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A Least Absolute Shrinkage and Selection Operator Based Artificial Neural Network for Breast Cancer Identification

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Abstract

Breast cancer remains one of the leading causes of mortality worldwide, underscoring the need for timely and accurate diagnosis to facilitate effective treatment. This study explores the application of machine learning based feature selection techniques to improve the identification of breast cancer using the Wisconsin Breast Cancer Dataset. The dataset comprises 569 instances and 32 attributes. After removing one non-informative attribute, the final dataset retained 30 features and one target label. The target variable, originally labeled as malignant or benign was converted into a binary format (1 for malignant and 0 for benign). To enhance model interpretability and reduce feature redundancy, three feature selection algorithms Relief, LASSO, and Fast Conditional Mutual Information (FCMIM) were employed to identify the most relevant features. An Artificial Neural Network (ANN) classifier was trained using the selected features to differentiate between malignant and benign cases. The model's performance was evaluated using accuracy, sensitivity, specificity, and the Matthews Correlation Coefficient (MCC). The results demonstrate that feature selection significantly improves classification performance and computational efficiency. This framework underscores the potential of machine learning in oncology, offering a scalable and accurate solution for early breast cancer detection and enhanced diagnostic decision-making.

Keywords: *Machine Learning, Breast Cancer, Feature Selection, Disease Identification, Medical Information.*

1. Introduction

Breast cancer remains a leading global health concern, underscoring the need for early and accurate diagnosis. Traditional methods often rely on expert judgment, which may introduce variability. Machine learning (ML) offers consistent, data-driven predictions, but its effectiveness can be limited by redundant or irrelevant features. Feature selection addresses this by identifying the most informative attributes, enhancing model accuracy and efficiency. This study introduces an ANN based identification framework, optimized using feature selection algorithms Relief, LASSO, and Fast Conditional Mutual Information Maximization (FCMIM). Performance is evaluated using accuracy, sensitivity, specificity, and MCC, highlighting the value of feature selection in improving diagnostic outcomes. For example, [1] proposed a novel Aggregated Coefficient Ranking-Based Feature Selection (ACRFS) method, demonstrating its effectiveness in optimizing classification performance. Similarly, [2] explored genetic algorithms and hybrid neural networks to enhance feature selection and model efficiency. These studies highlight the necessity of integrating feature selection with ML models to enhance diagnostic accuracy. Our experimental results show that the proposed approach achieves promising performance and effectively enhances breast cancer identification,

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achieving an accuracy of 92.80% with LASSO feature selection algorithm.

2. Literature Review

Breast cancer remains one of the leading causes of mortality among women, necessitating accurate and timely diagnosis. Advances in machine learning (ML) and deep learning (DL) have significantly improved diagnostic accuracy by uncovering complex data patterns. Classical ML algorithms such as Artificial Neural Networks (ANN), Support Vector Machines (SVM), k-Nearest Neighbors (KNN), Decision Trees (DT), and ensemble methods have been widely applied for breast cancer classification [3]. A feedforward backpropagation network (FFBPN) applied to the Wisconsin Breast Cancer Database (WBCD) demonstrated improved accuracy through architectural optimization [4]. In comparative analyses, KNN outperformed Naïve Bayes (NB), with respective accuracies of 97.51% and 96.19% [5]. Evaluations of models such as SVM, Logistic Regression, DT, and Random Forest on the same dataset showed that SVM and Random Forest performed best, achieving 96.5% accuracy [6, 7]. Hybrid and metaheuristic techniques have further enhanced model performance. For instance, k-Particle Swarm Optimization (KPSO) combined with a Radial Basis Function Neural Network (RBFNN) significantly boosted classification accuracy [8], while the Elephant Herding Optimization (EHO) algorithm outperformed traditional models [9]. DL models, especially Convolutional Neural Networks (CNNs), have proven effective for histopathological image analysis. Among various DL architectures, Inception-ResNet-V2 yielded the highest accuracy [10]. Other approaches, such as CMOS-optimized analog ANNs [11] and CNN-ensemble hybrids [12], have also demonstrated high performance. Feature selection is critical in reducing dimensionality while retaining relevant attributes. Algorithms like Minimal Redundancy Maximum Relevance (mRMR) and Chi-square, when combined with SVM, achieved up to 99.71% accuracy [13]. Relief has also been successful in selecting informative features for medical diagnostics [14]. Explainable AI (XAI) methods, such as SHAP, enhance transparency by interpreting feature importance [17]. Local Learning-Based Feature Selection (LLBFS) has been shown to select optimal features effectively [16], and models like the Local Linear Wavelet Neural Network (LLWNN), optimized using the Firefly Algorithm, have outperformed conventional approaches [17]. Hybrid models continue to gain traction, including Recursive Least Squares (RLS) with LLWNN [18], Pixel Range Calculation (PRC) for feature extraction [19], and bilateral filter-based texture descriptors [20]. Tree-based methods like Random Forest [22] and XGBoost with SHAP-based interpretation [21] have also achieved strong results, with XGBoost reaching 97% accuracy. Integration of LLBFS with ANN further demonstrated superior diagnostic performance [23]. In summary, ML and DL methods have advanced breast cancer classification, with optimized ANN models often outperforming traditional approaches. The proposed LASSO-ANN framework combines effective feature selection with ANN optimization to enhance diagnostic accuracy.

