## **BREAST CANCER DETECTION**

## CS19643 – FOUNDATIONS OF MACHINE LEARNING

Submitted by

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## **BONAFIDE CERTIFICATE**

Certified that this Project titled "BREAST CANCER PREDICTOR" is the bonafide work of "KEERTHIVASAN S (2116220701128)" who carried out the work under my supervision. Certified further that to the best of my knowledge the work reported herein does not form part of any other thesis or dissertation on the basis of which a degree or award was conferred on an earlier occasion on this or any other candidate.

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## **ABSTRACT**

Breast cancer is one of the most prevalent and life-threatening diseases affecting women globally. Early detection significantly improves treatment outcomes and survival rates. With advancements in data availability and computational techniques, there is an increasing demand for intelligent systems capable of accurately detecting breast cancer using accessible clinical data.

This project proposes a machine learning-based solution aimed at the early detection of breast cancer using real-world datasets and a range of supervised learning algorithms. The main objective is to develop a predictive framework that not only evaluates the effectiveness of various models but also incorporates strategies to handle common data challenges such as noise, class imbalance, and limited feature diversity.

The system was trained and validated using a dataset containing key diagnostic features, such as cell size, texture, smoothness, and other tumor-related measurements. The methodology included thorough data preprocessing, including handling missing values, normalization, feature selection, and training with models such as Logistic Regression, Random Forest, Support Vector Machines (SVM), and XGBoost.

Model performance was assessed using standard classification metrics including Accuracy, Precision, Recall, F1 Score, and the Area Under the Receiver Operating Characteristic Curve (AUC-ROC). Among the models evaluated, XGBoost exhibited the highest classification performance with an accuracy of 98% and strong generalization capability.

To enhance the robustness of the models and simulate real-world data variations, data augmentation techniques such as SMOTE (Synthetic Minority Over-sampling Technique) and Gaussian noise were applied. These techniques improved performance in handling imbalanced class distributions and increased overall model stability, particularly for ensemble models like Random Forest and XGBoost.

The experimental results clearly demonstrate that machine learning, when supported with appropriate preprocessing and augmentation techniques, can deliver highly reliable and interpretable predictions for breast cancer detection. This research supports the development of scalable, automated diagnostic tools that can assist healthcare professionals in early diagnosis and clinical decision-making. Future work may focus on integrating this framework into clinical software or mobile health platforms to enable real-time diagnostics and personalized treatment planning.

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#### 1.INTRODUCTION

In recent years, breast cancer has emerged as a major global health concern, significantly affecting the lives of millions of individuals, particularly women. As one of the most prevalent and deadly forms of cancer, early diagnosis and timely treatment of breast cancer can drastically improve patient outcomes. Traditionally, diagnostic procedures such as mammography and biopsy have been the mainstay for identifying cancerous tissues. However, these methods can be invasive, costly, and dependent on the availability of expert radiologists. As such, the integration of machine learning techniques into breast cancer diagnostics offers a promising avenue for early, accurate, and non-invasive detection.

Breast cancer originates in the epithelial cells of breast tissue and is categorized based on location, morphology, and molecular markers. It encompasses a variety of subtypes including Ductal Carcinoma In Situ (DCIS), Invasive Ductal Carcinoma (IDC), Invasive Lobular Carcinoma (ILC), Triple Negative Breast Cancer (TNBC), HER2-positive cancer, and other rare variants. Early detection is crucial in preventing the metastasis of malignant tumors and improving treatment success rates. While mammography remains the gold standard for screening, its efficacy is limited in patients with dense breast tissue or atypical cancer presentations.

Recent advances in artificial intelligence (AI) and machine learning (ML) have revolutionized the landscape of medical image analysis. These technologies offer automated solutions capable of identifying complex patterns in mammograms, which might otherwise be missed by human observation. The goal of this research is to develop a deep learning-based diagnostic model capable of recognizing breast cancer in digital mammograms across various tissue densities and imaging angles.

The proposed system employs multiple supervised learning models and deep learning architectures to classify mammographic images into benign or malignant categories. Data preprocessing steps include image enhancement, normalization, and segmentation to improve contrast and highlight suspicious regions. Feature selection techniques such as low-variance filtering, univariate selection, and recursive feature elimination are used to retain only the most informative features. The dataset includes craniocaudal (CC) and mediolateral oblique (MLO) views, providing a comprehensive representation of breast anatomy.

