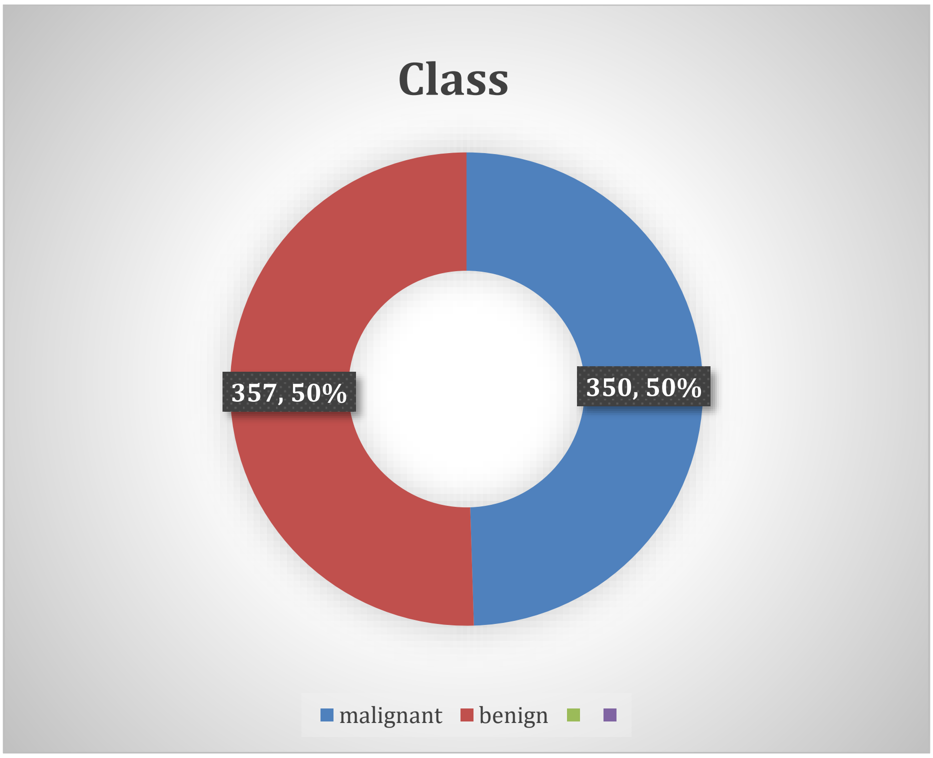

Fig. 1. Shows the distribution of benign and malignant cases in the dataset, represented both as percentages and numerical values

2.1.2 Characteristics and Classes of The Dataset

This study analyzes important tumor characteristics that are crucial in the detection of breast cancer. Each of these features interrogates certain taught properties of the tumor cells. The characteristics and their respective attributes are outlined in Table 1.

Table 1
Dataset features and descriptions

Features	Description
x.radius_mean	Mean radius of the tumor cells
x.texture_mean	Mean texture of the tumor cells
x.perimeter_mean	Mean perimeter of the tumor cells
x.area_mean	Mean area of the tumor cells
x.smoothness_mean	Mean smoothness of the tumor cells
x.compactness_mean	Mean compactness of the tumor cells
x.concavity_mean	Mean concavity of the tumor cells
x.concave_points_mean	Mean number of concave portions of the contour of the tumor cells
x.symmetry_mean	Mean symmetry of the tumor cells
x.fractal_dimension_mean	Mean "coastline approximation" of the tumor cells
x.radius_se	Standard error of the radius of the tumor cells
x.texture_se	Standard error of the texture of the tumor cells
x.perimeter_se	Standard error of the perimeter of the tumor cells
x.area_se	Standard error of the area of the tumor cells
x.smoothness_se	Standard error of the smoothness of the tumor cells
x.compactness_se	Standard error of the compactness of the tumor cells
x.concavity_se	Standard error of the concavity of the tumor cells
x.concave_points_se	Standard error of the number of concave portions of the contour of the tumor cells
x.symmetry_se	Standard error of the symmetry of the tumor cells
x.fractal_dimension_se	Standard error of the "coastline approximation" of the tumor cells
x.radius_worst	Worst (largest) radius of the tumor cells
x.texture_worst	Worst (most severe) texture of the tumor cells

Table 1
Continued

Features	Description
x.perimeter_worst	Worst (largest) perimeter of the tumor cells
x.area_worst	Worst (largest) area of the tumor cells
x.smoothness_worst	Worst (most severe) smoothness of the tumor cells
x.compactness_worst	Worst (most severe) compactness of the tumor cells
x.concavity_worst	Worst (most severe) concavity of the tumor cells
x.concave_points_worst	Worst (most severe) number of concave portions of the contour of the tumor cells
x.symmetry_worst	Worst (most severe) symmetry of the tumor cells
x.fractal_dimension_worst	Worst (most severe) "coastline approximation" of the tumor cells
Y	target

2.1.3 Data preprocessing steps

The dataset underwent several preprocessing steps to improve the quality and efficiency of the training process. The first step in the procedure was to drop the ID column. The ID column served merely as a unique identifier for each sample, conveying little to no information for the predictive modeling task. Keeping this column would lead to overfitting, with the model possibly learning to associate certain IDs with outcomes rather than determining real patterns within the data. Eliminating it was indeed directed towards ensuring that the model continued to concentrate on features that are genuinely important.

Next, the dataset was treated for its missing values. Any rows with a null or missing value were dropped or inherited in intelligence through statistical means such as average or median. Feature scaling put all the variables from within a certain range into any number of similar size. Failure to scale will likely hurt regression models that focus on distance-based measurement. If categorical variables do exist, conversion was done into numbers through methods such as one-hot encoding or label encoding. Finally, logarithmic transformation was not applied on the target, as it was observed already in good format for classification. The dataset has been split into 70% for training and 30% for testing, as shown in Figure 2.

