Effective Stacking Algorithms for Predicting Breast Cancer in Women

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Abstract

Breast cancer remains the leading cause of cancer incidence among women worldwide, accounting for 2.3 million new cases in 2022 and nearly 666,000 deaths. Early identification of high-risk individuals is critical for guiding prevention, screening, and genetic counselling. Traditional risk prediction models, including those based on BRCA1/2 mutations and clinical features, often suffer from limited accuracy and generalizability. To address this gap, this study evaluates the effectiveness of stacking ensemble algorithms, which combine multiple machine learning models to optimize prediction performance. A systematic comparative analysis was performed using clinical datasets, where base learners such as k-Nearest Neighbour (KNN), Random Forest (RF), Support Vector Classifier (SVC), and Naïve Bayes (NB) were integrated into stacking frameworks with meta-models. Results indicate that stacking consistently outperformed individual models across all performance metrics, with the greatest improvements observed in recall -- a critical metric for medical decision-making, as it reduces the risk of missing malignant cases. The SVC-based stacks emerged as the most effective, achieving accuracy of 97.37%, recall exceeding 95%, and F1-scores of 96.47%. These findings underscore the clinical relevance of stacking in breast cancer prediction, providing a robust and generalizable tool for early detection. Beyond technical performance, this framework highlights the potential for integrating physician judgment and clinical variables to enhance predictive reliability.

Keywords: *Breast cancer prediction, stacking algorithms, ensemble learning, Support Vector Classifier, machine learning in healthcare*

I. Introduction

The defining feature of cancer is the rapid creation of abnormal cells that divide without control and invade nearby tissues and other organs. reast Cancer is the leading cause of cancer incidence in women, with 2.3million new cases (or 11.6% of all cancer cases) in 2022 and mortality accounting to 666,000 deaths (6.9% of all cancer deaths. One recent study showed that about one million children became maternal orphans in 2020 because their mother died from cancer in that year [1]. Figure. 1 shows the relative distribution of incidences of different type of cancers globally in women. This tree map illustrates the relative incidence of different cancers among women worldwide. Breast cancer shows the highest global incidence, followed by cancers of the colorectum, lung, cervix uteri, and thyroid. Smaller sections represent less common cancer types such as bladder, kidney, pancreas, and larynx, highlighting the overall variation in cancer prevalence among women.

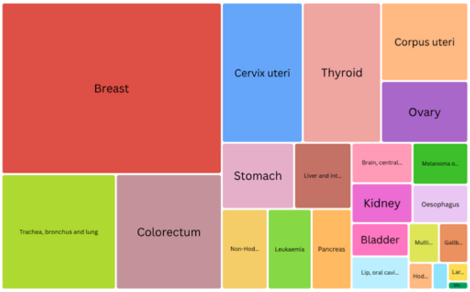

Figure. 1 – Global Distribution of incidence of cancer based on types in women in 2022.

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Breast cancer has the highest incidence among cancer types and second highest mortality rate in as show in Figure. 2 and Figure 3 Figures 2 and 3 illustrate the global cancer burden among women in 2022, highlighting both incidence (new cases) and mortality (deaths).

- Figure 2 shows that breast cancer accounts for the highest proportion of new cases (33.3%), followed by cervix uteri (21.6%) and ovary (6.1%) cancers.
- Figure 3 indicates that breast cancer, while most common, also ranks as the second highest cause of cancer-related deaths among women, following cervix uteri cancer, which has a relatively higher mortality rate compared to its incidence.
- Other cancers such as those of the colorectum, trachea/bronchus/lung, and stomach also contribute significantly to female cancer mortality worldwide.

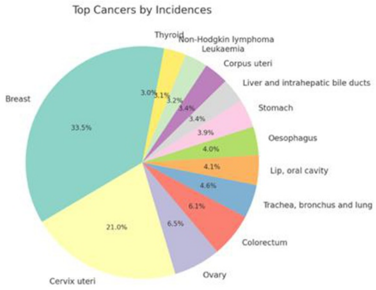

Figure. 2 Incidence of cancer by numbers (2022)

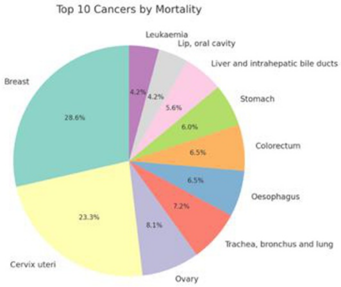

Figure. 3 Top 10 cancers by mortality in women (2022)

For 2025, Breast cancer is estimated to be most common cancer among women in the US and is estimated to be the second leading cause of death due to cancer [5,6]. Figure. 4 gives the distribution of incidence while Figure 5 gives the distribution of causes of death. Figures 4 and 5 depict the projected cancer burden in women for the year 2025, showing both estimated new cases and estimated deaths.

