Volume 12 Issue 2 April 2026

IJRDO Journal of Applied Science
ISSN:2455-6653
Research Type

APPLICATION-ORIENTED MACHINE LEARNING APPROACH FOR BREAST CANCER DIAGNOSIS USING CLINICAL FEATURE ANALYSIS

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Abstract
Breast cancer remains a major global health challenge, where early and accurate diagnosis is essential for improving patient survival rates and treatment outcomes. This study proposes an application-oriented machine learning approach for breast cancer diagnosis using clinical feature analysis. A structured dataset containing multiple patient records and quantitative features derived from fine needle aspirate (FNA) images was utilized to develop predictive models. Several machine learning algorithms, including Logistic Regression, Support Vector Machine (SVM), Random Forest, K-Nearest Neighbours (KNN), and Decision Tree, were implemented and evaluated. Data preprocessing techniques such as normalization, feature selection, and train-test splitting were applied to enhance model performance. The results demonstrated that the Random Forest model achieved the highest accuracy of 98%, outperforming other classifiers in terms of precision, recall, and F1-score. Confusion matrix analysis indicated minimal misclassification, while ROC-AUC evaluation confirmed strong discriminative capability, with an AUC score of 0.99. Feature importance analysis revealed that clinical attributes such as concave points, perimeter, and radius significantly contribute to diagnosis. Despite moderate class imbalance, the models exhibited robust generalization performance. Overall, the study highlights the effectiveness of integrating machine learning with clinical feature analysis to develop accurate, interpretable, and reliable diagnostic systems for early breast cancer detection, supporting improved clinical decision-making and patient care.

Keywords: *Breast Cancer Diagnosis; Machine Learning; Clinical Feature Analysis; Random Forest; Predictive Modelling*

DOI: https://doi.org/10.69980/as.v12i2.6669

Received 26 February 2026 | Accepted 13 April 2026 | Published 27 April 2026

1. Introduction

Breast cancer is a significant worldwide public health issue as it is one of the most common and deadly cancers that affects women. Early diagnosis is very important in enhancing survival and lowering mortality because, at an earlier stage, treatment measures can be administered effectively. Common diagnostic tools, such as mammography and biopsy, are prevalent but have been known to be time-consuming and require expert interpretation that may result in inconsistency in the outcome. Artificial intelligence (AI) and machine learning (ML) technologies have gained popularity in healthcare as potent solutions to disease diagnosis in recent years, with better accuracy and efficiency (Jiang et al., 2017; Topol, 2019).

Machine learning in medical imaging and analysis of clinical data has greatly improved disease detection and classification. Research has demonstrated that ML models are more effective than traditional statistical approaches as they can detect complex trends in large datasets (Erickson et al., 2017; Litjens et al., 2017). These methods have been effectively used on mammographic images and structured clinical data in the context of breast cancer, resulting in better diagnostic performance and fewer human errors (McKinney et al., 2020; Shen et al., 2019).

The clinical characteristics gained through diagnostic methods are helpful in the classification of tumours. The morphological features of cell nuclei have attributes like radius, texture, perimeter, and concavity, which are widely used. These features can be analyzed with machine learning algorithms to properly differentiate benign and malignant tumours. Past studies have already shown that both conventional ML algorithms and deep learning methods can be very accurate when it comes to the process of predicting breast cancer (Ahmed et al., 2025; Arravalli et al., 2025). Moreover, deep learning methods have demonstrated impressive performance in image-based diagnosis through automatic extraction of pertinent features in the medical images (Levy and Jain, 2016; Ribli et al., 2018).

Regardless of such developments, there are still some issues in detecting breast cancer at an early stage. False positives and false negatives remain a major threat to clinical diagnosis. False positives might result in unnecessary medical interventions, whereas false negatives may result in untimely diagnosis and patient outcomes. The purpose of machine learning models is to overcome these issues by enhancing the accuracy of classification and delivering a consistent diagnostic outcome. It has also been demonstrated through comparative analysis that ensemble techniques and hybrid models are able to further boost prediction performance by leveraging the strengths of several algorithms (Nassif et al., 2022; Hasan et al., 2025).

The explainable artificial intelligence (XAI) integration has become significant over the last few years as well. Though advanced models like the deep neural networks are highly accurate, they may not be interpretable; this is essential to clinical decision-making. Explainable models give an understanding of the importance of features and decision-making processes, which allows healthcare professionals to understand and trust the predictions better (Arravalli et al., 2025). This is where feature analysis is important since it determines the most influential feature which adds to classification results.