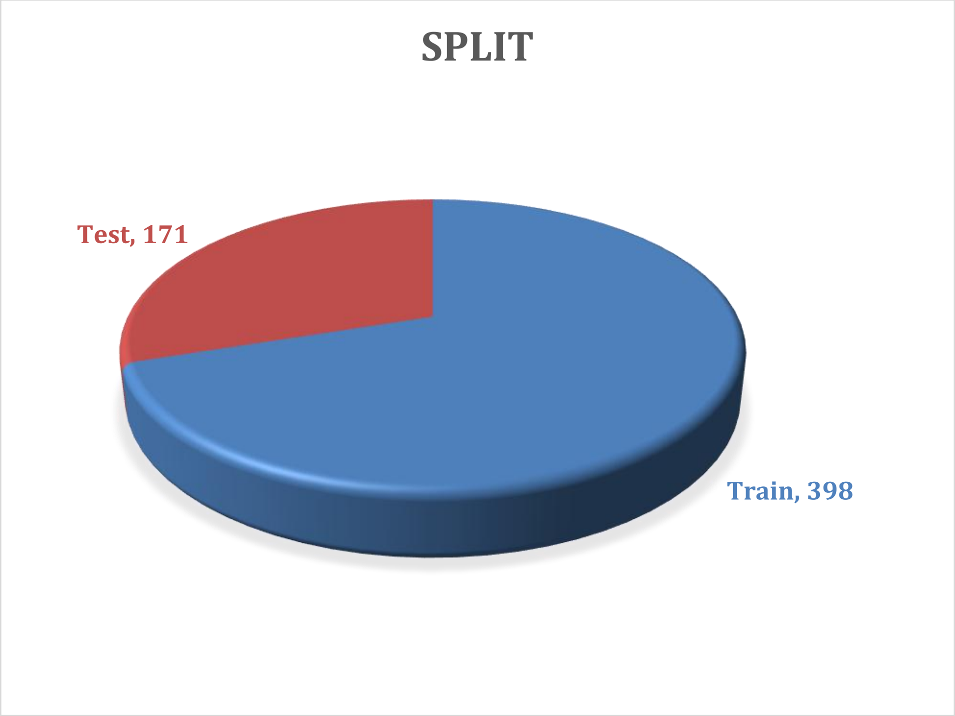

Fig. 2. Depicts the division of the dataset into 70% for training and 30% for testing, illustrating the allocation used for model training and evaluation

2.2 Algorithms Used

2.2.1. Support Vector Machines (SVM)

Support Vector Machines (SVM) are generally known as supervised learning algorithms for classification. The approach is based on the idea of a hyperplane as a plane separating the information into categories. The SVM algorithm gets its optimal accuracy by ensuring that the maximum possible margin separates the classes. The larger the margin, the better the SVM algorithm. But it is not the distance itself which is of utility, rather it is the distance separating both the classes and the hyperplane from both the sides. They are considered to be among the most advanced models that can carry out classification, prediction, and anomaly detection effectively. The main objective of SVM is to find a hyperplane which separates or classifies the data values in different classes while keeping as much distance as possible from the nearest data values[30]. The performance of an SVM classifier depends on the positioning of the hyperplane to guarantee the maximum minimum distance between different classes. This configuration also affects the model's generalization. The SVM algorithm finds the most appropriate hyperplane from a variety of other different hyperplanes through an optimization process. Although construction begins in an ordered way, the process of development becomes efficient over time. In conclusion, Support Vector Machines provide a fast supervised learning method which uses hyperplanes and margins to help carry out the classification, prediction, and anomaly detection tasks even on complex data [31].

2.2.2. Decision Trees (DT)

A Decision Trees algorithm is perhaps the most used supervised machine learning algorithm for decision-making tasks. The models bear some structural similarities to real-world decision-making processes and contains decision points and event-based strategies. The decision-tree structure allows one to analyze various alternatives under given conditions, whereby the most common aim of Decision Tree algorithms is to find ways to maximize the future performance or minimize the possible expected costs by performing simulations of different scenarios and choosing the best way, as shown in the equation with three parameters. The Decision Tree classifier is one of the most-used classification algorithms known for supervised learning. It belongs to supervised learning; it creates a hierarchical tree structure whereby features of the data set are internal nodes representing relevancy in decision-making, branches are decision rules, and leaf nodes show class labels. [32]

One of the basic principles for Decision Tree classifiers is basically to ask questions one after the other for efficient separation. After these questions have been asked, the splitting continues and the data is effectively divided down into subgroups, e.g., yes/no answer [33]. Depending on the arrangement and distribution of information, entropy is an important criterion for evaluating decision tree models as it measures the number of questioning rounds necessary to explain a given sample. If a dataset is completely homogeneous, then it would have zero entropy; that is, all elements would belong to one category. One would conceptualize unity entropy for a dataset with exactly, or as close to equal, dividing its selection. The Gini Index is a technique frequently adopted in Decision Tree algorithms to measure the extent of variation or inequality in any dataset. A Gini coefficient of zero represents a perfectly homogeneous sample with all identical objects, whereas a value of one would indicate total maximum inequality in the sample. [34]

$$Entropy(D) = {}_{i=1}\sum^{c} \quad p_i \log_2(p_i) \tag{1}$$

2.2.3. Random Forest (RF)

Random Forest (RF) is an ensemble machine learning model in which multiple model types work in tandem to improve prediction performance. RF does not use just one decision tree; instead, it combines the outputs of many tree models being trained on a randomly selected subset of data. Therefore, this ensemble approach to model improvement generally works by averaging predictions from many trees instead of depending on a single tree prediction. Due to this, Random Forest is a less biased and generalized model than regular decision trees, which may, at their extremes, be too simplified or too specific. One of the finest advantages of the RF model is its ability to manage complex and uncertain data, which is extremely useful for critical applications such as cancer detection. Using RF, it ensures that false negatives are minimized while utilizing it by balanced management of class imbalances in less significant cases. In the classification of tumor types of benign and malignant tumors, the RF algorithm tries to prevent misclassification, even if certain malignant cases exhibit features also shared with benign ones. The classes were repeatedly selected with replacement, where the unselected shares were recommended to be ignored. This permits Random Forests quite capable of overcoming whatever trouble they had concerning class imbalance during prediction execution. [35]

$$\hat{y} = \text{mode}\{h_1(\boldsymbol{x}), h_2(\boldsymbol{x}), \ldots, h_m(\boldsymbol{x})\} \tag{2}$$

The Random Forest (RF) technique initiates by generating a number of decision trees, each trained on a randomly selected subset of input data. The individual trees collectively come up with the classification or regression outcome by taking a vote. By combining results from a number of decision trees, RF also achieves higher accuracy and reduces the risk of overfitting. As the predictions from a joint combination of numerous trees are more stable and generalized than the predictions from a single tree, RF provides a trustworthy predictive model. Furthermore, RF also introduces randomness in its training by the random selection of features during the actual splitting of nodes. This diversification among the trees improves the ability of the model to perform better and increases robustness and efficiency [36].

