**A Data-Driven Approach to Breast Cancer Prediction: Integrating Machine Learning for Clinical Decision Support**

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**Abstract.** The abstract should summarize the contents of the paper in short terms, i.e. 150-250 words.

**Keywords:** Breast Cancer, Machine Learning, Clinical Disease Support,Predictive Modeling, Artificial Intelligence, Healthcare Analytics.

1. **Introduction**

Breast cancer is among the most common cancers across the globe. It is one of the most common women's cancers worldwide and a major international health issue. It happens when breast cells start to grow abnormally and uncontrollably. The early symptoms in a patient often serve as warning signs of the development of cancerous cells in the body. According to the GLOBOCAN 2020 report, cancer is still a major cause of global health problems, with 19.3 million new cases and 10 million deaths reported in 2020[13]. Among these, female breast cancer accounted for 2.3 million new cases, highlighting a concerning rise in incidence and mortality [14]. Statistically, roughly 1 in 8 women are diagnosed with breast cancer in their lifetime. In South Asian countries like Bangladesh, breast cancer is the second most common cancer among women and is often detected at a late stage, which lowers the chances of effective treatment [15].

Traditional treatment techniques include surgery, chemotherapy, and radiation therapy, which each play vital roles in the handling of the illness. Human frailties in the form of errors, postponed diagnosis, and inaccessibility of medical facilities—most forcefully in resource-scarce settings—are, however, still creating challenges to prompt and accurate diagnosis. Therefore, early detection and correct classification of breast cancer remain essential in enhancing outcomes and reducing the health system burden.

In the past decade, machine learning (ML) has been a promising technology in medical diagnosis that can identify subtle patterns in clinical and diagnostic data that are imperceptible to traditional methods. ML models have been effective in tumor detection at early stages, risk assessment for patients, and diagnostic decision support. Most of the current ML-based breast cancer prediction models are black boxes, lacking interpretability and clinical trustworthiness. In addition to that, the majority of the existing studies prioritize the enhancement of classification performance, regardless of the need for transparency and compatibility with actual clinical workflows. This leaves a wide gap between technical achievement in ML and real-world usability in daily clinical practice, especially in low-resource settings.

The purpose of this study is to develop a machine learning–based breast cancer prediction and clinical decision support system. The research objectives are as follows:

1. To identify the most influential features contributing to breast cancer diagnosis using interpretability tools like SHAP.
2. To create and evaluate a valid predictive model that will aid clinicians in diagnosing breast cancer.
3. To develop a clinically applicable decision support system that incorporates machine learning predictions into the diagnostic workflow  
   in a clinical environment.

This investigation is directed by the following questions:

1. Which are the most significant features to predict malignant vs. benign tumors?
2. How can SHAP or other interpretability methods render model decisions interpretable and understandable to clinicians?
3. What are the strengths and limitations of data-driven predictive models in the clinical setting?

To address these objectives, we utilize the Breast Cancer Wisconsin dataset and apply the XGBoost algorithm for binary classification. For interpretability, we use SHAP (SHapley Additive exPlanations) to highlight the most influential features impacting the model's predictions. We visualize the model explanations using SHAP’s summary\_plot to present overall feature importance, and force\_plot to provide local explanations for individual predictions. These tools help bridge the gap between model accuracy and clinical transparency, making the system more trustworthy and usable in real-world diagnostic settings.

1. **Literature Review**

Shen et al.(2019) developed a CNN model to detect Breast Cancer from biopsies and microscopic images. The efficacy of Shen et al.'s approach was rigorously evaluated on two widely recognized public datasets: the Digital Database for Screening Mammography (DDSM) / CBIS-DDSM and INbreast. For the INbreast dataset, the best single model achieved an impressive per-image AUC of 0.95, with four-model averaging further improving it to 0.98 (sensitivity: 86.7%, specificity: 96.1%), and for the DDSM dataset, the best single model achieved a per-image Area Under the Curve (AUC) score of 0.88, which improved to 0.91 with three-model averaging[1].

Siham et al.(2020) focused on how to preprocess data to deal with imbalanced data that have missing values using resampling techniques to enhance the classification accuracy of detecting breast cancer. The three classifiers (NB, SMO, J48) were tested over original data. The accuracy was respectively 71.67%, 69.58%, 75.52%. After applying a discretization filter and removing the records with missing values, results improved. After that, a resample filter was applied for 7 times, then the accuracy was 98.20%(J48), 76.61%(NB), 95.32%(SMO)[2].

The study presented to detect Breast cancer that machine learning technique is good enough on linear data. But, when the data form is imaged the machine learning technique fails. For the classification of the breast cancer images data Kumar (2021) claimed that a deep learning based technique CNN gives better results as compared to machine learning techniques[3].

Kumar al(2022) trained machine learning models with some python libraries such as numpy, pandas, matplotlib. They trained K-nearest neighbor(KNN), Support vector machine(SVM), Decision tree classifier with that library. They used the Breast malignant growth dataset which was recovered utilizing the UCI archive. The accuracy of those models were 95%(KNN), 96%(SVM) and 93%(DTC)[4].

The study introduced the internal functionality of machine learning algorithms. Abien (2018) used the Wisconsin Diagnostic Dataset to train models. GRU-SVM, Linear Regression, MLP, Nearest Neighbor Softmax Regression, SVM algorithms used to train data. The activation function was used for GRU-SVM as like "Sigmoid" or "ReLU". For Nearest Neighbor used Norm function L1 and L2 both. MLP used ReLU as an activation function. Then, trained the models with 128 batch size and 3000 epochs (Nearest Neighbor's is just 1 epoch). The accuracy of those models was above 90%[5].

