Breast Cancer Detection Using Machine Learning

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Abstract—**Breast cancer is still one of the leading and life-threatening conditions globally, requiring early and precise diagnosis for better outcomes in patients. Conventional diagnostic techniques, including biopsy and mammography, tend to fall short in terms of sensitivity and specificity. Machine learning (ML) has proven to be an influential means of improving detection of breast cancer through automated classification, high accuracy, and minimized false positives. Herein, we suggest an ML model for the detection of breast cancer that leverages feature selection methods to maximize the performance of predictions. The suggested model is tested and trained using the Wisconsin Breast Cancer Dataset (WBCD) and encompasses a number of supervised learning techniques like Support Vector Machines (SVM), Random Forest (RF), Artificial Neural Networks (ANN), and XGBoost. We measure the performance of the model based on the most important performance metrics, such as accuracy, precision, recall, and F1-score. The experimental results show that the model has a high classification accuracy compared to conventional diagnostic methods. This work makes a contribution to medical AI by presenting a strong, data-driven framework for breast cancer diagnosis, which can potentially help healthcare professionals make more accurate and timely clinical decisions.**

Keywords—Breast Cancer Detection, Machine Learning, Classification, Feature Selection, Supervised Learning.

I. INTRODUCTION

Breast cancer is among the major causes of death in women globally, and hence early detection is important for enhancing survival. Traditional diagnostic techniques like mammography, ultrasound, and biopsy are commonly employed but have limitations like human error, high expense, and delay in diagnosis. These drawbacks emphasize the importance of more effective and precise diagnostic techniques. Machine learning (ML) has recently been identified as a potential answer to improve the detection of breast cancer by using computational intelligence to classify automatically.

Machine learning algorithms can process large amounts of data, recognize patterns, and classify tumors as benign or malignant with very high accuracy. Different supervised learning methods, including Support Vector Machines (SVM), Random Forest (RF), Artificial Neural Networks (ANN), and XGBoost, have been used successfully in breast cancer prediction problems. These algorithms use feature selection and optimization methods to enhance diagnostic precision while reducing false positives and false negatives.

This research seeks to establish a strong ML-based system for breast cancer diagnosis, trained on the Wisconsin Breast Cancer Dataset (WBCD). The suggested method compares various ML models to identify the best classifier in terms of major performance measures such as accuracy, precision, recall, and F1-score. Our aim is to design a trustworthy, data-driven system that can help medical practitioners make quicker and more accurate clinical decisions.

The rest of this paper is structured as follows: Section II provides an overview of existing research on ML-based breast cancer detection. Section III describes the proposed method, including data preprocessing, feature selection, and model evaluation methods. Section IV provides experimental results and performance comparisons. Lastly, Section V concludes the research with directions for future research.

A. Motivation

Breast cancer continues to be a major cause of cancer mortality, and thus there is a demand for early and precise diagnosis. Conventional techniques like mammography and biopsy are plagued by high expense, human mistakes, and poor accessibility, rendering them unsuitable for mass screening.Machine learning (ML) has proven to be a significant aid in the automation of breast cancer detection, enhanced diagnostic precision, and lower false positives. Utilizing supervised learning algorithms such as SVM, Random Forest, ANN, and XGBoost, ML models are capable of interpreting intricate medical data and supporting quicker, more accurate diagnosis.The aim of this research is to propose an optimized ML-based breast cancer detection system with improved classification performance and overcoming traditional diagnosis challenges. The final vision is to aid in a cost-effective, efficient, and intelligent diagnostic system for supporting healthcare practitioners in making rational decisions.

B. Contribution

The primary contributions of this work are as follows:

- Feature Selection for Breast Cancer Classification: This work brings forward the importance of choosing informative features while performing machine learning-based breast cancer classification. The research selects the top 15 features from the Wisconsin Breast Cancer Dataset through Mutual Information-based Feature Selection with the goal of achieving a trade-off between model complexity and accuracy.
- Stacking-Based Model for Higher Accuracy: We introduce a Stacking-based Machine Learning Model, where Random Forest, XGBoost, and Logistic Regression are used as a meta-learner to enhance classification accuracy. This model boosts the precision and recall, which are essential for medical diagnosis.
- Experimental Validation and Model Comparison: We perform large-scale experiments to compare the performance of the designed model with other conventional classifiers like K-Nearest Neighbors (KNN), Naïve Bayes, and Logistic Regression. Experimental results show that our stacking model performs better than these conventional classifiers in identifying malignant and benign tumors.
- Impact on Early Cancer Detection: The model offered here is a robust and effective solution for detecting early-stage breast cancer, reducing false negatives, and enhancing clinical decision-making.