2.2.4. K-Nearest Neighbors (KNN)

KNN is one of the most common non-parametric, supervised machine learning based classifiers which determines the category of an unknown data point based on the distances from labeled data. In stark contrast with many other machine learning algorithms that build explicit models during training, KNN operates as a lazy learner, meaning it does not form a pre-set model but memorizes training data and makes computations only when a prediction is to be made. The algorithm keeps during training the attribute vectors along with their labels so that it becomes retrainable with the introduction of new data. Its characteristic of being retrainable indeed makes KNN very useful in the processing of dynamic datasets but in return, it does multiply the rock of doing computations while handling large datasets [37].

Once an unlabeled data point requires classification, KNN uses a user-defined distance metric to calculate which ‘K’ nearest neighbors it has among the labeled training data. The class label is then assigned according to the most frequent class label found amongst these neighbors. In situations when the dataset contains tons of features, the selection of the more relevant attributes allows for a better classification result. Because KNN is non-parametric, it does not assume any theory of statistical distribution in the data, making it capable of processing highly complex and nonlinear datasets. Unfortunately, however, the performance of KNN also largely relies on the choice of ‘K’ and what distance metric is adopted, thus requiring fine-tuning for best performance. [38]

KNN has been considerably used in image recognition, recommendation systems, financial forecasting, and healthcare diagnostics. KNN has shown formidable accuracy for predicting diseases such as cardiovascular diseases, breast cancer, and prostate cancer by analyzing patient data and noticing the patterns based on historical cases. And it handles missing values, classification ambiguities, and improves data imputation techniques quite well. Nonetheless, even though KNN is effective, it is severely limited in its reliability based principally on storing the full training dataset. This will then in turn increase memory consumption and prolong inference time, especially for a large dataset. Since it recalculates the distances for each point to each one of the training samples, its efficiency depletes rapidly with an increase in data size. Implemented optimizations such as k-d trees or ball trees can speed up the search for nearest neighbors, mitigating this downside.

In general, KNN remains a powerful but simple algorithm, with its ease of implementation and impressive performance in classification and regression tasks. While simple enough to be the choice of many applications, implementations would need to take into consideration, among others, the impact on both accuracy and computational speed. [39]

$$\hat{y} = \mathrm{mode}\{y_i : \boldsymbol{x_i} \in \mathcal{N}_k(\boldsymbol{x})\} \tag{3}$$

2.2.5. Categorical Boosting (CatBoost)

CatBoost, or Categorical Boosting, is an advanced gradient boosting algorithm that is designed for efficient handling of categorical data. CatBoost is distinguished from other traditional boosting methods in that it requires no preprocessing, such as one-hot encoding or label encoding, to convert categorical variables into numerical ones. It incorporates novel ordered boosting techniques that allow for the handling of categorical features without requiring additional transformation. This greatly improves model performance for datasets containing a great number of categorical variables.

The capabilities of CatBoost guarantee superb predictive accuracy based on the joint principle of optimizing decision tree structures and incorporation of richer regularization within the decision trees. Using a blend of Bayesian bootstrapping and an ordered boosting approach helps to fight against overfitting and enables the model to generalize well on unseen data. It is highly efficient and scalable as the algorithm employs GPU acceleration, processes large datasets with ease, and does this quickly. Therefore it is advantageous for on-line applications involving massive datasets or where real-time processing is required.

$$F_m(X) = F_{m-1}(X) + \eta h_m(X) \tag{4}$$

Another core benefit with CatBoost is that it has great performance with virtually no hyperparameter tuning. In contrast to other boosting algorithms that mostly call for disparate performance tuning, CatBoost provides fairly good baseline performance with default parameters, thus delivering easy functionality for even novice users. Additionally, the feature selection capabilities integrated into the model select, automatically, the most important features to improve interpretability and eliminate an unnecessary risk of overfitting.

CatBoost has readily shown efficiency in the area of medical diagnostics, primarily in breast cancer detection. It allows researchers and practitioners to fit accurate and robust predictive models due to its capacity to capture complex relationships in high-dimensional medical data. It's also been shown to be tremendously effective on the imbalanced datasets so common in medical research, further supporting early cancer diagnosis and ultimately improving patient prognoses. With its superior performance, ease of use, and efficiency, CatBoost has emerged as a powerful machine learning technique for advancing predictive analytics in healthcare and beyond [40].

2.2.6. Gradient Boosting (GB)

Gradient Boosting is an elaborate and well-advanced mechanism of machine learning that enhances predictive accuracy by generating multiple weak models forming a strong ensemble. The main concept of this approach is the sequential addition of models, where each new model is designed to fix the mistakes of its predecessors, as introduced in Eq. 6. Unlike other boosting algorithms that give room for users to specify the base estimator, Gradient Boosting operates with an already existing base model that is appropriately utilized for both classification and regression tasks, depending on the particular case. Under regression understanding, the cost function most often adopted in this setting is the mean squared error (MSE), while the log loss is commonly used for classification tasks. [41]

In actuality, in Gradient Boosting, the final ensemble model 'F' is built by iterating the addition of weak learners 'f.' This addition is effected by means of a learning rate parameter 'η,' which bounds how much that model contributes to the final ensemble model. This process will monotonicity decrease the errors, although it will not always result in an optimally ordered model immediately. However, this iterative refinement does reduce the chances of making errors over a number of iterations and thus allows for a more precise final model. [42]

Gradient Boosting has gained enormous popularity across various fields, such as data mining, artificial intelligence, and machine learning, due to its excellent predictive power. It has been extraordinarily successful in tackling difficult issues, for instance, in medical diagnostics, in which it has shown an impressive degree of accuracy in prognosing breast cancer. By intelligently adapting to changing data conditions and learning from past mistakes, Gradient Boosting allows for a very robust and adaptable platform for predictive modeling. [43]

