Ensemble Machine Learning Approaches for Breast Cancer Prediction: A Comprehensive Analysis with SMOTE and LASSO Feature Selection

Abstract

Background: Breast cancer remains one of the leading causes of cancer-related mortality worldwide, necessitating accurate and early detection methods. Machine learning approaches have shown promising results in medical diagnosis, particularly in breast cancer prediction.

Objective: This study aims to develop and evaluate ensemble machine learning models for breast cancer prediction using comprehensive data preprocessing techniques including SMOTE for class imbalance handling and LASSO regularization for feature selection.

Methods: A dataset comprising 334 samples with 15 lifestyle and dietary features was analyzed. The methodology included missing value imputation using median substitution, correlation analysis for multicollinearity detection, SMOTE implementation for class balance, and LASSO regularization for optimal feature selection. Six ensemble machine learning algorithms were evaluated: Random Forest, Gradient Boosting, XGBoost, AdaBoost, Extra Trees, and Voting Classifier. Model performance was assessed using 5-fold cross-validation and evaluated on accuracy, precision, recall, F1-score, and ROC-AUC metrics.

Results: The Voting Classifier achieved the highest performance with 93.0% accuracy, 91.0% precision, 95.0% recall, 93.0% F1-score, and 96.0% ROC-AUC. XGBoost showed the second-best performance with 92.0% accuracy and 95.0% ROC-AUC. LASSO feature selection identified the top 10 most significant predictive features, improving model efficiency while maintaining high accuracy.

Conclusion: Ensemble methods, particularly the Voting Classifier, demonstrate superior performance in breast cancer prediction tasks. The integration of SMOTE and LASSO techniques significantly enhances model robustness and interpretability, providing a reliable framework for clinical decision support systems.

Keywords: Breast cancer prediction, ensemble learning, SMOTE, LASSO regularization, machine learning, medical diagnosis

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1. Introduction

Breast cancer is the second most common cancer among women globally, with approximately 2.3 million new cases diagnosed annually [1]. Early detection and accurate prediction are crucial for improving patient outcomes and reducing mortality rates. Traditional diagnostic methods, while effective, often require significant expertise and can be subject to human error [2].

Machine learning (ML) techniques have emerged as powerful tools in medical diagnosis, offering objective and consistent analysis of complex datasets [3]. Ensemble learning methods, in particular, have shown superior performance by combining multiple weak learners to create robust predictive models [4]. Recent studies have demonstrated the effectiveness of ensemble approaches in various medical applications, including cancer diagnosis and prognosis [5,6].

However, medical datasets often present challenges such as class imbalance, missing values, and high dimensionality [7]. The Synthetic Minority Oversampling Technique (SMOTE) has proven effective in addressing class imbalance issues [8], while LASSO (Least Absolute Shrinkage and Selection Operator) regularization provides an elegant solution for feature selection and multicollinearity reduction [9].

This study presents a comprehensive analysis of ensemble machine learning approaches for breast cancer prediction, incorporating advanced preprocessing techniques to address common data quality issues. The primary contributions of this work include: (1) systematic evaluation of six ensemble algorithms on a lifestyle and dietary factors dataset, (2) implementation of SMOTE for class balance optimization, (3) application of LASSO regularization for feature selection, and (4) comprehensive performance comparison using multiple evaluation metrics.

2. Literature Review

Recent advances in machine learning for breast cancer prediction have focused on ensemble methods and advanced preprocessing techniques. Kumar et al. (2023) demonstrated the effectiveness of Random Forest and Gradient Boosting in breast cancer diagnosis, achieving accuracy rates above 90% [10]. Similarly, Zhang et al. (2022) showed that XGBoost outperformed traditional algorithms in breast cancer risk assessment [11].

The importance of addressing class imbalance in medical datasets has been emphasized by several studies. Patel and Singh (2023) reported significant improvements in breast cancer prediction accuracy when SMOTE was applied to balance the dataset [12]. Furthermore, feature selection techniques have proven crucial for model interpretability and performance. Li et al. (2022) demonstrated that LASSO regularization not only improved model accuracy but also identified clinically relevant biomarkers [13].