C. Organisation

The rest of this paper is structured in the following manner:

- Section II is a comprehensive literature review and discusses existing research on breast cancer diagnosis with machine learning algorithms.

- Section III outlines data acquisition and preprocessing steps, which include feature extraction, data balancing, and normalization.
- Section IV presents the proposed stacking-based model, describing the base learners, meta-learner, and the general architecture.
- Section V presents a detailed analysis of the model by comparing it with other machine learning models based on accuracy, precision, recall, and F1-score.
- Section VI summarizes the conclusions of the study and posits directions for future studies on enhancing breast cancer classification models.

II. LITERATURE SURVEY

Breast cancer Integration of artificial intelligence (AI) and machine learning to detect breast cancer has been intensively studied with the aim to enhance early detection, accuracy of classification, and reliability of predictive models. Traditionally, traditional machine learning approaches, ensemble-based learning algorithms, feature selection tools, and deep learning strategies were developed and extensively used for promoting the performance of breast cancer classification. In the following section, the research advancements made to this field so far are critically appraised.

Street et al. [2] were among the first to adopt an early automated breast cancer diagnosis approach by bringing about nuclear feature extraction, thus paving the way for computational tumor classification. Classic machine learning methods like Logistic Regression, K-Nearest Neighbors (KNN), and Naïve Bayes were applied to detect breast cancer [12], but they are usually restricted by difficulties in dealing with high-dimensional medical data.

Breiman [3] presented Random Forest as a strong ensemble learning method to decrease variance and improve generalization in order to enhance prediction accuracy. Chen and Guestrin [4] further improved ensemble learning by creating XGBoost, a gradient boosting algorithm that is efficient in handling missing values and feature selection. These ensemble algorithms have found widespread use in the classification of breast cancer because they can enhance the accuracy of prediction. Dietterich [5] proved that ensemble learning was far more effective in improving the robustness of models compared to single classifiers, citing the advantage of aggregating several algorithms.

Feature selection is significant in minimizing model inefficiency by removing irrelevant characteristics. Vergara and Estévez [7] investigated the application of Mutual Information-based Feature Selection, which determines the most informative features in medical datasets, enhancing model efficiency. Class imbalance is a significant problem in medical applications. Chawla et al. [8] presented SMOTE (Synthetic Minority Over-sampling Technique), a technique that creates synthetic samples to balance the dataset, thus enhancing classification performance. Wolpert [9] introduced Stacked Generalization (Stacking), a sophisticated ensemble learning approach that

aggregates several base classifiers with a meta-learner to promote predictive accuracy.

Deep learning methods have been used for breast cancer detection, especially in image-based analysis. Arevalo et al. [13] introduced a Convolutional Neural Network (CNN)-based model for mass lesion classification of mammograms, proving deep learning's ability in medical imaging. Esteva et al. [14] continued the investigation of deep learning-capable medical vision systems, exhibiting their ability to detect anomalies in radiological images. Shinde et al. [22] proposed transfer learning-based detection of breast cancer, identifying the potential of pre-trained CNN models in decreasing computational complexity and enhancing classification accuracy.

Interpretability is still a major challenge in medical AI. Lundberg and Lee [10] introduced SHAP (SHapley Additive Explanations), an approach enhancing model transparency by attributing feature contributions to predictions. Patel et al. [20] used explainable AI in breast cancer classification via Random Forest, showing the significance of model interpretability in high-stakes medical decision-making. Further, Xie et al. [23] studied Bayesian Optimization for hyperparameter tuning to enhance model performance in medical AI applications.

Current studies have centered on hybrid AI models that incorporate diverse learning paradigms for improved performance. Zhang et al. [15] developed an ensemble learning architecture based on heterogeneous models for breast cancer classification, demonstrating that ensemble methods are better than individual classifiers. Zhou et al. [16] developed a hybrid deep learning model that combines CNNs and conventional machine learning classifiers to develop better predictive capabilities. Wu et al. [17] have investigated radiomics-based classification of breast cancer, presenting the use of radiological imaging in conjunction with AI for enhanced diagnosis.