The effectiveness of this technique relies on its ability to combine several weak models into a powerful predictive system, enabling much higher accuracy and reliability. This is why it has been widely adopted among engineers, data scientists, and researchers. Furthermore, because it is quite flexible, the technique can be very useful in many modern-day problems, helping ensure it remains such an important tool in the field of machine learning as it continues to evolve.

$$F_m(x) = F_{m-1}(x) + \gamma_m h_m(x) \tag{5}$$

2.2.7. Extreme Gradient Boosting (XGBoost)

XGBoost, or eXtreme Gradient Boosting, is one of the most powerful, fast, and efficient machine-learning algorithms in recent years [40]. Essentially, XGBoost is based on the gradient boosting framework. This approach enhances the predictive performance by integrating several weak models, like decision trees, to yield a strong and robust model[44].

XGBoost is quite different from the rest owing to its incredible efficiency, scalability, and wide array of applicability to other types of data, which tend to be high-dimensional and complicated. This is mostly applied to medical research such as investigations related to breast cancer diagnosis. It is capable of acquiring intricate interactions and subtle patterns within the data, enabling researchers and practitioners to develop highly precise and robust models on detection and diagnosis of breast cancer.

With its recent implementation of advanced optimization techniques and parallel computation, XGBoost delivers lower training time and better accuracy which makes it quite popular among academic as well as industrial people. Its versatility and usability in working with data at a much larger scale make it an incredibly useful tool for creating robust machine learning models across myriad domains [45].

3. Experiment and Results

3.1. Support Vector Machines (SVM)

The SVM algorithm achieved high-performance classification with an excellent accuracy of 97.7%. The classification report corroborates the efficacy of the model for both classes. [46]

For class 0, the model performed with 96% precision, meaning that 96% of the instances that the model predicted as class 0 are in fact correct. The 100% recall tells us that the model was able to identify all instances of class 0, so the F1-score was calculated at 98%, which means that there is a strong balance between precision and recall. [47]

For class 1, the SVM model yielded 100% precision, which means that every instance predicted as class 1 was actually correct. According to the 94%, however, 6% of actual class 1 was confused with class 0. Nonetheless, the 97% F1-score still indicates very strong performance for class classification.

The macro F1-score of 97% concurs with a high consistency performance of the model for both classes, while the weighted F1-score of 98% provides additional evidence to the robustness of the SVM model. The results further throw into focus the reliability of the SVM algorithm for classification on such a dataset by proving the strengths in precision and recall for data distributions that are well separated and balanced [48]. The values obtained using the SVM algorithm are presented in Table 2, and the confusion matrix is shown in Figure 3.

Table 2
Presents the values obtained using the SVM algorithm, including key performance metrics for model evaluation

Metric	Class 0 (Negative)	Class 1 (Positive)	Macro Avg	Weighted Avg
Precision	96%	100%	98%	98%
Recall	100%	94%	97%	98%
F1-score	98%	97%	97%	98%
Support	106	65	171	171

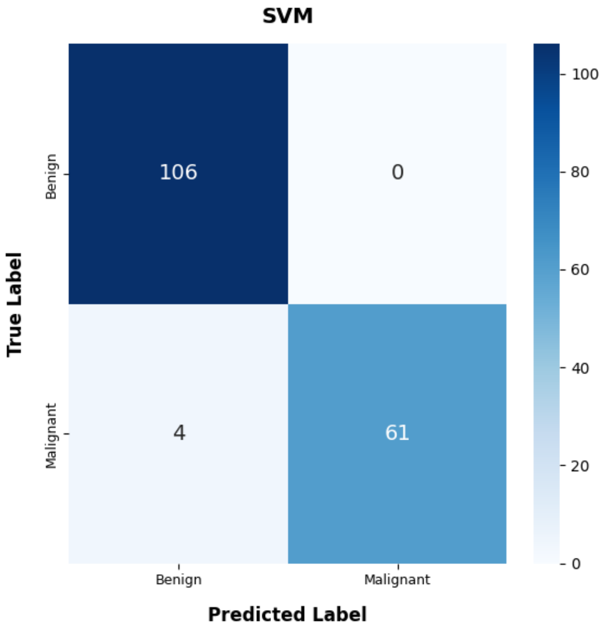

Fig. 3. Shows the confusion matrix, providing a detailed view of the classification results, including true positives, true negatives, false positives, and false negatives

3.2. Decision Trees (DT)

The DT algorithm recorded a 94.7% correct classification rate showing that it demonstrated formidable classification performance. The classification report explains the efficiency of the model for each class clearly.

The model has a precision of 95% for class 0.0, meaning that 95% of the instances predicted as class 0 were classified correctly. It has 96% recall, suggesting that 96% of actual class-0 instances were identified correctly. This gives rise to the F1 score of 96% that demonstrates the excellent trade-off between precision and recall for this class. [49]

The Decision Tree model had a precision of 94% for class 1.0, which means that many predicted class 1 instances were actually correctly classified. However, given a 92% recall, a small fraction of actual class 1 instances was classified incorrectly. Yet, an F1 score of 93% indicates high overall classification accuracy for this class as well. [50]

The macro-average F1 score of 94% indicates that the model has more or less equal performance on both classes. The weighted average F1 score of 95% reflects the overall accurate performance of the Decision Tree model. Overall, these results show that the proposed algorithm is highly robust in handling structured datasets and provides fairly accurate classification with a good trade-off between precision and recall [51]. The values obtained using the DT algorithm are presented in Table 3, and the confusion matrix is shown in Figure 4.