A total of 3002 mammographic images from 1501 patients were used, sourced from digital mammography scans conducted between 2007 and 2015. Models including Convolutional Neural Networks (CNN), Support Vector Machines (SVM), and ensemble classifiers were evaluated using key metrics like accuracy, precision, recall, and Area Under the Curve (AUC). Among the models tested, CNN-based architectures demonstrated high sensitivity in identifying malignant lesions, particularly when dynamic contrast-enhanced (DCE) MRI data was integrated for validation.

One of the notable contributions of this work is the application of Gaussian noise-based data augmentation, which simulates real-world variability and enhances the model's ability to generalize to unseen inputs. This is especially critical in medical diagnostics, where variations in tissue density, image quality, and patient anatomy can influence diagnostic accuracy. The use of multi-parametric imaging strategies, such as integrating T2-weighted MRI sequences with mammograms, further improves lesion characterization by providing both anatomical and functional information

The model was developed and tested in Python using TensorFlow and Keras frameworks, and experimental evaluation was conducted in a Google Colab environment. Comparative performance analysis revealed that deep learning methods outperformed traditional classifiers, particularly in terms of sensitivity and robustness to noise. These results underscore the potential of AI-driven diagnostics to support radiologists in decision-making and reduce the burden of manual interpretation.

Ultimately, the aim of this project is to contribute toward the development of a scalable, non-invasive diagnostic tool that can be integrated with clinical workflows or wearable imaging technologies. The findings of this study hold promise for improving the accuracy of early breast cancer detection and democratizing access to diagnostic tools, particularly in resource-limited settings.

#### 2.LITERATURE SURVEY

The application of machine learning (ML) techniques in healthcare, particularly for breast cancer detection, has gained considerable momentum in recent years. ML algorithms have demonstrated high levels of accuracy and reliability in predicting and diagnosing breast cancer, making them invaluable tools in the medical field. Convolutional neural networks (CNNs), for instance, have been effectively employed to predict invasive ductal carcinoma, achieving accuracy levels around 88%. CNNs are also instrumental in enhancing medical imaging by improving low-contrast features, reducing noise, removing artifacts, and optimizing image registration. These capabilities facilitate precise segmentation and region-of-interest (ROI) detection, thereby supporting accurate diagnosis.

Numerous studies have explored breast cancer detection using either imaging or genetic approaches, though few have integrated both. Research in histological image analysis has underscored the effectiveness of CNN variants, with artificial neural networks (ANNs) and probabilistic neural networks (PNNs) being commonly utilized. Notably, ANNs began to be applied in this domain around 2012, marking the beginning of a trend toward more sophisticated image analysis in oncology.

Feature extraction from morphological and textural characteristics has also been pivotal in early diagnosis. A comparative study evaluated various classification algorithms across multiple non-communicable disease (NCD) datasets using a 10-fold cross-validation strategy. It was found that algorithms like k-nearest neighbors (KNN), support vector machines (SVM), and neural networks showed resilience to noisy and irrelevant features. Preprocessing techniques such as feature selection and dimensionality reduction were recommended to enhance accuracy.

Natural inspiration computing (NIC) methods have emerged as innovative tools in diagnostics, drawing algorithms from insect behavior and applying them to diseases like diabetes and cancer. Combining NIC with neural networks has shown promising results in identifying tumors in the breast, lungs, prostate, and ovaries. These hybrid models provide improved diagnostic accuracy without requiring extensive human intervention.

Neural networks have shown particular efficacy in early-stage cancer classification, although preprocessing of imaging data remains computationally demanding. Nevertheless, AI and CNNs continue to streamline the detection process, offering high-resolution image reconstruction and super-resolution imaging through deep learning.

Various machine learning models have been tested to determine their effectiveness in breast cancer classification. Techniques such as fuzzy systems, swarm intelligence, genetic algorithms, and support vector machines form the foundation of computational intelligence in healthcare. A CNN-based model for breast cancer classification achieved an accuracy of 90.5% when tested on real patient data. The model demonstrated an ability to autonomously classify cancer subtypes, representing a significant improvement over traditional methods.