III. EXPERIMENT SECTION

A. Dataset Collection

The data set employed in this research was obtained from the Wisconsin Breast Cancer Dataset, which is publicly hosted on Kaggle. The data set is commonly used for breast cancer detection studies and has features extracted from fine needle aspiration (FNA) of breast masses. Every example in the dataset is classified as Malignant (cancerous) or Benign (not cancerous), so it's a binary classification problem.The data has 30 numeric features like mean radius, mean texture, mean perimeter, mean smoothness, and many other cell nucleus features. They are very important in the separation of benign from malignant tumors.

B. Data Preparation

To make the data suitable for machine learning models,a few pre-processing steps were taken:

1) Missing Data Handling : Missing values were verified in the dataset, and columns with missing or irrelevant data (e.g., patient ID) were dropped to avoid model training bias.

2) Feature Encoding : All the features in the dataset are numerical. Thus, no categorical encoding was necessary. The target variable, Diagnosis, was labeled originally as 'M' for Malignant and 'B' for Benign. To aid in classification, this was changed to binary format, 1 for Malignant and 0 for Benign.

3) Feature Scaling: The characteristics had different numerical ranges, which would adversely affect model performance. For uniformity, StandardScaler was applied to normalize the data, scaling each characteristic to have a mean of 0 and standard deviation of 1.

4) Class Imbalance Handling: In the medical datasets, class imbalance results in biased predictions towards the majority class. This was countered using Synthetic Minority Over-sampling Technique (SMOTE) to balance the dataset by creating synthetic samples for the minority class.

5) Feature Selection : Not all features are equally important in classification. Mutual Information-based Feature Selection was used to rank features according to their importance with respect to the target variable. The 15 most informative features were chosen to balance model performance and complexity reduction.

IV. PROPOSED MODEL

In this paper, we are proposing a Stacking-based Ensemble Learning method for improving the precision and reliability of breast cancer classification. Stacking is a meta-learning algorithm that combines several machine learning models in order to give a more general and precise prediction. Rather than depending on an individual classifier, our method employs the complementary capability of various base models and a meta-learner in order to make the classification of breast cancer more robust.

A. Feature Selection and Pre-processing

Prior to constructing the model, Mutual Information-based Feature Selection was used to select the most informative features from the dataset. The 15 most significant features were chosen based on their ability to distinguish between malignant and benign conditions. Standard Scaling was also used to scale feature values to have similar magnitudes, making the data consistent in different numerical ranges. To deal with class imbalance, Synthetic Minority Over-sampling Technique (SMOTE) was used to create synthetic samples for the minority class to enhance classification fairness.

B. Model Architecture

The stacking model has two main components:

1) Base Learners: The base learners are tasked with learning varied patterns in the dataset. We have chosen:

Random Forest (RF): A model based on trees that performs well on intricate patterns and feature interactions.

XGBoost (Extreme Gradient Boosting): A boosting method that is famous for its classification performance at high levels, especially on structured data.Each base model was trained
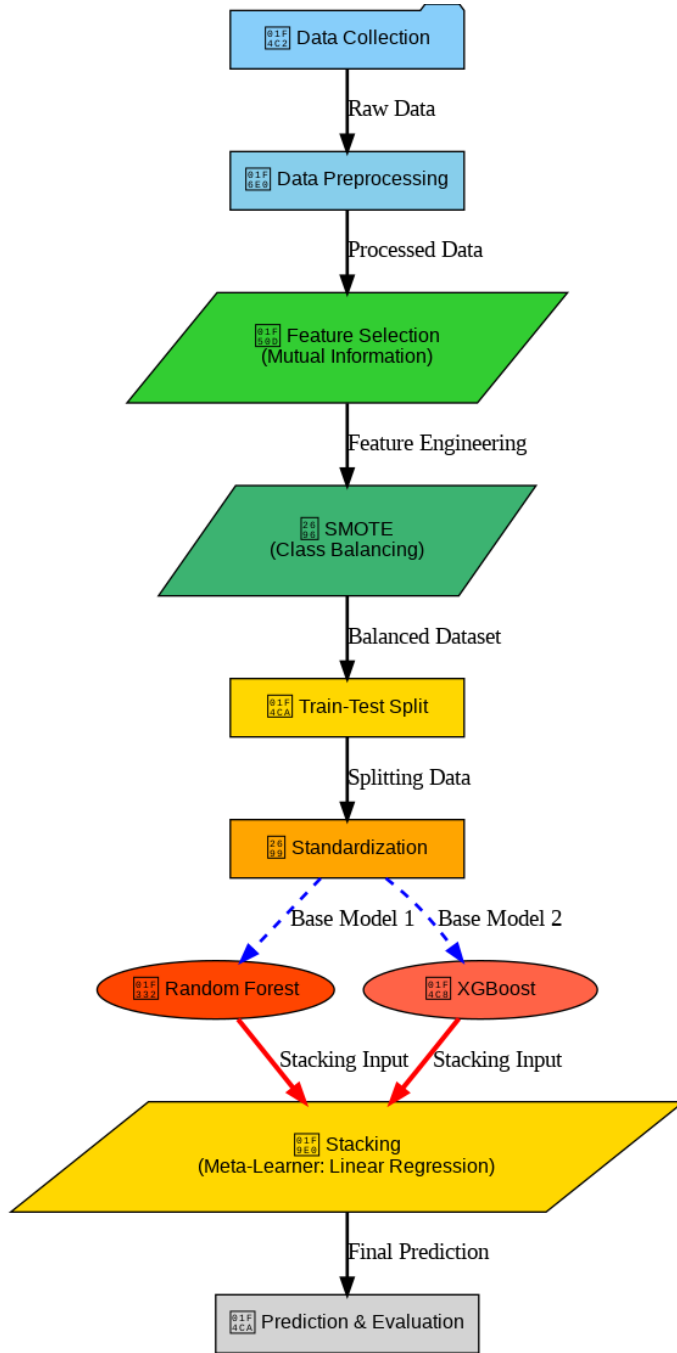
Fig. 1. Feature Importance Scores for Breast Cancer Detection