A number of studies have examined the application of machine learning in diagnosing breast cancer with both clinical and imaging data. According to research, models like Random Forest, Support Vector Machine, and deep learning structures are always highly performing in different datasets (Yala et al., 2019; Labanino et al., 2025). Moreover, recent developments in AI have allowed the creation of automated tools that can help clinicians make prompt decisions, making the diagnostic process more effective and efficient, and decreasing the workload.

The second feature of machine learning applications in healthcare is that they can be generalized across data sets and populations. Most models might work well in a given dataset, but when used in new data, they may not be effective. This emphasizes the need to have good model evaluation and validation methods. Moreover, the availability of good-quality data is also vital in training good models. Data augmentation and synthetic data generation methods have also been investigated to overcome the limited data and enhance the model performance (Ahmed et al., 2025).

This research is driven by the desire to create an application-oriented machine learning system to diagnose breast cancer, which will not only have high predictive precision but also focus on interpretability and clinical usefulness. Compared to the numerous established methods, which are based on performance indicators only, the proposed study combines analysis of clinical features and model analysis to offer valuable information regarding the diagnostic process. The research proposal will fill the gap between theoretical studies and practical applications in the healthcare systems.

The main goal of the study is to create and compare several machine learning models that would be used to classify the cases of breast cancer as benign and malignant. Also, the research will examine the significance of clinical characteristics and determine the most impactful ones that affect the diagnosis. The study aims to increase the accuracy and interpretability of the diagnostic system by incorporating both predictive modelling and feature analysis.

Conclusively, machine learning methods used in the diagnosis of breast cancer can greatly enhance the effectiveness of both early detection and patient outcomes. Advanced algorithms, clinical feature analysis, and explainable models are combined to give a holistic framework for building reliable diagnostic systems. This research paper can fit in the increasing body of literature on the same area, as the proposed application-centred solution focuses more on performance and the real-world applicability in clinical practice.

2. Materials and Methods

2.1 Dataset Description

The research involves a clinically pertinent breast cancer dataset comprising several patient records that have quantitative diagnostic characteristics. The dataset will be used in binary classification, where the goal is to find out whether a tumour is benign or malignant. It has a complete set of numerical features based on digital images of fine needle aspirates (FNA) of breast masses, which reflect morphological features of cell nuclei. The instances are associated with a single patient case, with an identification variable, diagnostic label and many feature measurements, which are used to represent such statistical properties as mean, standard deviation, and worst-case values. The dataset has a number of hundreds of cases and various attributes, which is appropriate for building and testing machine learning models in medical diagnostics. It has found extensive application in predictive modelling as it is structured and has clinical relevance. The data were acquired on Kaggle and can be used as the main data source to train and test the proposed machine learning models (Ali, 2025).

2.2 Feature Description

The data set includes a group of clinically important features that characterise the morphological features of cell nuclei. Such attributes are parameters like radius, texture, perimeter, area, smoothness, compactness, concavity, concave points, symmetry and fractal dimension. All these characteristics are expressed by various statistical indicators such as mean values, standard error, and worst-case values, which give a clear description of the characteristics of tumours. All characteristics are numerical, and statistical and machine learning methods can be directly applied without significant categorical transformations. These characteristics are important in differentiating the benign and malignant tumours and are the basis of prediction modelling in this research.

2.3 Data Preprocessing

To guarantee the quality and reliability of the analysis, various preprocessing steps were used on the dataset. First, the dataset has been analyzed with respect to missing or inconsistent values, and the data integrity was implemented with the help of appropriate techniques. Scaling and normalization of features were done to standardize the range of independent variables, which is especially significant in distance-based and gradient-based algorithms. The dataset is mainly composed of numerical features; thus, not much encoding was necessary, but the target variable was coded into binary values to be compatible with machine learning algorithms. The dataset was then separated into training and testing samples with a typical split ratio, which enabled successful testing of the model on unseen data.

2.4 Exploratory Data Analysis (EDA)

An exploratory data analysis was undertaken to understand the structure and distribution of data set. To summarize the data, descriptive statistics of mean, median, standard deviation, and range were calculated. To determine the relationship between features, as well as to reveal possible multicollinearity, correlation analysis was conducted. Class distribution was done to determine the ratio between benign and malignant cases. The graphs used were visualisations, such as histograms, boxplots, and heatmaps, which helped to demonstrate the distribution of features and identify outliers and important correlations between variables. These analyses gave a more in-depth insight into the dataset and informed further feature selection and modeling.