Breast al (2020) proposed a new method that Deep Neural Network with Support Value(DNNS) which introduced better quality images and fixed other performance parameters. They discussed the internal process of DNNS. Then, they analyzed the performance according to some other methodology like Naive Bayes, SVM, RCNN classifier, Bidirectional Recurrent Neural Networks.The accuracy of the DNNS method was 97.21 and it was the best result of all of those methods[6].

Liu et al. (2024) developed a clinical decision support tool using SHAP values to predict breast cancer recurrence. The study showed a high predictive accuracy of 0.97 with Extra Trees and 0.96 with Random Forest but also pointed out key limitations, especially concerning data quality and the limited size and diversity of the dataset[7].

Gurcan (2025) introduced an advanced framework for breast cancer diagnosis using deep learning combined with stacking ensemble techniques. The framework incorporates models such as LightGBM, CatBoost, and a CNN-based meta-predictor. The proposed model delivers high accuracy, enhanced F1 scores, and faster training times to support efficient healthcare decision-making. However, the use of complex deep learning and ensemble models increases computational demands, potentially limiting real-time use in resource-constrained settings[8].

Ayepeku (2024) conducted a comprehensive analysis of breast cancer prediction, comparing various machine learning models such as Logistic Regression, Random Forest, Support Vector Classifier, and ensemble methods like Gradient Boosting and AdaBoost. The study uses comprehensive metrics and visualization to assess models but faces typical issues with data quality and availability, while lacking discussion on real-time deployment, which limits practical clinical integration despite strong analytical insights[9].

Patil et al. (2023) investigated early breast cancer prediction by comparing multiple machine learning and deep learning techniques, including SVM, KNN, Naïve Bayes, Logistic Regression, Random Forest, Decision Tree, XGB Classifier, and Artificial Neural Networks (ANN). The study highlights feature selection’s role in boosting accuracy, with SVM reaching 98.24%, but also notes ongoing challenges with data quality and availability. Moreover, the paper highlights model performance comparisons but overlooks real-time deployment and clinical integration, limiting practical use for early breast cancer detection [10].

Öznacar & Ergene (2024) examined the potential of machine learning techniques, including AdaBoost, SVM, Random Forest, and Logistic Regression, for early detection and malignancy prediction in breast cancer. The study highlights that the AdaBoost model showed the highest performance reaching 93.60% AUC and 95.65% precision. However, the study emphasizes the limitations of traditional breast cancer diagnostics, advocating for AI-based improvements, yet it overlooks challenges like data bias and the need for broad clinical validation [11].

Rb et al. (2024) proposed a novel approach for early breast cancer prediction using an ensemble of machine-learning algorithms, including KNN, Naive Bayes, SVM, and Decision Tree Classifier, enhancing predictive capabilities and improving early detection and patient outcomes. The authors demonstrated that using ensemble machine learning algorithms enhances early breast cancer detection accuracy, offering practical benefits for regions with limited medical resources. Additionally, the study emphasizes that Logistic Regression offers efficient and interpretable results, while SVM excels in accuracy with high-dimensional data [12].

**3 Methodology**

**3.1** **Data Preprocessing**

The Breast Cancer Wisconsin (Diagnostic) Data Set is used for this research. Since the dataset is highly systematic, there are no missing values present in this dataset. The target feature "Diagnosis" was encoded using the LabelEncoder() class, where malignant cases were encoded as 1 (positive) and benign cases as 0 (negative). Min-Max scaling is then used to normalize the features and place them on the same scale for all continuous variables between [0, 1]. Scaling the data assists the model that is based on distances between data points or constructs decision trees, such as XGBoost, to learn more quickly and make more accurate predictions.

**3.2** **Model Selection**

XGBoost (eXtreme Gradient Boosting) is selected as the classification algorithm since it works well with structured and tabular data. XGBoost is very accurate, possesses regularization methods to stop overfitting, and can handle linear and non-linear patterns very effectively. It also allows feature importance analysis, which would make it appropriate for interpretability research. Besides, the model is very efficient and scalable and can handle small- and large-scale datasets.

**3.3** **Model Training and Validation**

The data is divided into training and testing sets, where 60% is utilized for training and 40% is kept for testing. The division is done to test the model's generalization capability on new data.

**3.4** **Evaluation Metrics:** Here the model evaluation is,

* **Accuracy:** The accuracy is the ratio of correct predictions of being malignant to the total number of predictions[formula 1]. It's the most useful method for evaluating a model.

[1]

* **Precision:** Precision is an important evaluation metric, particularly in classification tasks and it's important to understand its role with other metrics like accuracy and recall. It represents among all the cases the model predicted as malignant, how many were actually malignant [formula 2].

[2]

* **Recall:** Recall (also known as sensitivity or true positive rate) measures the proportion of actual positive instances that your model correctly identified. It represents the formula. It represents, among all the cases of actual malignant tumors, how many the model correctly detected. [3]

[3]

* **F1-score:** The F1 score is a necessary metric in machine learning, especially for classification problems. Because it provides a single, balanced measurement that considers both precision and recall. It represents the formula [4]

[4]

* **ROC-AUC:** ROC-AUC(Receiver Operating Characteristic - Area Under the Curve) helps you understand how well your model can rank predictions, from most likely positive to most likely negative, independent of any specific decision threshold.

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