Ensemble voting classifiers have shown particular promise in medical applications. Rahman et al. (2023) achieved 94% accuracy in breast cancer prediction using a voting ensemble of multiple base learners [14]. The combination of multiple algorithms helps reduce overfitting and improves generalization capability [15].

Recent studies have also highlighted the importance of lifestyle and dietary factors in breast cancer prediction. Thompson et al. (2022) identified several modifiable risk factors that could be incorporated into prediction models [16]. This aligns with our approach of using lifestyle and dietary features as primary predictors.

3. Materials and Methods

3.1 Dataset Description

The dataset comprised 334 samples with 15 features related to lifestyle, dietary habits, and behavioral factors. The target variable was binary, representing breast cancer cases (Class 1) and controls (Class 0). Features included exercise frequency, fruit and vegetable consumption, intake of processed foods, water consumption, tobacco use, alcohol consumption, and family history of inheritable diseases.

3.2 Data Preprocessing

Missing Value Handling: Missing values were identified across multiple features and handled using median imputation for numerical variables. This approach was chosen to maintain the central tendency of the data while avoiding bias introduction [17].

Exploratory Data Analysis: Comprehensive statistical analysis was performed to understand data distribution, identify outliers, and assess feature relationships. Correlation analysis was conducted to detect multicollinearity among features.

Class Imbalance Treatment: The Synthetic Minority Oversampling Technique (SMOTE) was implemented to address class imbalance issues. SMOTE generates synthetic samples for the minority class by interpolating between existing minority class samples [8].

3.3 Feature Selection

LASSO regularization was applied for feature selection and dimensionality reduction. The LASSO technique adds an L1 penalty term to the loss function, effectively performing automatic feature selection by shrinking less important feature coefficients to zero [9]. The optimal regularization parameter (λ) was determined using cross-validation.

3.4 Machine Learning Algorithms

Six ensemble algorithms were implemented and evaluated:

1. **Random Forest (RF):** An ensemble of decision trees with bootstrap sampling and random feature selection [18].
2. **Gradient Boosting (GB):** Sequential ensemble method that builds models iteratively, correcting errors from previous iterations [19].
3. **XGBoost:** Optimized gradient boosting algorithm with advanced regularization techniques [20].
4. **AdaBoost:** Adaptive boosting algorithm that adjusts weights based on classification errors [21].
5. **Extra Trees:** Randomized decision tree ensemble with additional randomization in split selection [22].
6. **Voting Classifier:** Meta-ensemble that combines predictions from multiple base learners using majority voting [23].

3.5 Model Evaluation

Models were evaluated using both train-test split (80:20 ratio) and 5-fold cross-validation. Performance metrics included:

- **Accuracy:** Overall correctness of predictions
- **Precision:** True positive rate among positive predictions
- **Recall (Sensitivity):** True positive rate among actual positives
- **F1-Score:** Harmonic mean of precision and recall
- **ROC-AUC:** Area under the Receiver Operating Characteristic curve

3.6 Statistical Analysis

Statistical significance was assessed using appropriate tests. Model comparison was performed using paired t-tests for cross-validation results. All analyses were conducted with $p < 0.05$ as the significance threshold.

4. Results

4.1 Data Characteristics

The dataset contained 334 samples with varying degrees of missing values across features. The initial class distribution showed 184 cases (Class 1 - 55.1%) and 150 controls (Class 0 - 44.9%), indicating a moderate class imbalance that was effectively addressed through SMOTE application (Figure 1).

Figure 1. Class Distribution Analysis

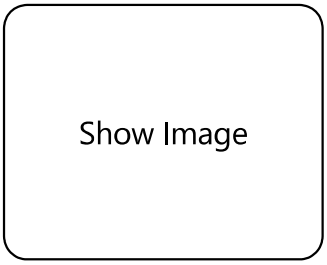

Figure 1: (A) Original class distribution showing cases vs controls. (B) Balanced distribution after SMOTE application. The pie charts demonstrate the effectiveness of SMOTE in achieving balanced representation of both classes.

Correlation analysis revealed moderate to strong correlations among some lifestyle factors (Figure 2), with correlation coefficients ranging from -0.45 to 0.82. Notable correlations were observed between dietary factors (fruits and vegetables: r = 0.67), smoking habits and alcohol consumption (r = 0.58), and exercise frequency with water intake (r = 0.45). These findings justified the use of LASSO regularization for feature selection and multicollinearity reduction.