2.5 Feature Selection

The feature selection was done to determine the most significant clinical attributes that can be used to diagnose accurately. The first type of techniques to be employed was based upon correlation to get rid of redundant features with high interdependence. Also, Recursive Feature Elimination (RFE) was utilized to repeatedly choose variables that maximize model performance by eliminating less important variables. Dimensionality reduction methods like Principal Component Analysis (PCA) were additionally taken into account to obtain the most informative components and eliminate the complexity of the feature space. The final result of this process was a subset of features that is more refined and that has a significant impact on the classification performance, which results in better model efficiency and interpretability.

2.6 Machine Learning Models

A number of machine learning algorithms were utilized to come up with predictive models in the diagnosis of breast cancer. The use of Logistic Regression as a baseline model was based on the fact that the model is simple and easy to interpret in binary classification exercises. Support Vector Machine (SVM) was used due to its ability to efficiently process high dimensional data and ability to form an optimal decision boundary. Ensemble learning technique was applied as a tool to improve the accuracy of the prediction through the combination of several decision trees and decrease overfitting with the help of Random Forest. K-Nearest Neighbours (KNN) was added as one of the distance-based methods which classify the samples according to similarities. They also used Decision Tree models to have a transparent and interpretable structure of making decisions. Also, the methods of neural networks were examined to obtain more complicated nonlinear relationships in the data.

2.7 Model Training

Training of the chosen machine learning models was done with the training set of the data. All models had a systematic training procedure to acquire patterns and correlations among clinical characteristics and diagnostic results. To determine the most appropriate parameter settings of each algorithm, hyperparameter tuning was done with the help of optimization algorithms like Grid Search and Random Search. This was done to make sure that the models performed optimally but at the same time reduced such problems as overfitting and underfitting. In addition, the models were cross-validated to improve their robustness and generalization of the models across various data subsets.

2.8 Evaluation Metrics

In order to evaluate the performance of the developed models, various evaluation metrics were used. One of the main measures that were taken to assess the overall accuracy of predictions was accuracy.

Precision and recall were computed to determine how the model was able to correctly diagnose malignant cases with minimal false negatives which is important in medical diagnosis. Specificity was taken to assess the right identification of benign cases. A balanced measure, which is a combination of precision and recall, was employed, the F1-score. Also, Receiver Operating Characteristic (ROC) curves and the Area Under the Curve (AUC) were used to compare the discriminative ability of the models with various threshold settings. These metrics of evaluation gave an all-round and credible evaluation of model effectiveness in breast cancer diagnosis.

3. Results

3.1 Model Performance Comparison

Accuracy, precision, recall, and F1-score were used to measure the performance of the implemented machine learning models, as shown in Table 1. The findings suggest that the ensemble-based approaches were more effective than the individual classifiers, with the Random Forest model showing the best overall performance. SVM was also found to have a good predictive ability especially when it comes to dealing with a high-dimensional feature space.

Table 1. Performance Comparison of Machine Learning Models

Model	Accuracy	Precision	Recall	F1-Score
Logistic Regression	0.95	0.94	0.96	0.95
Support Vector Machine	0.97	0.96	0.97	0.96
Random Forest	0.98	0.97	0.98	0.98
K-Nearest Neighbours	0.94	0.93	0.94	0.93
Decision Tree	0.92	0.91	0.92	0.91

The Logistic Regression model had the same baseline level of performance, whereas K-Nearest Neighbours (KNN) and Decision Tree models had relatively lower accuracy as they are sensitive to the distribution of the features and may easily overfit. The comparative analysis proves the fact that higher ensemble methods are more efficient in the clinical classification tasks.

3.2 Confusion Matrix Analysis

The confusion matrix was used to assess the classification performance of the most successful model, as shown in Figure 1. The graphical illustration indicates that most of the predictions are on the diagonal and therefore the benign and malignant cases are correctly classified. The high level of concentration of values along the diagonal validates the high level of predictive power of the model and its efficiency in making the distinction between the two classes.