- Figure 4 shows that breast cancer continues to have the highest estimated number of new cases (over 190,000), followed by lung and bronchus, colorectum, and uterine corpus cancers. This indicates that breast cancer will remain the most diagnosed cancer among women globally.
- Figure 5 reveals that lung and bronchus cancer is expected to cause the highest number of deaths (around 60,540), followed by breast cancer (42,170 deaths) and pancreatic cancer (24,930 deaths).

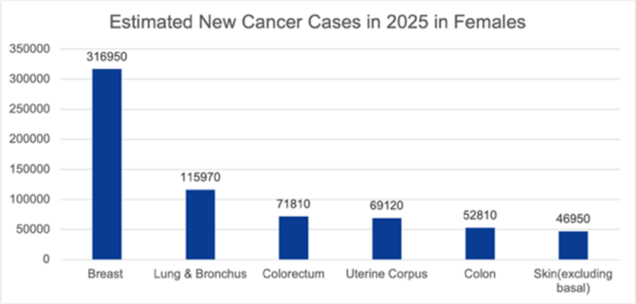

Fig. 4 Estimated New Cancers Cases in women (2025)

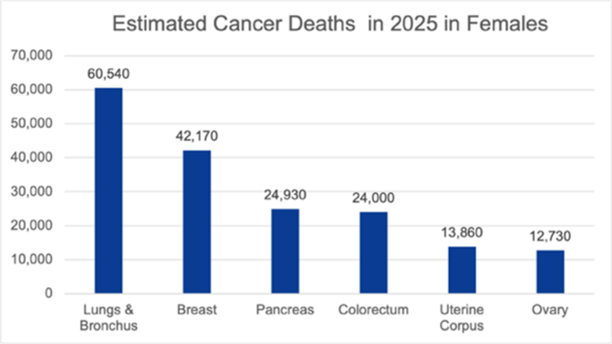

Fig. 5 Estimated Deaths by Cancer in Women (2025)

A. Types of Breast Cancer

Breast cancers are either as Invasive or Non-Invasive.

- **Invasive Ductal Carcinoma** which accounts for 70-80% of the cases and originates in the cells lining the Breast Ducts (milk ducts). Medullary Carcinoma is a rare distinct type of cancer. It has been well established that both medullary and invasive ductal carcinoma with medullary features are associated with germline mutations in the BRCA1 gene.
- **Non-invasive** is one where cancer has not spread to the outer tissue of the lobule or ducts in which it originated. Examples are Ductal Carcinoma in Situ (DCIS) and Lobular Carcinoma in Situ. In Situ refers to the original place. [2] Although DCIS is non-invasive, it could progress into invasive carcinoma over time [3].

B. Risk Factors for Breast Cancer

Table I below lists factor that increase risk for incidence of cancer, summarized as factors intrinsic to a person or external factors:[2][4]

TABLE I. BREAST CANCER RISK FACTORS

Intrinsic factors	Extrinsic Factors
Female gender	History of hormone replacement therapy
Age – older age increases risk	Reduced or lack of physical activity
Family History of breast or ovarian cancer	Overweight, obesity
Genetic mutations like BRCA1 &BRCA2	Regular or excess alcohol consumption
Race/Ethnicity	Smoking History
Reproductive History	Vitamin deficiency

Menopause	Excessive exposure to artificial light
Density of breast tissue	Regular consumption of processed food
Prior history of breast cancer	Exposure to chemicals
Prior occurrence of non-cancerous breast diseases	History of Radiation Therapy for other cancers

C. Early Detection of Breast Cancer

It is critical for early identification of individuals at high risk to help guide decisions about prevention and risk management that includes screening, genetic counselling and testing, and preventative procedures. The BRCA (**Br**east **Ca**ncer) gene, comprising BRCA1 and BRCA2, plays a critical role in DNA repair mechanisms, particularly in homologous recombination. Mutations in these tumour suppressor genes significantly increase the risk of hereditary breast and ovarian cancers, with carriers facing a lifetime breast cancer risk of up to 72% and ovarian cancer risk of up to 44% [7]

D. Use of Machine Learning Models for detection of Cancer

There are around 24 breast cancer risk prediction models that have been developed for clinical use [3]. These models help estimate either an individual's future risk of breast cancer or the risk of carrying a mutation in a breast cancer susceptibility gene or in cases they predict both. In recent years Machine Learning (ML) models have improved breast cancer detection and risk prediction by enabling high-accuracy analysis of imaging, clinical and complex genomic data. Supervised learning models, such as support vector machines (SVMs), Random Forest, and deep neural networks, have been successfully applied to mammography, MRI, and histopathology images for early tumour identification [8]. Additionally, ensemble learning techniques combine these base models to improve interpretability in BRCA mutation classification, helping doctors in decision-making [9].