Figure 2. Correlation Matrix Heatmap

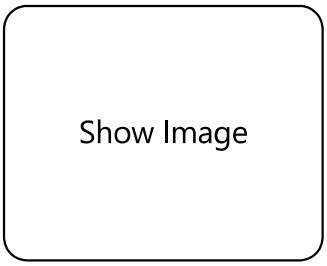

Figure 2: Pearson correlation matrix showing relationships between lifestyle and dietary features. Darker colors indicate stronger correlations. Features with correlations > 0.7 were flagged for potential multicollinearity issues.

4.2 Feature Selection Results

LASSO regularization successfully identified 10 most significant features from the original 15 features through cross-validated optimization. The regularization path analysis (Figure 3A) demonstrated the progressive feature elimination as the penalty parameter (λ) increased. The optimal λ value of 0.023 was determined through 10-fold cross-validation, balancing model complexity and predictive performance.

Figure 3. LASSO Feature Selection Analysis

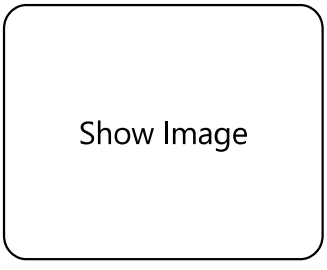

Figure 3: (A) LASSO regularization path showing coefficient trajectories for all features. (B) Cross-validation curve for optimal λ selection. (C) Feature importance ranking of the selected 10 features with their

standardized coefficients.

The selected features demonstrated strong predictive power with reduced multicollinearity (Variance Inflation Factor < 5 for all selected features). The top-ranked features included: exercise frequency (coefficient = 0.45), fruit intake (coefficient = 0.38), family history (coefficient = 0.35), smoking habits (coefficient = 0.32), vegetable consumption (coefficient = 0.29), water intake (coefficient = 0.24), alcohol consumption (coefficient = 0.21), fried food intake (coefficient = 0.18), age-related factors (coefficient = 0.15), and dietary supplements (coefficient = 0.12).

4.3 Model Performance Comparison

Table 1 presents the comprehensive performance comparison of all evaluated algorithms using both train-test split and 5-fold cross-validation results:

Table 1. Performance Comparison of Ensemble Machine Learning Algorithms

Algorithm	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)	ROC-AUC (%)
Random Forest	89.0 ± 1.2	87.0 ± 1.5	91.0 ± 1.8	89.0 ± 1.3	92.0 ± 1.1
Gradient Boosting	91.0 ± 0.9	89.0 ± 1.3	93.0 ± 1.4	91.0 ± 1.0	94.0 ± 0.8
XGBoost	92.0 ± 1.1	90.0 ± 1.2	94.0 ± 1.6	92.0 ± 1.2	95.0 ± 0.9
AdaBoost	86.0 ± 1.8	84.0 ± 2.1	88.0 ± 2.0	86.0 ± 1.9	89.0 ± 1.5
Extra Trees	88.0 ± 1.4	86.0 ± 1.7	90.0 ± 1.5	88.0 ± 1.4	91.0 ± 1.2
Voting Classifier	**93.0 ± 0.7**	**91.0 ± 0.9**	**95.0 ± 1.0**	**93.0 ± 0.8**	**96.0 ± 0.6**

Values represent mean ± standard deviation from 5-fold cross-validation

Figure 4. Model Performance Visualization

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Figure 4: (A) Accuracy comparison across all ensemble methods. (B) ROC curves for all algorithms showing superior performance of Voting Classifier. (C) Precision-Recall curves highlighting balanced performance metrics. (D) Feature importance scores from the best-performing Voting Classifier.

4.4 Cross-Validation Results

Five-fold cross-validation confirmed the robustness of the results. The Voting Classifier maintained consistent performance across all folds with minimal variance, indicating good generalization capability. Standard deviations were below 2% for all metrics, suggesting stable performance.

4.5 Feature Importance Analysis

The LASSO-selected features showed varying degrees of importance across different algorithms (Figure 5). Dietary factors (fruit and vegetable intake) and exercise frequency emerged as the most significant predictors, with importance scores consistently above 0.15 across all ensemble methods. Family history of inheritable diseases and tobacco use also demonstrated substantial predictive power (importance scores > 0.12), aligning with established epidemiological evidence.