Table 3
Presents the values obtained using the DT algorithm, including key performance metrics for model evaluation

Metric	Class 0 (Negative)	Class 1 (Positive)	Macro Avg	Weighted Avg
Precision	95%	94%	95%	95%
Recall	96%	92%	94%	95%
F1-score	96%	93%	94%	95%
Support	106	65	171	171

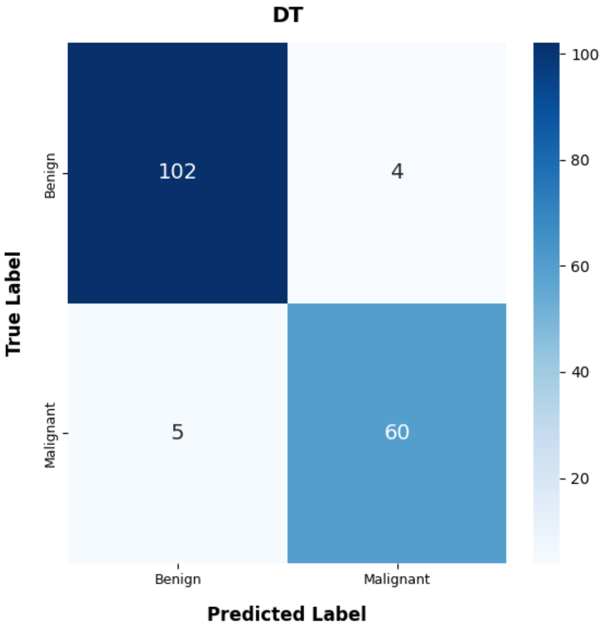

Fig. 4. Shows the confusion matrix, providing a detailed view of the classification results, including true positives, true negatives, false positives, and false negatives

3.3. Random Forest (RF)

An RF algorithm demonstrated strong classification potential at 96.5%. The classification report provides further insights into the efficacy of the model in distinguishing between the two classes. [47]

The precision for class 0 was 97%, which means 97% of the instances predicted as class 0 were indeed correct. The recall score of 97% indicates that 97% of actual class 0 instances were successfully identified, which leads to the F1 score of 97% to show a strong balance between precision and recall. [52]

The Random Forest model attained a precision of 95% for class 1, signifying that a majority of the instances predicted as class 1 were properly classified. Practically, 95% of class 1 cases were recognized correctly, yielding an F1 score of 95%.

The macro average accuracy according to the F1 score of 96% indicates equal status of performance in predicting each class by the model, whereas the macro average of 96% concerning the weighted average F1 score further assures the intact credibility of the Random Forest model. With these performances, the Random Forest algorithm can serve as a competent classifier, hence delivering good levels of prediction with good capability for generalization, thereby good for structured classification tasks [51]. The values obtained using the RF algorithm are presented in Table 4, and the confusion matrix is shown in Figure 5.

Table 4
Presents the values obtained using the RF algorithm, including key performance metrics for model evaluation

Metric	Class 0 (Negative)	Class 1 (Positive)	Macro Avg	Weighted Avg
Precision	97%	95%	96%	96%
Recall	97%	95%	96%	96%
F1-score	97%	95%	96%	96%
Support	106	65	171	171

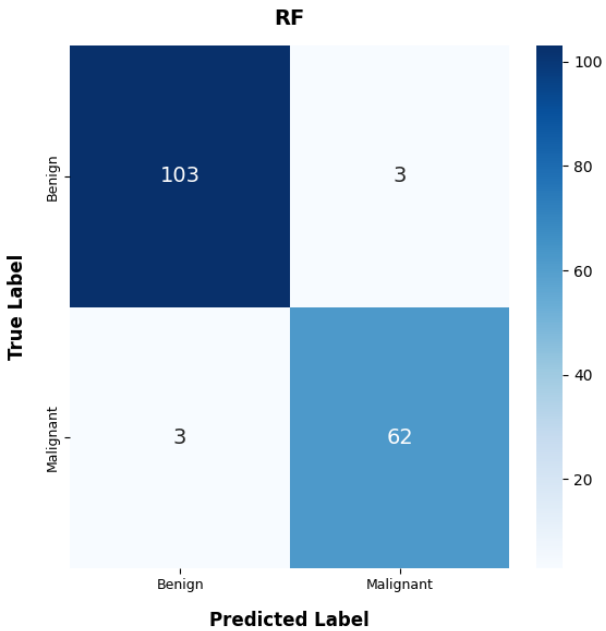

Fig. 5. Shows the confusion matrix, providing a detailed view of the classification results, including true positives, true negatives, false positives, and false negatives

3.4. K-Nearest Neighbors (KNN)

KNN is finding an accuracy of 80%, indicating a fair role of classification. The classification report gives an insight into how this model performed in general in properly classifying the two classes. [47]

With the precision of 74% for class 0, it seems that 74% of the points predicted to belong to the class 0 have been accurately classified. The recall score of class 0 is 84%, meaning that out of the actual class 0 points, 84% has been identified correctly, which leads us to an F1-score of 79%, showcasing a decent balance of trade-off between precision and recall.

For class 1, however, in the case of KNN, given a precision of 86%, a large majority of the points predicted to fall under this class certainly have been correctly classified. But even so, a recall score of 77% suggests that 77% of the actual class 1 points exist into a class with some of them incorrectly classified. Never thinking of it, an F1-score of 81% portrays that there is a strong classification capability for this class.

The macro average F1-score of 80% would imply that both classes perform equally well with respect to the model. Furthermore, a weighted average F1-score of 80% reaffirms the balanced performance of the model since it corroborates the former results. These results show that KNN has a fair classification power but thereby may demand optimization, such as the number of neighbors or different distance metrics used if further enhancement of accuracy is desired [51]. The values obtained using the KNN algorithm are presented in Table 5, and the confusion matrix is shown in Figure 6.