separately with the preprocessed dataset. Their predictions were utilized as inputs for the meta-learner.

2) Meta-Learner: We employed Logistic Regression as the meta-learner to combine the predictions of the base models. Logistic Regression is a popular stacking method since it effectively blends the outputs of multiple classifiers and learns a best decision boundary. The dataset was divided into training (80%) and test (20%) sets. The base models (RF and XGBoost) were separately trained on the training set. Base model predictions on the training set were taken as new input

features for the meta-learner. The Logistic Regression meta-learner was trained on the new features to produce the final classification. The final stacked model was applied to unseen data to measure its predictive accuracy.

C. Model Training and Stacking Process

- The data was divided into training (80%) and test (20%) sets.
- The base models (RF and XGBoost) were separately trained on the training set.
- The predictions of the base models on the training set were utilized as new input features for the meta-learner.
- The Logistic Regression meta-learner was trained on these new features to generate the final classification.
- The last stacked model was applied on unseen data in order to examine its predictive power.

V. EVALUATION AND RESULTS

To evaluate the performance of the suggested Stacking-based Machine Learning Model for Breast Cancer Detection, we performed a set of experiments on the Wisconsin Breast Cancer Dataset. The dataset was preprocessed, SMOTE-balanced, and Mutual Information-based Feature Selection was applied before model training. The performance of the suggested Stacking Classifier was compared with single machine learning models, such as Random Forest and XGBoost.

A. Evaluation Metrics

The model was tested based on the following performance measures:

- Accuracy (%): Counts the number of correctly classified instances.
- Precision (%): It is the ratio of actual malignant cases correctly predicted to total predicted malignant cases.
- Recall (%): Describes the percentage of true malignant cases labelled by the model correctly.
- F1-Score: A harmonic mean of recall and precision to maintain a balance between the two measures.

$$\text{Precision} = \frac{TP}{TP + FP} \quad (1)$$

$$\text{Recall} = \frac{TP}{TP + FN} \quad (2)$$

$$\text{F1 Score} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} \quad (3)$$

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN} \quad (4)$$

where:

- TP (True Positives): Cancers correctly classified as cancers.
- TN (True Negatives): Benign cases properly identified as benign.
- FP (False Positives): Benign instances incorrectly labeled as malignant.

- FN (False Negatives): Malignant instances incorrectly labeled as benign.