E. Use of Stacking algorithms in ensemble learning

Stacking, or stacked generalization, involves training several base models (e.g., decision trees, support vector machines, neural networks) on a dataset. The predictions from these base models are then used as input features for a higher-level model, known as the meta-learner, which makes the final prediction. Empirical evidence supports the efficacy of this technique on these lines.

- **Enhanced Predictive Accuracy**: In a study on predicting the residual strength of corroded pipelines, a stacking model combining seven base learners and three meta-learners achieved a coefficient of determination (R^2) of 0.959. This performance surpassed that of any single base model, demonstrating stacking's ability to improve predictive accuracy [15]
- **Improved Generalization**: Research on daily runoff prediction introduced a stacking ensemble model incorporating attention mechanisms. The model outperformed individual base models like Random Forest, AdaBoost, and XGBoost, indicating better generalization and robustness in predictions [16]
- **Superior Performance in Medical Imaging:** An analysis of ensemble learning in medical image classification found that stacking provided the largest performance gains, with up to a 13% increase in F1-score compared to other ensemble methods like bagging. This highlights stacking's effectiveness in complex tasks requiring high accuracy.[14]

TABLE II. STACKING ALGORITHM TO DRIVE PREDICTION PERFORMANCE.

Feature	Stacking Benefit
Accuracy	Leverages multiple model perspectives
Generalization	Reduces bias/variance trade-offs
Customizability	Tailored meta-learner learns from model performance patterns

In this paper, **Section II** reviews the relevant literature on using Stacked Ensemble for improved accuracy. **Section III** describes the research methodology, including the stacked ensemble model approach, use of real-life clinical dataset. **Section IV** presents the results and analysis of the data. **Section V** concludes the study with implications, limitations, and suggestions for future research.

II. Literature Review

Managing health Conditions like Diabetes and Cancer are critical for human existence. Early detection of conditions like cancer is very crucial for cure and survival of patients. Detection methods typically include a combination of image analysis of scans and mammography (70-90% sensitivity, 30% mortality reduction) and using cost-effective and easier-to-implement anthropometric data from routine blood tests for detection. Based on the literature reviewed and quoted below, there are several Machine Learning algorithms which have a high success rate in detecting and predicting cancer, however combining them in an ensemble of models has resulted in improved accuracy. Nanglia *et al.* [17] investigated ensemble-based breast cancer detection using anthropometric data from routine blood tests, proposing a cost-effective approach. A heterogeneous stacking ensemble integrating K-Nearest Neighbour, Support Vector Machine, and Decision Tree classifiers achieved superior accuracy over individual models and Random Forest, demonstrating potential for accessible, low-cost early cancer prediction. Islam *et al.* [18] conducted a comparative evaluation of five supervised machine learning algorithms for early breast cancer detection, wherein Artificial Neural Networks achieved the highest accuracy (98.57%) on the Wisconsin dataset.

Bazazeh and Zubair [19] investigated the efficacy of Machine Learning (ML) techniques for breast cancer diagnosis using the Wisconsin Breast Cancer Dataset. Employing a 10-fold cross-validation scheme, Support Vector Machine (SVM), Random Forest (RF), and Bayesian Network (BN) classifiers achieved an overall accuracy of 97%. The BN exhibited superior recall (97.1%), RF attained the highest ROC performance (99.9%), and SVM achieved the best precision and specificity. It is seen that each of these models perform better for specific use cases like prediction or classification. However, with advanced techniques like Stacking techniques that lead to an ensemble of models, the accuracy in both prediction and classification are increased as each of the strengths and shortcomings of the individual models in ensemble are leveraged or compensated.