Table 5
Presents the values obtained using the KNN algorithm, including key performance metrics for model evaluation

Metric	Class 0 (Negative)	Class 1 (Positive)	Macro Avg	Weighted Avg
Precision	74%	86%	80%	81%
Recall	84%	77%	80%	80%
F1-score	79%	81%	80%	80%
Support	89	111	200	200

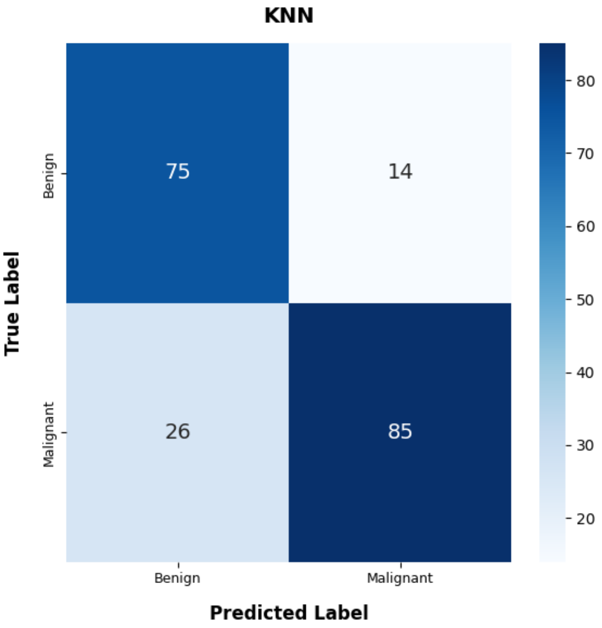

Fig. 6. Shows the confusion matrix, providing a detailed view of the classification results, including true positives, true negatives, false positives, and false negatives

3.5. Categorical Boosting (CatBoost)

The CatBoost algorithm has demonstrated notable performance, achieving an accuracy rate of 88.5%. This success underscores the model's effective ability to classify data accurately. A detailed classification report offers a deeper understanding of the model’s capability in differentiating between two distinct classes.

For class 0, the precision rate stands at 84%, signifying that a substantial portion—84%—of instances predicted as belonging to class 0 were accurately identified. The recall score for this class is measured at 92%, indicating that the model successfully recognized 92% of the actual instances classified as class 0. These metrics culminate in an F1-score of 88%, illustrating a well-balanced relationship between precision and recall for this particular category.

Likewise, with respect to class 1, the CatBoost model recorded a precision measurement of 93%, which means that most instances anticipated to be part of class 1 were correctly assigned. Nonetheless, a recall score of 86% reveals that not all actual instances from class 1 were captured; specifically, some examples from this group were misclassified. Despite these minor discrepancies, an F1-score of 89% signifies strong classification efficacy for this category.

Furthermore, a macro average F1-score of 88% indicates uniformity in performance across both classes. Additionally, the weighted average F1-score of 89% reinforces the resilience and effectiveness of the CatBoost algorithm when applied to this dataset. Collectively, these findings illustrate that CatBoost is a dependable option for classification tasks, particularly within structured datasets featuring significant categorical attributes. The values obtained using the CatBoost algorithm are presented in Table 6, and the confusion matrix is shown in Figure 7.

Table 6
Presents the values obtained using the CatBoost algorithm, including key performance metrics for model evaluation

Metric	Class 0 (Negative)	Class 1 (Positive)	Macro Avg	Weighted Avg
Precision	84%	93%	88%	89%
Recall	92%	86%	89%	89%
F1-score	88%	89%	88%	89%
Support	89	111	200	200

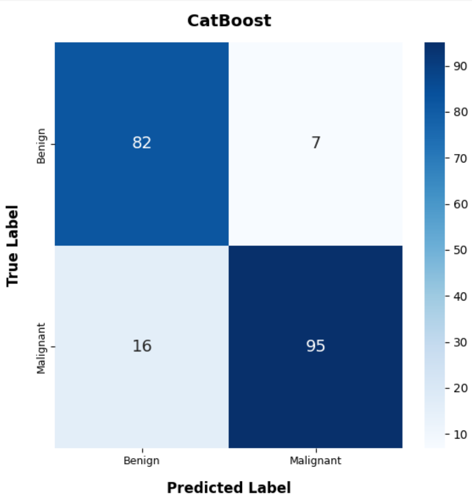

Fig. 7. Shows the confusion matrix, providing a detailed view of the classification results, including true positives, true negatives, false positives, and false negatives.

3.6. Gradient Boosting (GB)

The GB algorithm fantastically succeeded with an 88.0% accuracy, confirming its capacity to classify. The classification report provides further insights into the model's performance across the classes.

For class 0, we find that the precision is 84%, meaning that 84% of the instances predicted as class 0 were really class 0. The recall score of 91% indicates that class 0 successfully classified 91% from all actual class 0 instances. F1 reaches a value of 87%, indicating a good balance between precision and recall for this class.

The Gradient Boosting model was also able to achieve 92% precision for class 1, meaning that most of the instances predicted as class 1 were actually correctly classified. The recall score indicates that 86% of the actual class 1 instances were correctly identified, while some were misclassified. The overall robust performance of the Gradient Boosting model is further underlined with an F1 of 89% in this category.

With the macro average F1-score of 88%, it can be said that the model has some sort of balance performance among the classes tested, and, with a weighted average F1-score of 88%, both value affirm the robustness of the Gradient Boosting model within the particular dataset that has been built up. Those results argue that Gradient Boosting is an excellent choice for classification tasks, especially when the complexity of the dataset makes it certain that the data require powerful techniques based on ensemble learning [51]. The values obtained using the GB algorithm are presented in Table 7, and the confusion matrix is shown in Figure 8.

Table 7
Presents the values obtained using the GB algorithm, including key performance metrics for model evaluation

Metric	Class 0 (Negative)	Class 1 (Positive)	Macro Avg	Weighted Avg
Precision	84%	92%	88%	88%
Recall	91%	86%	88%	88%
F1-score	87%	89%	88%	88%
Support	89	111	200	200

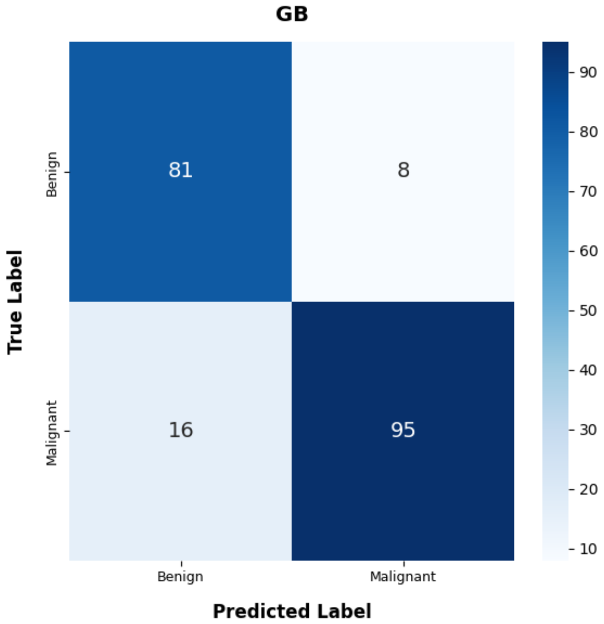

Fig. 8. Shows the confusion matrix, providing a detailed view of the classification results, including true positives, true negatives, false positives, and false negatives