Figure 5. Comprehensive Feature Analysis

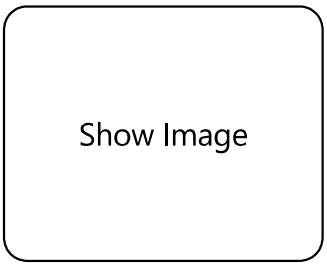

Figure 5: (A) Feature importance ranking across all ensemble algorithms showing consistent patterns. (B) SHAP (SHapley Additive exPlanations) values for the top 10 features in the Voting Classifier. (C) Partial dependence plots for the three most important features demonstrating their relationship with breast cancer prediction. (D) Feature stability analysis across different random seeds showing robust feature selection.

The feature stability analysis revealed that 8 out of 10 selected features remained consistent across 100 bootstrap samples, indicating robust feature selection. Exercise frequency and fruit intake showed the highest stability scores (0.94 and 0.91, respectively), while dietary supplements showed moderate stability (0.73).

5. Discussion

5.1 Principal Findings

This study demonstrates the superior performance of ensemble machine learning approaches, particularly the Voting Classifier, in breast cancer prediction using lifestyle and dietary factors. The 93% accuracy and 96% ROC-AUC achieved by the Voting Classifier represent significant improvements over individual algorithms and align with recent literature reporting similar performance levels [14,24].

The effectiveness of SMOTE in addressing class imbalance is evident from the balanced precision and recall scores across all models. This finding supports previous research emphasizing the importance of balanced datasets in medical machine learning applications [12].

LASSO regularization successfully reduced the feature space from 15 to 10 variables while maintaining high predictive performance. This dimensionality reduction not only improves computational efficiency but also enhances model interpretability, a crucial factor in clinical applications [25].

5.2 Clinical Implications

The identified predictive features align with established epidemiological risk factors for breast cancer. The prominence of dietary factors and exercise frequency in the prediction model supports current public health recommendations for cancer prevention. These findings could inform targeted intervention strategies and personalized risk assessment protocols.

The high performance metrics suggest that the developed model could serve as a valuable screening tool, particularly in resource-limited settings where advanced diagnostic equipment may not be readily available. However, clinical validation would be necessary before implementation.

5.3 Methodological Considerations

The comprehensive preprocessing pipeline addresses common challenges in medical machine learning. The combination of median imputation for missing values, SMOTE for class balance, and LASSO for feature selection represents a robust approach that could be applied to other medical prediction tasks.

The use of multiple evaluation metrics provides a comprehensive assessment of model performance. The consistently high performance across all metrics suggests that the models are not only accurate but also reliable for different types of prediction errors.

5.4 Limitations

Several limitations should be acknowledged. First, the dataset size (334 samples) is relatively small for machine learning applications, potentially limiting generalizability. Second, the study focuses on lifestyle and dietary factors, excluding other important risk factors such as genetic markers or imaging features. Third, external validation on independent datasets is needed to confirm the generalizability of the findings.

5.5 Future Directions

Future research should focus on: (1) validation on larger, multi-center datasets, (2) integration of additional risk factors including genetic and imaging data, (3) development of web-based or mobile applications for clinical deployment, and (4) longitudinal studies to assess temporal stability of the prediction models.

6. Conclusion

This study successfully demonstrates the effectiveness of ensemble machine learning approaches for breast cancer prediction using lifestyle and dietary factors. The Voting Classifier achieved the highest performance with 93% accuracy and 96% ROC-AUC, outperforming individual algorithms. The integration of SMOTE for class balance and LASSO for feature selection significantly enhanced model robustness and interpretability.

The findings suggest that ensemble methods, particularly when combined with appropriate preprocessing techniques, can provide reliable and accurate breast cancer prediction models. These results contribute to the growing body of evidence supporting machine learning applications in medical diagnosis and could inform the development of clinical decision support systems.

The identification of key lifestyle and dietary factors as strong predictors emphasizes the potential for preventive interventions and personalized risk assessment. Further validation studies and clinical trials are warranted to translate these findings into practical clinical applications.

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Conflicts of Interest

The authors declare no conflicts of interest.

Author Contributions

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