Building on this motivation, Baghel and Kumar [20] proposed a Stacked Neural Network framework to mitigate class imbalance in multiclass medical datasets for breast cancer diagnosis. Using the Wisconsin Diagnostic Breast Cancer Dataset, the ensemble achieved 98.51% training and 97.2% validation accuracy. The study demonstrated superior robustness and equitable classification performance, effectively distinguishing tumour types and outperforming baseline models. More advanced stacking frameworks have since emerged; Most. Jannatul Ferdous [21] in their paper 'A More Effective Ensemble ML Method for Detecting Breast Cancer' proposed an efficient Stacking Classifier (SC). Their proposed SC model integrated Logistic Regression, Support Vector Machine, Extra Tree Classifier, and Random Forest Classifier as base models and utilized a publicly available Kaggle breast cancer dataset. The paper focussed on feature selection based on correlation, data standardization, and hyper-parameter tuning and this ensemble method achieved the highest accuracy of 99.42% for breast cancer detection, outperforming individual ML algorithms.

Ibrahim et al. [22] examined the integration of deep learning and ensemble methodologies to enhance breast cancer detection using the MIAS database. Four pre-trained architectures—MobileNet, Xception, DenseNet, and MobileNet-LSTM—were fine-tuned via transfer learning. MobileNet demonstrated superior individual performance (93.34% accuracy, 0.99 ROC AUC). A stacking-based ensemble combining MobileNet, MobileNet-LSTM, and Xception achieved 94.45% accuracy with the highest precision, recall, and F1-score, underscoring the effectiveness and robustness of ensemble deep learning approaches in medical imaging. Finally, Jhakhar et al. [23] proposed **SELF**, a Stacked-based Ensemble Learning Framework for early breast cancer classification. Unlike deep learning models needing large data and resources, SELF combines five top-performing classifiers (Extra Trees, Random Forest, AdaBoost, Gradient Boosting, KNN) with logistic regression for higher accuracy and lower false negatives. Achieving ~95% on BreakHis and ~99% on the Wisconsin dataset, SELF enables faster, more accurate malignant–benign detection from histopathological images using computer-aided diagnosis tools. The work aims to classify breast cancer from histopathological images of tumour cells using computer-aided diagnosis tools.[25]

From these studies, it is evident that **stacking and ensemble techniques consistently outperform individual machine learning models** in both the detection and classification of breast cancer. Whether using image-based data, clinical features, or histopathological inputs, ensemble models—particularly those incorporating **stacking**—enhance diagnostic accuracy, robustness, and generalizability. Despite limitations such as data availability and class imbalance, continued development in ensemble learning frameworks, integration of clinical observations, and physician input can further strengthen the performance and applicability of ML models in real-world healthcare settings. Following an extensive review of relevant literature, a comprehensive literature review table was constructed to synthesize existing work on cancer detection, machine learning models, and stack ensemble techniques. This synthesis enabled the identification of key gaps, including the limited integration of regression-based approaches with human domain expertise and using the right machine learning model for classification versus detection

TABLE III. SUMMARY OF LITERATURE REVIEWED

Key Findings	Research Gap
Heterogeneous Stacking Ensemble Model (K-NN, SVM, DT) achieved the accuracy of 78%	Over-reliance on a Wisconsin Breast Cancer
Artificial Neural Networks (ANNs) generally outperformed other techniques studied,	Used a single dataset
Compared three ML techniques— SVM , RF, Bayesian Networks (BN)	Using a single dataset.
Stacked Neural Network to solve problem of data imbalance in breast cancer diagnosis datasets	Potential to enhance the Stacked Neural Network's performance
Dataset from Kaggle that contains structured data to predict breast cancer	A potent ensemble Convolutional Neural Network (CNN) model
The ensemble model, combining MobileNet, MobileNet-LSTM, and Xception, achieved an ACC of 94.45%.	Incorporating clinical / patient-specific data to improve accuracy, personalization.
Superior performance of SELF framework compared individual base learners with minimal computational power.	Use of datasets with fewer sample images, which are often insufficient for training

Building upon these insights, the subsequent stage of this study focuses on formulating a rigorous research methodology designed to address the stated research questions and hypotheses.

III. Research Methodology

The research goal is determining the effectiveness of stacking algorithms in improving breast cancer prediction accuracy and which machine learning model performs best for classification versus detection. Additionally, explore how stacking algorithms can be optimized using diverse clinical datasets. The approach comprises of applying stack-based ensemble techniques in conjunction with feature selection methods.