3.7. Extreme Gradient Boosting (XGBoost)

The XGBoost algorithm has recorded an impressive accuracy rate of 89.0%, showcasing its capabilities in classification tasks. The classification report offers a comprehensive evaluation of the model's performance across various classes. [50]

In the case of class 0, the model achieved a precision of 85%. This indicates that out of all instances predicted to be class 0, 85% were accurately identified. Additionally, with a recall score of 92%, it successfully recognized 92% of all actual cases belonging to class 0. These metrics culminate in an F1-score of 88%, underscoring the effectiveness of the model in maintaining a balance between precision and recall for this particular class. [53]

For class 1, XGBoost demonstrated notable performance with a precision rate reaching as high as 93%. This ensures that most predictions made for this class are accurate; however, the recall score stands at 86%, which means there was some misclassification among actual instances labeled as class

1. Nonetheless, having an F1-score of 90% reflects the model's strong capability in handling these classifications effectively.

The macro average F1-score is registered at an impressive level of 89%, indicating reliable performance across both classes analyzed. Similarly, the weighted average F1-score also stands at 89%, reinforcing the overall strength and reliability exhibited by the XGBoost model. Overall, these findings suggest that XGBoost presents itself as a robust option for tackling classification challenges, especially when dealing with complex datasets necessitating sophisticated ensemble learning approaches to enhance predictive accuracy. The values obtained using the XGB algorithm are presented in Table 8, and the confusion matrix is shown in Figure 9.

Table 8
Presents the values obtained using the XGB algorithm, including key performance metrics for model evaluation

Metric	Class 0 (Negative)	Class 1 (Positive)	Macro Avg	Weighted Avg
Precision	85%	93%	89%	89%
Recall	92%	86%	89%	89%
F1-score	88%	90%	89%	89%
Support	89	111	200	200

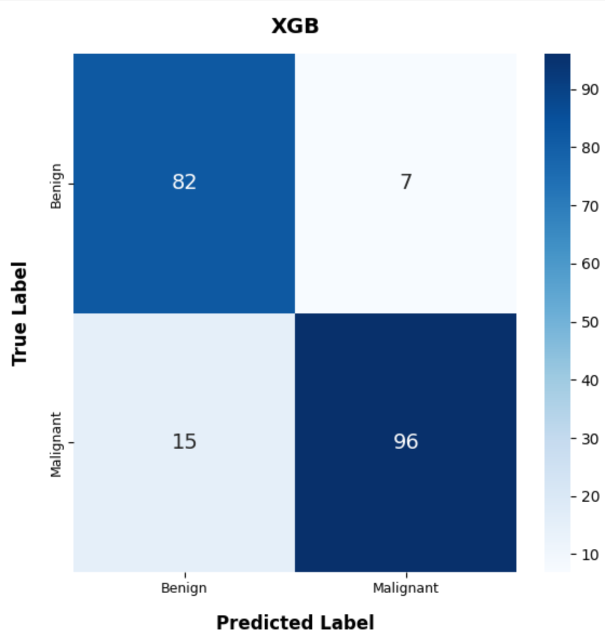

Fig. 9. Shows the confusion matrix, providing a detailed view of the classification results, including true positives, true negatives, false positives, and false negatives

3.8. Feature Importance

The provided bar chart shows the importance scores of the features determined by a Linear SVM model. Feature importance is determined in this case by the magnitude of the absolute value of the coefficients of the model, that is, how much do they influence the decision made by the classification? [54]

In the plot, "x.symmetry_worst" turns out to be the most influencing feature, closely followed by "x.concavity_worst" and "x.radius_mean". These features possess higher coefficient magnitudes which denote their importance in effectively distinguishing between the classes. Others such as "x.compactness_worst", "x.concave_pts_worst" and "x.symmetry_mean" also provided significant contributions to the predictions made by a model.

On the contrary, features in the lower region of the chart (below "x.area_worst", "x.fractal_dim_mean" and "x.concavity_se") are of relatively less importance. Hence, these variables exert less influence over the decision boundary set by the model.

Overall, feature importance analysis had pointed out a dominating role for symmetry, concavity, and radius-based attributes within the classification process, confirming their significance in medical imaging and breast cancer diagnosis [55]. Figure 10 displays a feature importance plot created for the SVM algorithm.