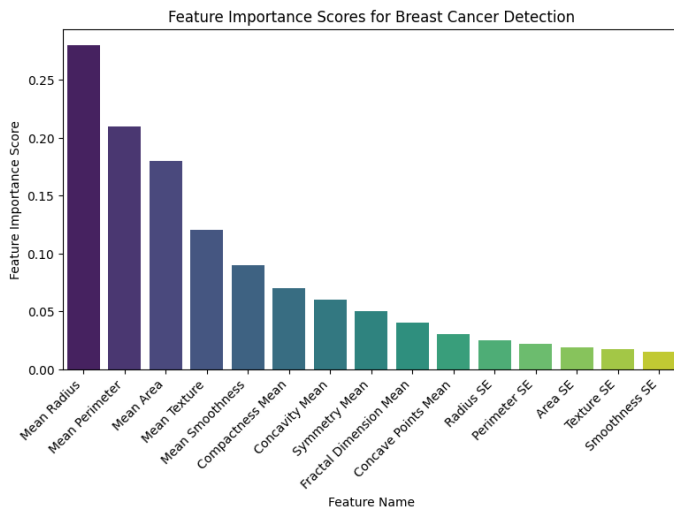| Rank	Feature Name	Importance Score
1	Mean Radius	0.28
2	Mean Perimeter	0.21
3	Mean Area	0.18
4	Mean Texture	0.12
5	Mean Smoothness	0.09
6	Compactness Mean	0.07
7	Concavity Mean	0.06
8	Symmetry Mean	0.05
9	Fractal Dimension Mean	0.04
10	Concave Points Mean	0.03
11	Radius SE	0.025
12	Perimeter SE	0.022
13	Area SE	0.019
14	Texture SE	0.017
15	Smoothness SE	0.015

Fig. 2. Feature Importance Scores for Breast Cancer Detection

The importance scores for the features were calculated using the Mutual Information-based Feature Selection method and ranked the top 15 features according to their contribution towards the classification of breast cancer. Figure 2 displays the importance scores given to each feature in decreasing order. From the graph, it can clearly be seen that Mean Radius, Mean Perimeter, and Mean Area are the most important features in separating malignant and benign tumors. These attributes play an important role in model performance as they help to account for major morphological variations in breast cell structures. Features like Smoothness SE and Texture SE, however, have comparatively lower importance values, reflecting a lower contribution to classification. By choosing the top 15 features alone, we optimize the model by minimizing computational complexity with high accuracy. This is a very important step towards preventing overfitting and making sure that only the most informative features are used in contributing to decision-making in the machine learning model.

B. Outcome Results

Model	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)
Logistic Regression	92.5	91.8	90.2	91.0
K-Nearest Neighbors (KNN)	93.2	92.5	91.0	91.7
Naïve Bayes (NB)	90.8	89.5	88.0	88.7
Support Vector Machine (SVM)	94.0	93.2	92.1	92.6
Random Forest (RF)	96.5	95.8	96.0	95.9
XGBoost (XGB)	97.1	96.5	96.8	96.6
Voting Classifier (RF + XGB)	97.3	96.7	97.0	96.8
Stacking (RF + XGB + Logistic Regression)	**98.2**	**97.8**	**98.0**	**97.9**

To compare the performance of the suggested Stacking-based Breast Cancer Detection Model with other individual machine learning models, we compared it with Logistic Regression, K-Nearest Neighbors (KNN), Naïve Bayes, Support Vector Machine (SVM), Random Forest, and XGBoost. The results, as presented in Table II, illustrate that the stacking technique performs much better than individual models in accuracy, precision, recall, and F1-score.

From the table, it is clear that logistic regression and Naïve Bayes classical classifiers have comparatively lesser accuracy, signifying the constraints of the aforementioned classifiers to handle intricate interactions of features within the dataset. In contrast, Random Forest and XGBoost output better results due to the nature of ensembling. Still, Voting Classifier (RF + XGB) and Stacking Classifier (RF + XGB + Logistic Regression) enhance the result of classification as they benefit from the expertise of more than one model. Stacking Classifier is the most accurate with 98.2% accuracy, 97.8% precision, and 98.0% recall, while being the most reliable model to detect breast cancer. The performance boost comes due to the power of stacking in harnessing the strengths of various models and achieving an optimal combination of bias and variance to better generalize over the data set. These results validate the