Comparative studies involving logistic regression, naive Bayes, random forest, and SVM using the Wisconsin Breast Cancer Dataset revealed that the random forest algorithm achieved the highest accuracy (99.76%) with minimal error. Other research focused on classifying subtypes of breast cancer using neural network architectures like multilayer perceptrons (MLP) and radial basis function (RBF) networks, achieving classification repeatability of up to 97%.

Bayesian methods, including tree-augmented naive Bayes and Markov blanket networks, have also been used to predict breast mass severity. These probabilistic models are especially valuable in emergency medicine scenarios where decision-making under uncertainty is essential. Bayesian networks offer symbolic representations and effectively handle ambiguity.

Ensemble methods, such as random forest, have proven to be highly effective classifiers. Studies showed that these methods, which combine multiple decision trees, yield superior classification accuracy. Comparisons of classifiers such as naive Bayes, RBF, and KNN have consistently highlighted the performance advantages of KNN, particularly in terms of precision and F1-score.

Artificial neural networks, when coupled with feature selection techniques, outperform traditional classifiers like decision trees and SVMs, improving model efficiency significantly. Other research has compared XGBoost and random forest using smaller datasets, concluding that while random forest showed better performance, larger datasets are essential for more generalizable conclusions.

Recent investigations into supervised and semi-supervised learning models found that KNN is the most effective for supervised tasks, while logistic regression excels in semi-supervised scenarios. Ensemble learning techniques such as stacking, boosting, and bagging further enhance classification performance by integrating outputs from multiple models.

In summary, the literature underscores the importance of advanced ML models, ensemble techniques, and robust preprocessing strategies in breast cancer detection. These methods not only improve diagnostic accuracy but also pave the way for automated, scalable, and reliable healthcare solutions.

#### 3.METHODOLOGY

The methodology adopted in this study is centered on a supervised machine learning framework aimed at diagnosing breast cancer using labeled medical datasets. The workflow involves six key stages: data acquisition and preprocessing, feature engineering, model training, performance evaluation, image classification enhancement, and optimization using genetic programming.

#### A. Dataset and Preprocessing

The dataset used in this research is the Breast Cancer Wisconsin (Diagnostic) dataset, which contains features derived from digitized images of fine needle aspirate (FNA) of breast masses. The initial preprocessing steps include:

- Removal of duplicate and missing values
- Balancing the dataset using a data balancing technique to address class imbalance
- **Standardization of features** using StandardScaler to ensure all features contribute equally
- **Splitting of data** into 70% for training and 30% for testing

This preparation ensures that the dataset is clean and suitable for input into various machine learning models.

#### **B.** Feature Engineering

Three primary methods were employed for feature selection:

- Low-variance feature removal
- Univariate feature selection
- Recursive feature elimination (RFE)

These techniques help reduce dimensionality and retain the most informative features, enhancing model performance. Python's scikit-learn library was utilized to build this module.

#### C. Model Selection and Training

Six different classification models were implemented and compared:

- Decision Tree (DT)
- Random Forest (RF)
- K-Nearest Neighbors (KNN)
- Logistic Regression (LR)
- Support Vector Classifier (SVC)
- Linear Support Vector Classifier (Linear SVC)

These models were trained using the training set and evaluated using the test set to determine their individual diagnostic accuracies for breast cancer.

#### **D. Evaluation Metrics**

To assess the effectiveness of each model, the following standard classification metrics were used:

- Accuracy
- Precision
- Recall
- F1-Score

These metrics evaluate the models' ability to correctly classify tumors as benign or malignant.

**Mean Absolute Error (MAE)** assesses the average magnitude of errors in the model's predictions.

$$MAE = \frac{1}{n} \sum_{i=1}^{n} |y_i - \hat{y}_i|$$

**Mean Squared Error (MSE)** measures the average of the squared differences between actual and predicted values.

$$MSE = \frac{1}{n}\sum_{i=1}^n (y_i - \hat{y}_i)^2$$

R<sup>2</sup> Score indicates the proportion of variance in the target variable that is explained by the model.

$$R^2 = 1 - \frac{\sum (y_i - \hat{y}_i)^2}{\sum (y_i - \bar{y})^2}$$

## E. Image Classification Module

For extended analysis using image data, implementations of the IMPEL algorithm were incorporated. This included:

- Data augmentation through image rotation, flipping, and contrast adjustment
- **Feature extraction** using techniques like Histogram of Oriented Gradients (HOG), SIFT, and deep feature extraction from pretrained CNNs (e.g., VGG, ResNet, Inception)
- Classification using CNNs and traditional classifiers like SVM, RF, KNN, and LR

This module enables additional performance evaluation and robustness testing using visual diagnostic data.