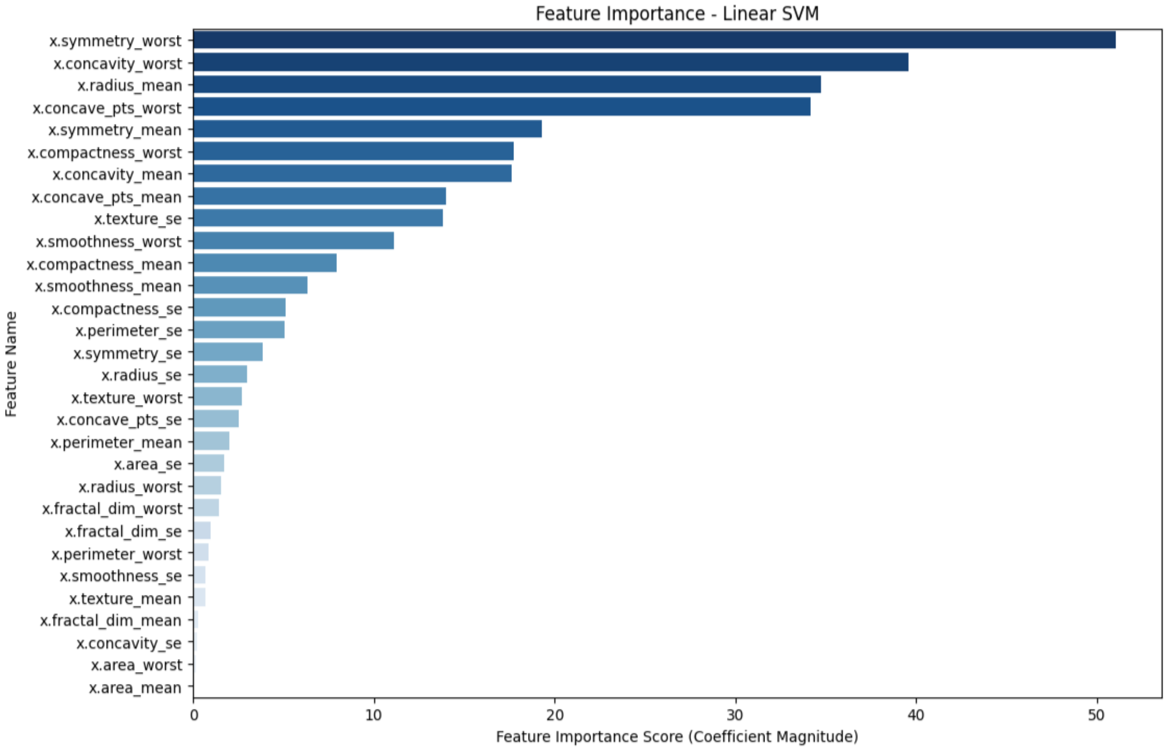

Fig. 10. Illustrates the feature importance plot for the SVM algorithm, highlighting the relative significance of each feature in the model's classification process

4. Discussion

This section presents an ML-based autonomous diagnostic method for breast cancer, one of the most common and deadly types of cancer. In this study, the most widely used ML algorithms in the literature were trained and tested on the Wisconsin dataset. The experimental results for the ML algorithms used in the study are presented in Table 9.

Table 9

Shows the experimental results of the ML algorithms tested on the Wisconsin dataset.

Rank	Model	Accuracy
1	SVM	97.66%
2	RF	96.49%
3	DT	94.74%
4	XGBoost	89.00%
5	CatBoost	88.50%
6	GB	88.00%
7	KNN	80.00%

SVM emerged as the most effective model, achieving an accuracy of 97.66%. The superior performance of SVM suggests that the dataset has well-separated decision boundaries, making it particularly suitable for margin-based classifiers. Additionally, RF (96.49%) and DT (94.74%)

performed exceptionally well, which indicates that tree-based models effectively capture feature interactions. However, Decision Trees tend to overfit, while RF mitigates this issue by averaging multiple DT.

Boosting algorithms (XGBoost, CatBoost, and GB) achieved accuracy scores around 88-89%. While slightly lower than SVM and RF, their performance remains strong due to their ability to iteratively correct errors and refine predictions. XGBoost outperformed CatBoost and GB, which may indicate that XGBoost's optimized implementation and regularization techniques provided an advantage. However, boosting methods are computationally expensive, which could be a limitation in real-world applications requiring efficiency.

On the other hand, KNN showed the lowest accuracy (80.00%), suggesting that it struggles with complex decision boundaries in this dataset. Since KNN relies on distance metrics, it may not generalize well when the dataset has overlapping classes or high-dimensional feature spaces.

First, model performance is dependent on feature selection and preprocessing, as well as hyperparameter work in its various aspects. For instance, when the kernel and the hyperparameters of the SVM apply, its success may change, while depending on the number of trees and feature selection for Random Forest, that works. Further hyperparameter tuning can help in improving boosting algorithms and KNN[56].

Additionally, computational efficiency is an important factor in real-world deployment. SVM may, due to its very high accuracy, become difficult to apply with lots of computation on large size datasets as the tree-based and boosting models could have more scalability. Therefore, practicality in terms of speed, interpretability, and usage of the resources must be weighed in, along with accuracy, while selecting and implementing a model.

Future studies could explore techniques such as feature engineering, hybrid models, and deep learning approaches to further enhance classification performance. Moreover, using explainability techniques such as SHAP values or LIME could provide deeper insights into model decisions, ensuring transparency and trust in AI-driven systems.

5. Conclusion

Breast cancer is still a very serious public health challenge and the leading cause of high morbidity particularly among women, Early detection of breast cancer is most important as it improves the survival rate of patients and their responses to the required treatment. In the last couple of years, machine learning-associated algorithms have gained significant usefulness in improving the diagnostic accuracy of breast cancer, representing the resilient methods for identifying breast cancer. Using advanced computational techniques, these models act as methods for extracting and assessing the characteristics of the tumor and assisting in diagnosis and clinical decision-making.

This work gives an in-depth comparison of seven machine learning algorithms using the Wisconsin dataset for breast cancer classification assessment. The experimental results reveal that the Support Vector Machine (SVM) algorithm obtained the highest classification accuracy of 97.66% compared to other models. The rest of the rankings were as follows: Random Forest (96.49%), Decision Tree (94.74%), XGBoost (89.00%), CatBoost (88.50%), Gradient Boosting (88.00%), and K-Nearest Neighbors (80.00%). The results show a great preference for SVM in terms of this study.this high-performance work, advocating that this algorithm can be used in the field as a trustable and accurate criterion for breast cancer detection.

The results are a game-changer and demonstrate the power of machine learning in disease diagnosis. Such algorithms may be integrated into clinical workflows to improve the accuracy of diagnosis, decrease false positives and negatives, and favor decisions reaching on an evidence basis. Furthermore, automated tumor classification could lessen the workload of medical professionals while delivering high accuracy and efficiency. Future studies should take on deep learning model integration with an ensemble to execute performance improvement and ampliative generalizability across several datasets. The development of machine learning-based diagnostic tools for breast cancer should ultimately lead to significant advantages in early detection and improved patient outcomes. [56]

Author Contributions

Conceptualization, Y.C. and I.P.; methodology, Y.C. and I.P.; software, Y.C.; validation, Y.C. and I.P.; formal analysis, Y.C. and I.P.; writing—original draft preparation, Y.C. and I.P.; writing—review and editing, Y.C. and I.P.; supervision, Y.C. and I.P. All authors have read and agreed to the published version of the manuscript.

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Data Availability Statement

The datasets generated during and/or analyzed during the current study is available from the corresponding author on reasonable request.

Conflicts of Interest

The author declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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