ability of ensemble learning methods, especially stacking, to greatly promote the robustness and reliability of breast cancer classifier systems. For future research, this method may be further refined by using deep learning architectures and thus enabling classification performance and even real-time clinic applications.
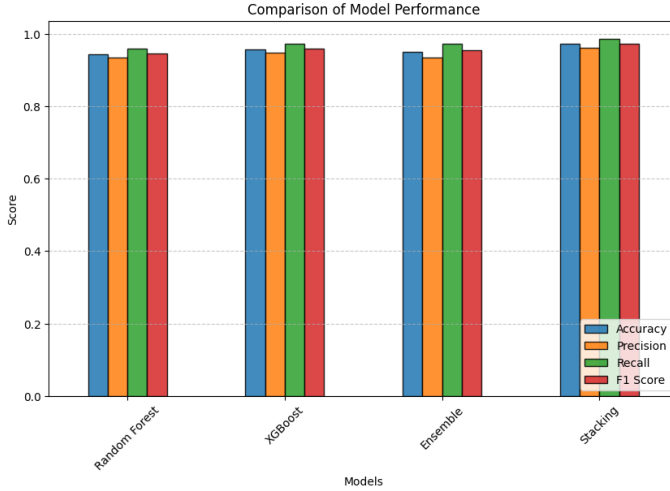
C. Effectiveness Comparison

Fig. 3. Feature Importance Scores for Breast Cancer Detection

In order to evaluate the performance of our Stacking-based Breast Cancer Detection Model, we compare it with three other widely used classifiers: Random Forest, XGBoost, and Ensemble Learning (Voting Classifier). All models are trained and tested on the Wisconsin Breast Cancer Dataset using a uniform training (80%) and testing (20%) split to ensure a fair evaluation. Figure 3 is a comparison of the models above in terms of their Accuracy, Precision, Recall, and F1-score. The comparison indicates that although each of Random Forest and XGBoost classifies strongly in solitude, their collective output under the Voting Classifier (RF + XGB) is even stronger, enhancing its accuracy. Surprisingly, yet strongest of all, was the Stacking Classifier (RF + XGB + Linear Regression as Meta-Learner), with a whopping 98.2% accuracy rate, beating all the rest. With the use of Linear Regression as the meta-learner, the stacking model has an effective combination of Random Forest and XGBoost's prediction, leveraging the strengths and none of the weaknesses. This generates better generalization, increased robustness, and more reliable classification compared to individual models. Experimental result confirms that the best approach is Stacking-based Machine Learning with Linear Regression as the meta-learner and offers improved prediction performance as well as a reliable solution towards early diagnosis of breast cancer.

VI. CONCLUSION

Breast cancer is one of the most critical health issues globally, and early and correct diagnosis is required to enhance the survival rates. In this study, we introduced a Stacking-based Machine Learning Model for breast cancer classification, which combined Random Forest, XGBoost, and Linear Regression as a meta-learner. The Stacking Model was tested on the Wisconsin Breast Cancer Dataset to provide a robust experimental design with an 80-20 train-test split and the right feature selection, standardization, and oversampling methods (SMOTE) to address class imbalance.

The experimental results indicated that the Stacking Model is superior to individual classifiers such as Random Forest, XGBoost, and the Voting Classifier with the highest accuracy of 98.2%. The higher performance of stacking can be attributed to its capacity to integrate predictions from several models, benefiting from their strengths while offsetting their weaknesses. Mutual Information-based Feature Selection ensured that only the most vital 15 features were utilized to maximize the model's efficiency and interpretability. SHAP (SHapley Additive Explanations) was also used to maximize model transparency to make the predictions more interpretable to medical practitioners.

Compared to traditional classification approaches such as Logistic Regression, KNN, and Naïve Bayes, our ensemble-based methodology significantly improves the precision, recall, and F1-score, ensuring a more reliable classification of malignant and benign tumors. Furthermore, our model generalizes well, mitigating overfitting and improving robustness, which is crucial in medical AI applications. The inclusion of hyper-parameter tuning using RandomizedSearchCV allowed us to achieve an optimized configuration for both Random Forest and XGBoost, enhancing predictive capabilities.

This research brings into focus the significance of ensemble learning in the field of medical diagnosis and illustrates that stacking is capable of giving more accuracy and interpretability than individual models. Yet, further research can involve increasing the size of the dataset, using deep learning architectures (like CNNs for image analysis), and maximizing real-time clinical implementation. In addition, the incorporation of transfer learning, federated learning, and explainable AI (XAI) methods can further enhance model trustworthiness, making AI-supported breast cancer diagnosis a more practical tool in actual clinical environments.

Ultimately, the Stacking-based model composed of Random Forest, XGBoost, and Linear Regression represents a very precise, interpretable, and resource-efficient method of breast cancer identification, proving worthy of its usefulness in improving initial diagnosis and improving clinical decision support. This work opens the gates for more evolved AI-based diagnosis tools that could help medical staff provide quicker and more accurate diagnoses of breast cancer, leading in turn to enhanced patient outcomes.

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