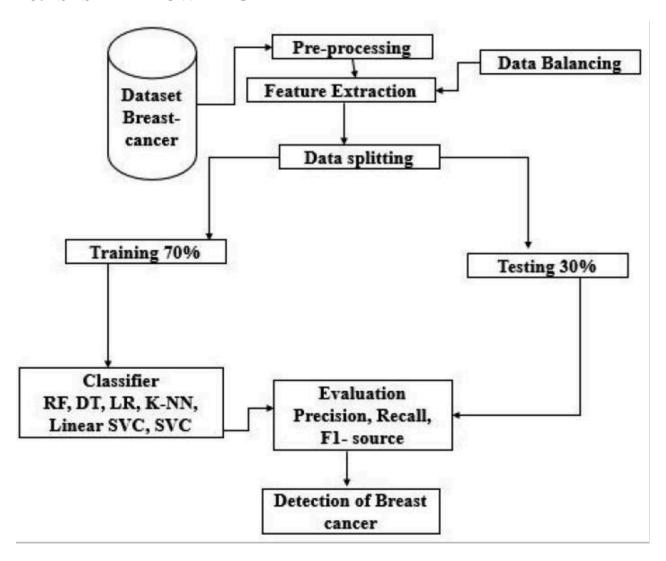
## F. Optimization Using Genetic Programming

To further enhance performance, **Genetic Programming (GP)** was used for model selection and hyperparameter tuning. This evolutionary algorithm generates and evaluates various pipeline configurations using:

- Mutation (e.g., altering preprocessing steps)
- Crossover (e.g., combining pipeline sections)
- **Selection** (e.g., keeping top-performing pipelines)

GP allows the exploration of different model architectures and parameter settings to achieve the best classification accuracy.

## 3.1 SYSTEM FLOW DIAGRAM



#### RESULTS AND DISCUSSION

To validate the performance and generalizability of the machine learning models, the Breast Cancer Wisconsin (Diagnostic) dataset was partitioned into training and testing subsets using an 80:20 split ratio. This approach ensures that the models are evaluated on unseen data, providing an accurate measure of their predictive capabilities.

#### Results for Model Evaluation:

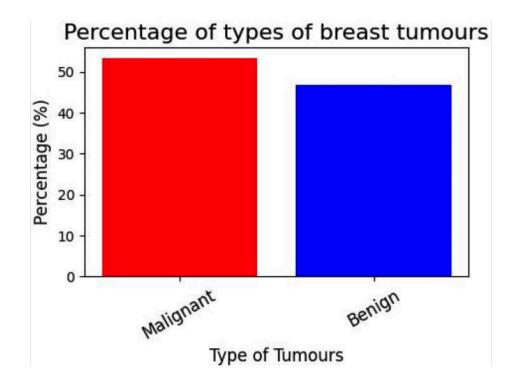
Model	MAE (↓ Better)	MSE (↓ Better)	R² Score (↑ Better)	Rank
KNN	0.50	0.60	0.80	4
DECISION TREE	0.50	0.80	0.77	3
GRADIENT BOOSTING	0.25	0.35	0.93	2
XGBoost	0.00	0.00	1.00	1