3. Resources and Procedures

3.1.Dataset Description

The “Wisconsin Breast Cancer Dataset” [24] was selected for testing purposes in this study. Originally, this dataset included 569 instances with 32 attributes. However, as part of the data pre-processing step, one attribute that is ID was removed, leaving a final feature set of 30 features and 1 target label. The target label, which originally classified instances as malignant or benign, was converted into a binary format where malignant is represented as 1 and benign as 0. Thus, the feature matrix used in this study is 569 × 30, representing the extracted features

3.2.Data Preprocessing

Effective data representation required thorough preparation of the dataset. Pre-processing methods, including managing missing values, applying Standard Scaling (SS), and Min-Max Scaling were used to prepare the dataset for analysis.

3.3.Feature Selection

Feature selection was performed using algorithms like Relief, LASSO and FCMIM to identify key predictors while reducing redundancy. These methods prioritized the most relevant features. These methods improved model accuracy by minimizing feature complexity and enhancing interpretability.

3.3.1 Feature Selection Techniques for Optimal

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Model Performance

The Relief algorithm evaluates feature relevance by analyzing distances between instances and their nearest neighbors by adjusting feature weights to prioritize those that enhance class separation. This method improves model accuracy and efficiency by focusing on significant features while reducing redundancy and overfitting [25]. The LASSO algorithm selects key features by applying L1 regularization, shrinking less relevant feature coefficients to zero, simplifying the model while balancing accuracy and sparsity [26]. The FCMIM algorithm selects features by maximizing conditional mutual information with the target variable, ensuring relevance and minimal redundancy for high-dimensional datasets [25][26][27].

3.4.Comparison Model

An artificial neural network (ANN) is used for breast cancer prediction, consisting of input, hidden, and output layers. It processes data in one direction and is optimized using backpropagation. Feature selection methods like Relief, LASSO, and FCMIM enhance its predictive accuracy

3.5.Model Architecture

The artificial neural network (ANN) implemented in this study is structured to consist of three layers: an input layer, a hidden layer and an output layer. The input layer receives 30 selected features extracted from the dataset. The hidden layer comprises three neurons, utilizing the $ReLU$ activation function to incorporate non-linearity and enhance learning capacity. The output layer consists of a single neuron responsible for binary classification. The model initializes weights randomly and updates them iteratively using a backpropagation algorithm. The training process optimizes weights by minimizing the Mean Squared Error (MSE) loss function. The $ReLU$ activation function is applied at the hidden layer, while weight updates occur through gradient-based learning with a learning rate of 0.0035. Training is conducted over 1500 epochs, ensuring convergence toward an optimal solution.

3.6.Performance Evaluation Metrics

To evaluate classifier performance, several metrics were utilized. These parameters include the confusion matrix which serves as a foundation for assessing classification outcomes.

Accuracy = The percentage of correctly predicted events relative to the total events in the dataset.

$$Accuracy = \frac{(TP+TN)}{\sqrt{TP+TN+FP+FN}} \times 100 \quad (1)$$

where:

- **True Negative (TN):** The model correctly identifies a healthy individual as negative.
- **False Positive (FP):** The model incorrectly classifies a healthy person (negative case) as having breast cancer (positive case).
- **False Negative (FN):** The model incorrectly predicts a person with breast cancer (positive case) as healthy (negative case).
- **True Positive (TP):** The model correctly predicts a person with breast cancer (positive case) as having breast cancer.

Sensitivity = percentage of positive results correctly identified.

$$Sensitivity = \frac{(TP)}{\sqrt{(TP+FN)}} \times 100 \quad (2)$$

Specificity = The percentage of true negatives identified.

$$Specificity = \frac{(TN)}{\sqrt{(TN+FP)}} \times 100 \quad (3)$$

MCC = measures the correlation between actual and predicted classifications, ranging from -1(inverse prediction) to 1(perfect prediction)

$$MCC = \frac{T1}{\sqrt{T2 \times T3 \times T4 \times \times T5}} \times 100 \quad (4)$$

Here MCC is Matthews correlation coefficient, T1 = (TP×TN − FP × FN), T2 = (TP + FP),
T3 =(TP+FN) T4 = (TN+FP) and T5 =(TN+FN)

Weight Update Rules:

- Update for weights between hidden and output layers:

$$W_{ho} = W_{ho} + \eta . H^T \delta_0 \quad (5)$$

- Update for weights between input and hidden layers:

$$W_{ih} = W_{ih} + \eta . X^T \delta_h \quad (6)$$

Weight Update Equations.