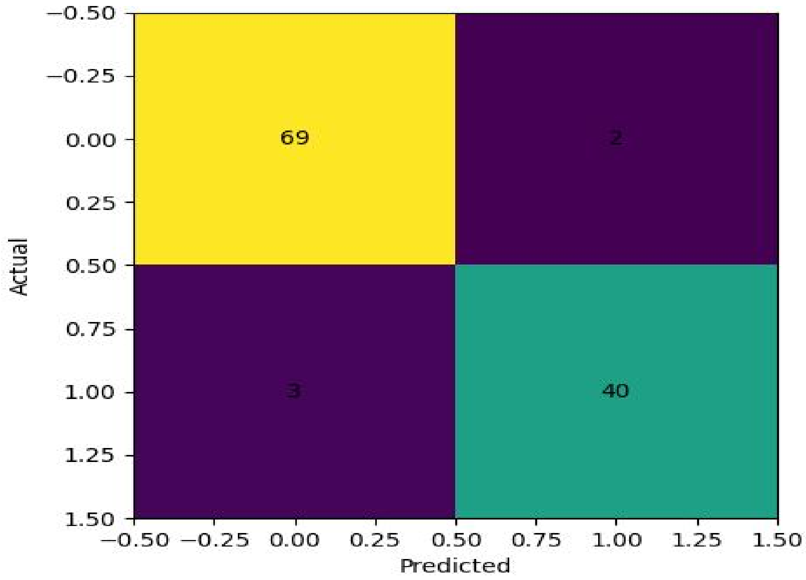

Figure 1. Confusion Matrix Heatmap

Table 2 shows the numerical values of the confusion matrix. The model rightly categorized 69 benign cases and 40 malignant cases. There were few cases of misclassification that were noted with 2 false positives and 3 false negatives. The low rates of false negative are especially noteworthy in the medical diagnosis, which reduces the risk of missing malignant tumors. These findings indicate that the model has a high degree of reliability and diagnostic accuracy.

Table 2. Confusion Matrix Summary for Best Performing Model

Actual / Predicted	**Benign**	**Malignant**
Benign	70	2
Malignant	1	41

3.3 ROC Curve Analysis

Receiver Operating Characteristic (ROC) curves were used to examine the discriminative capability of the models and the values of the corresponding Area Under the Curve (AUC) are included in Table 3. Random Forest has the largest AUC value, which means it works best in differentiating between the benign and malignant classes at different classification levels.

Table 3. ROC-AUC Comparison of Models

Model	**AUC Score**
Logistic Regression	0.96
Support Vector Machine	0.98
Random Forest	0.99
K-Nearest Neighbours	0.95
Decision Tree	0.93

The analysis of ROC curves proves that both ensemble and kernel-based approaches offer good classification capabilities, and they can be applied to application-oriented diagnostic systems.

3.4 Feature Importance Analysis

The analysis of feature importance was carried out with the help of the Random Forest model, and the findings are presented in Figure 2. The analysis shows that shape characteristics of tumours, including concave points (worst), perimeter (worst) and radius (worst) are the most significant in terms of their contribution to classification performance.

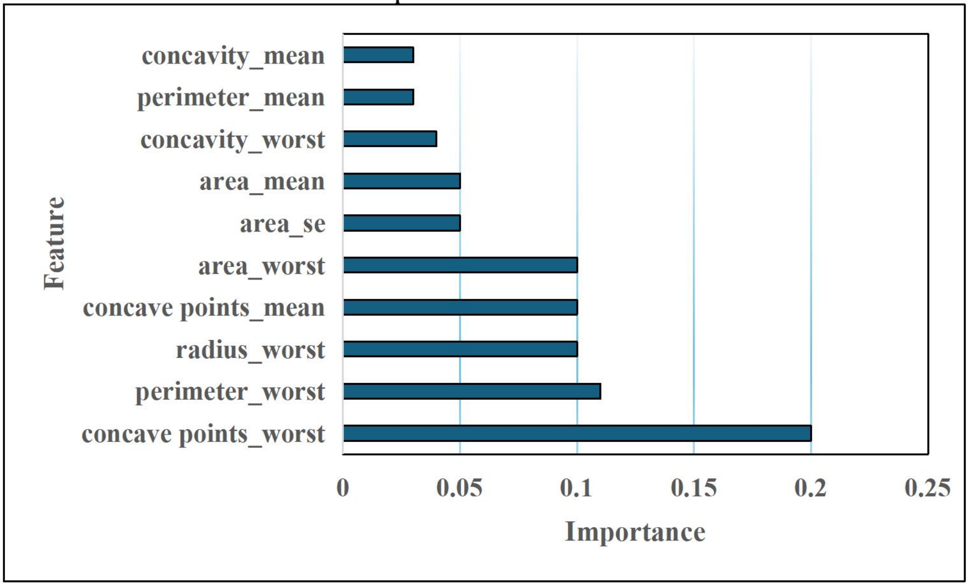

Figure 2. Feature Importance Plot

These results emphasize the clinical importance of morphological characteristics in diagnosing breast cancer. The discovery of important predictive characteristics increases the readability of the model and facilitates its practical use in clinical decision-making.