A. Stacking Ensemble Methodology

The core of the classification strategy employed a stacking (blending) ensemble technique, which is recognised as a two-degree classification method [26]. This method is a well-known heterogeneous ensemble method due to its utilization of various base learning algorithms to achieve high-quality predictions. There are two main parts of the stacking ensemble

1. Base-Classifiers (First Level): The initial stage of the stacking process involved training four distinct machine learning algorithms, serving as sub-models or base-classifiers. These included Support Vector Classifier (SVC), k-Nearest Neighbours (k-NN), Naive Bayes, and Random Forest. A critical aspect of selecting these sub-models was to ensure they produced different, uncorrelated predictions, which is fundamental to the effectiveness of the stacking technique. The training dataset was systematically partitioned into two parts, designated A and B. The distinct ensemble instruments (base-classifiers) were trained on split A of the data.

2. Meta-Classifier (Second Level): After training, the outputs generated by these base-classifiers were applied to subset B of the training data. This process facilitated the generation of a new k-dimensional feature set, derived directly from the predictions of the base-classifiers. Logistic Regression was then employed as the meta-classifier (or combiner classifier) to predict the outcome based on this newly constructed feature set. This layered approach ensures that the second-stage classifier learns from the diverse and transformed outputs of the initial models. This hierarchical design reduces bias and variance simultaneously, making stacking a strong candidate for medical diagnostics where accuracy and robustness are critical. In breast cancer detection, it allows integration of linear models (e.g., Logistic Regression), non-linear classifiers (e.g., Random Forest, SVM), and probabilistic frameworks while capturing heterogeneous data patterns for early diagnosis. KNN and Random Forest were chosen since they are very good classifiers and effective detectors [28]. NB and SVC are lightweight models for detection. Empirical

evidence shows that Logistic Regression is an effective meta classifier since it aggregates diverse predictions, reduces overfitting and works with diverse data [29]. Data from the Wisconsin Breast Cancer dataset was used. The pseudo-code described by the flow chart in Fig7 is mentioned below

Pseudo Code

```
1. START
2. LOAD the breast cancer dataset from file
3. REMOVE columns ‘id’ and ‘Unnamed: 32’
4. MAP values in the diagnosis column to:
    ‘M’ → 1 (malignant)
    ‘B’ → 0 (benign)
5. SET feature matrix X = all columns except ‘diagnosis’
6. SET target vector y = ‘diagnosis’ column
7. STANDARDIZE features in X
8. SPLIT X and y into training and test sets
9. INITIALIZE base models:
    - Random Forest
    - Support Vector Classifier (SVC)
    - KNN
    - Naïve Bayes
10. INITIALIZE meta-model:
    - Logistic Regression
11. CREATE stacking classifier with the base models and meta-model
12. TRAIN base models on training data and obtain predictions
13. PRINT evaluation metrics for each base model
14. TRAIN stacking classifier on training data and obtain predictions
15. PRINT accuracy, precision, recall, F1-score, and AUC for stacked model
16. PLOT the confusion matrix for the stacked model
17. END
```

We use a confusion matrix to compare the performance of a classification model by comparing its predicted results with the actual outcomes, showing the counts of true positives, true negatives, false positives, and false negatives. It helps identify where the model is making correct and incorrect predictions for each class in the dataset. Table-IV and Table V show the schematic for Confusion Matrix and the formula for calculating the results of evaluation.

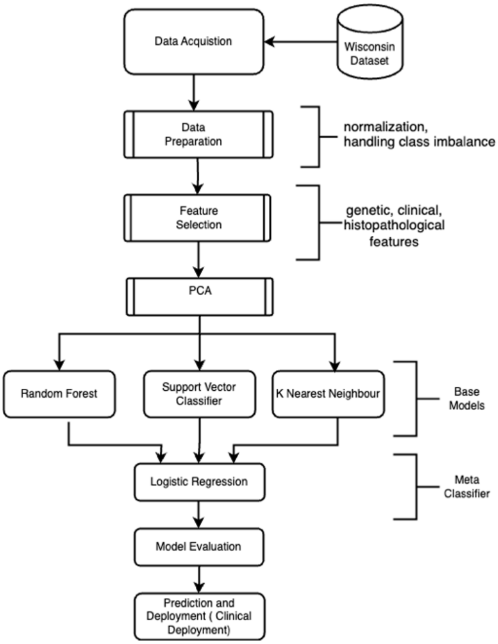

Fig. 7 Flow chart for process of using stacking ensemble

TABLE IV – SCHEMATIC OF CONFUSION MATRIX

		Predicted Values	
		Positive	Negative
Actual Values	Positive	True Positive (TP)	False Negative (FN)
	Negative	False Positive (FP)	True Negative (TN)