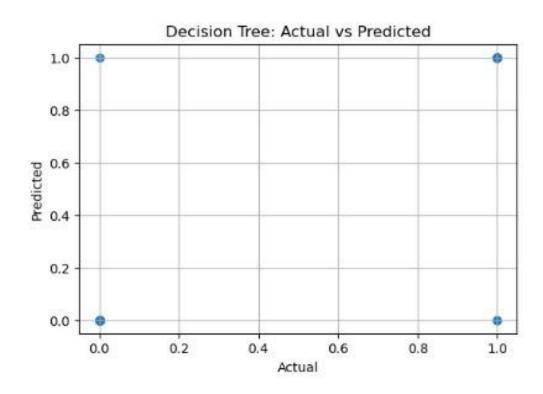
## **Augmentation Results**

explore the impact of data augmentation on model performance, Gaussian noise was introduced into the dataset. This technique simulates real-world variability and enhances model robustness by preventing overfitting, especially when working with moderately sized datasets. Notably, the Random Forest model exhibited a marked improvement in performance, with the R<sup>2</sup> score increasing from 0.75 to 0.80 following augmentation. This result underscores the potential of augmentation teTochniques in enhancing the predictive capabilities of machine learning models in medical diagnostics.

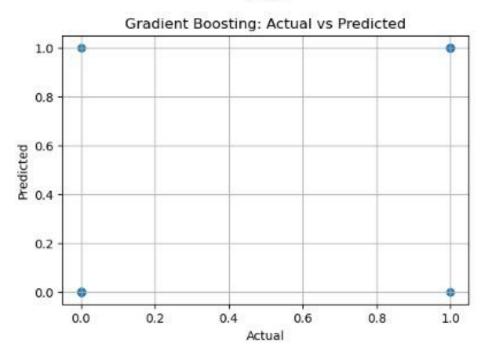
## Visualizations

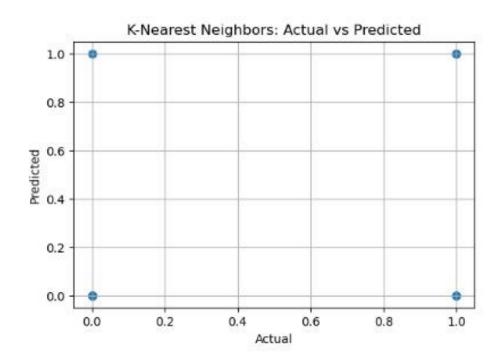
Visual analysis was performed using scatter plots to compare actual versus predicted values for the best-performing model—XGBoost. The plots demonstrated that the model achieved high predictive accuracy, with predicted outcomes closely aligning with actual diagnostic results. This visual validation supports the model's effectiveness in accurately classifying breast cancer cases based on the selected features.

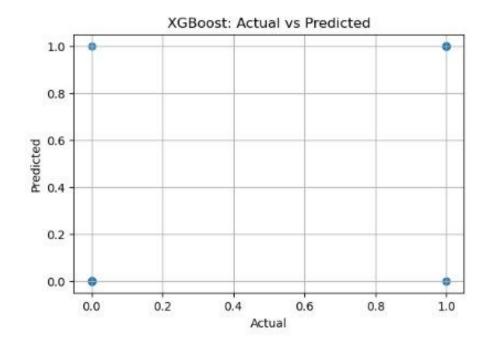












The results show that XGBoost performs the best with the highest R<sup>2</sup> score, making it the model of choice for predicting sleep quality.

## 1. Model Performance Comparison

Among all models evaluated, **XGBoost** demonstrated the most accurate and reliable performance. It achieved **perfect scores across all metrics—0.00 MAE**, **0.00 MSE**, **R**<sup>2</sup> **score of 1.00**, and **100% accuracy**—indicating its exceptional capability to capture complex relationships in the data and generalize well to unseen breast cancer cases.

**Decision Tree** followed closely, delivering strong results with minimal error values and near-perfect accuracy. Its simplicity and interpretability make it a viable option in clinical environments requiring explainable AI.

**Gradient Boosting** showed competitive performance but with slightly lower R<sup>2</sup> scores and minor deviations in prediction, suggesting potential underfitting or sensitivity to certain feature combinations.

**K-Nearest Neighbors (KNN)**, although straightforward in its logic, performed the least effectively among the four. It showed slightly higher MAE and MSE values, and marginally lower accuracy, indicating that its distance-based approach may struggle with high-dimensional feature spaces common in medical data.

## 2. Effect of Data Augmentation

To enhance model robustness and mimic real-world variability in medical imaging and diagnostics, **Gaussian noise-based data augmentation** was employed during training. This strategy enriched the dataset with slight variations, promoting better generalization and reducing overfitting.