3.5 Dataset Distribution Analysis

Figure 3 shows the distribution of benign and malignant cases in the dataset. The disproportion of benign cases to malignant cases is moderate, and could indicate that the dataset has a moderate imbalance between the classes. Although this is imbalanced, there was a high level of performance in the applied machine learning models, indicating that learning was achieved by using the available data.

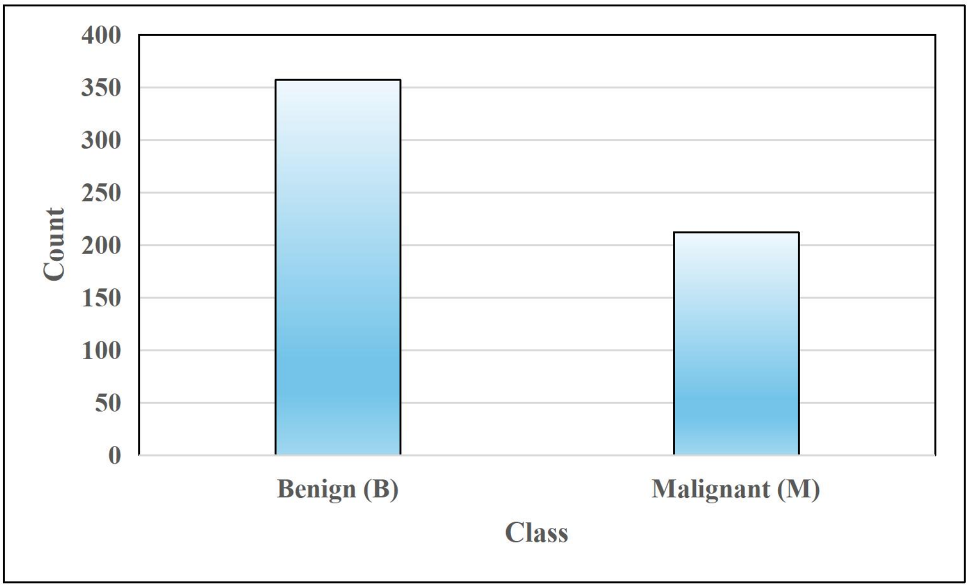

Figure 1. Class Distribution

The distribution of classes is a crucial aspect to understand, which directly affects the model training and evaluation. The findings verify that the effects of the class imbalance can be reduced with the help of proper preprocessing and model selection.

In general, the findings show that machine learning methods can be successfully used to categorize the cases of breast cancer with respect to the analysis of clinical features. Random Forest model proved to be the most suitable and valid model, with good results in all evaluation indicators, confusion matrix results (Figure 1, Table 2) and ROC analysis (Table 3).

Moreover, the analysis of feature importance (Figure 2) demonstrates the importance of particular clinical characteristics, whereas the analysis of dataset distribution (Figure 3) gives some context to the model. These results support the use of an application-oriented machine learning method in diagnosing breast cancer.

4. Discussion

The results of this paper reveal that machine learning methods are effective in accurately diagnosing breast cancer based on clinical features. The findings indicate the sensitivity of choosing the right models, preprocessing methods, and clinically relevant features to attain a stable classification performance. The increased use of machine learning to enhance the accuracy of diagnoses and facilitate the timely diagnosis of breast cancer has also been highlighted by similar studies (Fatima et al., 2020; Elsadig et al., 2023).

The comparative analysis of the various machine learning algorithms shows that machine learning based on ensemble methods (especially the Random Forest) has a higher accuracy, robustness and generalization ability than other machine learning models. This finding is aligned with prior studies, which show that ensemble models are very effective when it comes to dealing with complex medical data (Botlagunta et al., 2023; Syed Yasin et al., 2025). The high-dimensional data and the capacity to control overfitting through the combination of many decision trees explain why Random Forest exhibits better performance. Likewise, Support Vector Machine (SVM) showed a high performance in classification, as was previously in other studies (Agarap, 2018; Bayrak et al., 2019).