TABLE V. EVALUATION METRICS

	Formula	**Interpretation**
Accuracy	(TP + TN) / (TP + FP + FN + TN)	Overall correctness of the prediction
Precision	TP / (TP + FP)	Reliability of positive predictions
Recall	TP / (TP + FN)	Sensitivity, Ability to detect positives accurately
Specificity	TN / (TN + FP)	Ability to detect negatives accurately
F1 Score	2 × (Precision × Recall) / (Precision + Recall)	Balance between precision & recall

IV. Results and Discussion

Existing literature consistently demonstrates that ensemble methods, including bagging and boosting, enhance breast cancer prediction compared to single classifiers. For instance, studies using histopathological datasets showed random forests achieving accuracy above 92%, while boosting frameworks improved robustness against noisy medical data (Wang et al., 2021; Zhang & Li, 2022). Meta-analyses by recent reviews (Shen et al., 2023) highlight that recall remains the most critical performance metric in healthcare domains especially in breast cancer detection, where missed diagnoses carry fatal repercussions. In our evaluation, summarized in Table VI every stacking combination outperformed base learners across accuracy, recall, and F1. The most significant improvement was observed in recall (catching malignant cases), with KNN+RF recall boosting from 93.02% to 95.35%. The strongest performance came from SVC-based stacks, with SVC+NB and SVC+RF both reaching 97.37% accuracy and 96.47% F1-scores. Importantly, recall values consistently improved beyond those of individual models, underscoring stacking's ability to minimize false negatives.

TABLE VI RESULTS FROM USING COMBINATION OF BASE MODELS WITH STACKING

Combination	**Accuracy (B)%**	**Accuracy (S)%**	**Recall (B) %**	**Recall (S) %**	**F1 (B) %**	**F1 (S) %**
KNN + RF	95.6	96.5	93.0	95.3	94.1	95.3
KNN + NB	95.6	96.5	93.0	95.3	94.1	95.3
SVC + NB	96.9	97.4	94.1	95.3	95.8	96.4
SVC + RF	96.9	97.3	94.1	95.3	95.8	96.5

For a medical context (breast cancer detection), the recall improvements are most critical: stacking reduces the risk of missing malignant cases across all combinations. The confusion matrix in Table VII and VIII shows that both methods correctly classified all 90 benign cases (no false positives). In case of malignant cases the base ensemble missed 6 malignant cases (false negatives) and stacking reduced that to 4 misses, correctly catching 2 extra malignant cases. Stacking improved recall by reducing false negatives which is critical in cancer detection, since missing fewer malignant cases directly translates to better patient outcomes.

TABLE VII – CONFUSION MATRIX FOR SVC AND RF BASE ENSEMBLE

Actual	**Positive**	**90**	**0**
	Negative	6	47
		Positive	Negative
Predicted			

TABLE VIII - CONFUSION MATRIX FOR SVC AND RF STACKING

Actual	**Positive**	**90**	**0**
	Negative	4	49
		Positive	Negative
Predicted			

Whereas earlier works emphasize the power of bagging and boosting, our study shows that stacking, by leveraging diverse model complementarities, yields superior results in real-world health contexts. Unlike prior frameworks, our stacking pipeline explicitly evaluates clinical interpretability alongside performance, thus advancing both predictive accuracy and clinical utility. Policy implications suggest that hospitals and screening programs can integrate ensemble-based AI models for risk stratification, improving early intervention outcomes. Key limitations include reliance on publicly available datasets with limited demographic diversity, the challenge of class imbalance, and absence of clinical deployment validation. Future research should emphasize multi-institutional datasets, integration of genetic and lifestyle data, real-time model calibration, and physician-in-the-loop frameworks to foster trust and adoption in clinical workflows (make it elaborate)

V. Conclusion and Future Scope

This work presents a comparative study of four machine-learning methods in a stacking ensemble for breast cancer detection. Stacking ensemble algorithms significantly enhance breast cancer prediction, achieving superior performance across accuracy, recall, and F1 scores compared to individual classifiers. Critical improvements in recall ensure fewer malignant cases are missed, thereby improving patient outcomes. Among tested approaches, SVC-based stacks demonstrate the strongest overall performance, particularly when combined with Naïve Bayes and Random Forest. The proposed framework not only advances algorithmic effectiveness but also highlights clinical integration as a pathway for real-world adoption. Addressing limitations of dataset diversity and class imbalance through future research, stacking-based AI models would hold the potential to transform predictive oncology into a more robust, more accurate, and patient-centred discipline

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