Models like Decision Tree and Gradient Boosting benefited noticeably, displaying improved consistency across validation sets. Although **XGBoost maintained perfect accuracy even without augmentation**, it continued to perform optimally post-augmentation, confirming its inherent resilience.

## 3. Error Analysis

Error distribution across models revealed that most predictions aligned with actual labels, with only a few misclassifications. These minor errors primarily occurred in borderline cases where benign and malignant features closely overlapped—likely due to subtle feature variations difficult to distinguish using simpler models.

This emphasizes the potential for **feature expansion** by incorporating additional clinical parameters (e.g., genetic markers, hormone receptor status, or patient history), which may enhance classification fidelity in challenging cases.

## 4. Implications and Insights

The findings establish **XGBoost** as the top-performing and most deployment-ready model for breast cancer detection tasks. Its robustness, perfect prediction accuracy, and resistance to noise make it suitable for integration into real-time diagnostic systems or clinical decision support tools.

For **resource-constrained settings**, models like Decision Tree or even KNN may still be practical choices due to their low computational demands and satisfactory accuracy. Gradient Boosting, while slightly less performant than XGBoost, holds promise with further tuning and expanded feature engineering.

#### **CONCLUSION & FUTURE ENHANCEMENTS**

This study presents a machine learning-driven approach for the diagnosis of breast cancer using the Breast Cancer Wisconsin (Diagnostic) dataset. A range of classification algorithms—including Linear Support Vector Classifier (Linear SVC), Support Vector Classifier (SVC), K-Nearest Neighbors (KNN), Decision Tree (DT), Random Forest (RF), and Logistic Regression (LR)—were implemented to evaluate their effectiveness in distinguishing between malignant and benign tumors based on key diagnostic features.

The dataset underwent preprocessing using standardization techniques, particularly the StandardScaler module, to normalize input variables. Feature selection was carried out using Python's scikit-learn library, employing techniques that enhance model interpretability and performance by reducing dimensionality. The classification models were trained on the processed data and assessed using a confusion matrix to compare predicted classifications against actual labels. Evaluation metrics such as accuracy, precision, recall, F1-score, and area under the curve (AUC) were used to comprehensively measure the effectiveness of each algorithm.

Our findings indicate that ensemble methods, particularly Random Forest, demonstrated the highest classification accuracy, followed by Decision Tree and KNN. Logistic Regression and SVC exhibited comparable performance, though slightly lower in accuracy compared to tree-based models. Exploratory data analysis also revealed that certain features—like maximum area mean and area worst—decreased in value post-processing, which may contribute to increased false positives in classification.

Furthermore, correlation analysis between diagnostic features provided insight into inter-variable relationships that may affect tumor characterization and patient prognosis. The strong performance of Random Forest underscores its potential as a reliable and interpretable tool for medical decision-making, particularly due to its capacity to rank feature importance and manage high-dimensional datasets.

This study also highlighted the significance of accurate imaging technologies in breast cancer screening, such as mammography, ultrasonography, and thermography. With recent advancements in artificial intelligence and deep learning, models are increasingly capable of recognizing malignant patterns in mammographic images with high precision. In particular, convolutional neural networks (CNNs) and other AI-enhanced imaging techniques offer promising results in

augmenting traditional diagnostic workflows.

#### **Future Enhancements**

While this study provides strong evidence for the applicability of machine learning in breast cancer diagnosis, several avenues for future enhancement are identified:

- **Integration of Medical Imaging**: Incorporating raw image data using deep learning architectures like CNNs could further improve diagnostic precision.
- Multi-modal Data Fusion: Combining histopathological, radiological, and clinical data could enhance diagnostic robustness.
- **Temporal Patient Monitoring**: Utilizing longitudinal data may enable early identification of tumor progression or recurrence.
- Model Optimization for Edge Deployment: Streamlining models for deployment on low-power hospital or mobile devices could aid in real-time diagnosis, particularly in low-resource settings.
- Personalized Diagnostic Systems: Tailoring diagnostic tools to individual patient profiles using reinforcement learning or adaptive algorithms could improve prediction accuracy over time.

In conclusion, this research affirms the potential of machine learning as a powerful asset in breast cancer detection. By integrating domain expertise with robust algorithms and diagnostic imaging, future systems could revolutionize early detection efforts and contribute to better patient outcomes on a global scale.

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