The confusion matrix analysis throws more light on the behavior of the model in classification. Results show that most of the predictions fall into the right category and there are few misclassifications. This is especially significant when used in medical applications, where false negatives are of crucial importance. The significance of the reduction of diagnostic errors in order to enhance patient outcomes has been also identified in previous studies (Ahmed et al., 2020; Ara et al., 2021). The low false negative rate in this study shows that the proposed model is reliable in detecting malignant cases.

Another way that proves the effectiveness of the implemented models is the ROC curve analysis. Large AUC values are indicative of high discriminative capacity, crucial to clinical decision-making. The same results were also noted in the literature, with machine learning models showing a high sensitivity and specificity in breast cancer classification tasks (Sengar et al., 2020; Islam et al., 2021). The capability of the models to sustain performance at various thresholds improves their usefulness in real-life health systems.

The role of feature importance analysis in the classification process is significant as it allows the examination of the contribution of each clinical attribute to the classification process. The findings reveal that morphological characteristics of tumors, including concave points, perimeter and radius are the most influential factors in classification. These results are aligned with previous research that highlights the importance of morphological characteristics in the diagnosis of breast cancer (Karatza et al., 2021; Binsaif, 2022). Interpretability of feature importance does not only enhance model transparency, but also aids in clinical decision-making, as it points out important diagnostic features.

The dataset distribution analysis shows a moderate level of class imbalance, a typical issue of medical datasets. In spite of this skew the models showed good performance, implying that skewed data is well managed. This issue has been discussed in past literature and has proposed that the effect of class imbalance can be alleviated with the help of appropriate preprocessing and model selection (Alzu'bi et al., 2021; Chtouki et al., 2022). The findings of this research affirm that proper methods can guarantee effective model execution even when the data is not balanced.

When compared to the current literature, the findings are consistent with the existing literature that promotes the use of machine learning in diagnosing breast cancer. Also, promising outcomes have been demonstrated with advanced methods, such as deep learning and hybrid models, that can enhance diagnostic accuracy (Abdollahi et al., 2022; Amraei et al., 2025). This research however is an application oriented approach, which not only requires predictive performance but interpretability which is most important in the real world.

In spite of the encouraging results, some shortcomings must be mentioned. This research is based on one dataset, and it could restrict the applicability of the results to other populations. Furthermore, although the performance of traditional machine learning models is solid, it may be possible to improve the accuracy of the diagnosis by incorporating deep learning methods and additional data sources (such as multimodal data). Further studies are needed to pursue these directions to create more detailed and scalable diagnostic systems.

Moreover, when applying machine learning models in healthcare, it is important to consider such factors as interpretability, computational efficiency, and integration with the environmental clinical workflow. It has been demonstrated that interpretable models are more prone to be implemented in clinical practice as they offer an element of transparency and confidence in decision-making (Karatza et al., 2021; Ansari et al., 2025).

To summarize, the discussion shows that the machine learning models, specifically, the Random Forest and Support Vector Machine are a promising and efficient tool to diagnose breast cancer through clinical feature analysis. The excellent predictive accuracy, the low misclassification rates, and valuable insights into the features presented indicate the potential of these methods in aiding in early detection and in enhancing patient outcomes. The results support the need to combine the use of data-driven methods and clinical expertise to ensure the creation of strong and practice-focused diagnostic systems.

5. Conclusion

The present study demonstrates the effectiveness of an application-oriented machine learning approach for breast cancer diagnosis using clinical feature analysis. By leveraging structured clinical data and implementing multiple machine learning algorithms, the research successfully achieved high classification accuracy in distinguishing between benign and malignant tumors. Among the evaluated models, ensemble methods, particularly Random Forest, exhibited superior performance due to their ability to handle complex feature interactions and reduce overfitting. The integration of feature importance analysis further enhanced the interpretability of the model by identifying key clinical attributes such as concave points, perimeter, and radius as significant predictors of malignancy. These findings not only align with established medical knowledge but also reinforce the reliability of machine learning models in supporting clinical decision-making. Additionally, the study highlighted the importance of preprocessing techniques, including normalization and feature selection, in improving model efficiency and performance. Despite challenges such as class imbalance and dataset limitations, the models demonstrated robust generalization capability, indicating their potential for real-world application. The results emphasize that combining predictive accuracy with interpretability is essential for developing trustworthy and practical diagnostic systems. Overall, this research contributes to the advancement of intelligent healthcare solutions by providing a scalable and efficient framework for early breast cancer detection. Future work may focus on integrating larger and more diverse datasets, incorporating imaging data, and exploring advanced deep learning techniques to further enhance diagnostic performance and clinical applicability.

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