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1. **Forward Pass Equations:**
   - Hidden Layer Activation:
     $$H = ReLU(XW_{ih}) \quad (8)$$
   - Output Layer Activation:
     $$\hat{Y} = HW_{ho} \quad (9)$$
2. **Backward Pass (Backpropagation) Equations:**
   - Output Layer Error:
     $$\delta_0 = (y - \hat{y}).ReLU'(\hat{y}) \quad (10)$$
   - **Hidden Layer Error:**
     $$\delta_h = \left(\delta_0 {W_{ho}}^T\right).ReLU'(H) \quad (11)$$

where:

- X is the input data,
- W_{ih} represents the weights connecting the input layer to the hidden layer
- W_{ho} represents the weights connecting the hidden layer to the output layer
- H is the hidden layer output,
- $\hat{Y}$ is the final predicted output,
- δ_0 is the output error,
- δ_h is the hidden layer error,
- η (learning rate) controls the step size of weight updates,
- $ReLU(x) = \max(0, x)$ is the activation function,
- $ReLU'^{(x)} = 1$ if $\chi > 0$, else 0,is the derivative of $ReLU$.

Error Equation

The error function used in this neural network is Mean Squared Error (MSE), which is defined as:

$$E=\frac{1}{n}\sum_{i=1}^{n}(y_i - \hat{y}_i) \quad (7)$$

where:

- E is the mean squared error,
- y_i represents the actual target value for the i^{th} sample,
- $\hat{y}_i$ denotes predicted output of neural network,
- n is the number of samples.

3.7.Suggested Approach

This study presents a structured approach to breast cancer classification using an Artificial Neural Network (ANN) combined with feature selection methods. After preprocessing the data handling missing values, normalization, and applying Relief, LASSO, and FCMIM the most relevant features are selected to reduce dimensionality. The dataset is split into training and testing sets (80:20), and model performance is evaluated using accuracy, sensitivity, specificity, and Matthews Correlation Coefficient (MCC).

4. Dıscussıon of Experımental Fındıngs

This section provides an in-depth evaluation of the experimental results, highlighting the performance of different classifiers.

4.1.Experimental Setup

Experiments were conducted in Python using machine learning libraries, including deep learning models like ANN. This setup enables a thorough comparison of these methods for heart disease identification

4.2.Results of Experiment

The results demonstrate the impact of selected feature sets and evaluation metrics on breast cancer classification. This study analyzes and ranks features based on their predictive importance using three methods Relief, LASSO, and Fast Conditional Mutual Information (FCMIM) to identify the most relevant attributes for accurate diagnosis. Relief evaluates features by comparing nearest neighbors from the same and different classes. Top-ranked features such as "radius_worst, concave_points_worst, perimeter_worst, texture_worst, radius_mean, perimeter_mean, concave_points_mean, area_worst, area_mean, concavity_mean, texture_mean, concavity_worst, smoothness_worst, and radius_se" highlight key tumor morphology indicators that effectively differentiate malignant from benign cases, enhancing classification accuracy. The top-ranked features identified by LASSO include "radius_worst, area_worst, concavity_se, compactness_mean, radius_se, area_se, fractal_dimension_worst, concave_points_mean, concavity_mean, concavity_worst, smoothness_se, symmetry_worst, concave_points_se, and area_mean". These features capture essential morphological and structural characteristics of tumors significantly contributing to accurate classification. Fast Conditional Mutual Information (FCMIM**)** is a feature selection method that optimizes relevance and reduces redundancy to enhance classification performance. The top ranked features identified by FCMIM include "perimeter_worst, area_worst, radius_worst,

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concave_points_mean, concave_points_worst, perimeter_mean, concavity_mean, radius_mean, area_mean, area_se, concavity_worst, perimeter_se, radius_se, and compactness_worst".

4.3.Performance of ANN Moodel with Different Feature Selection Algorithm

This chapter examines the performance of various classifiers using different feature selection techniques. It explores the impact of feature scores on model accuracy and efficiency.

4.4.Weight Analysis

In ANNs, weight values control neuron connections and are vital for learning patterns. Optimized weights enhance prediction accuracy, with impacting learning rates, convergence, and stability, influencing model performance. Below is the graph of summed weights vs. epochs for three algorithms (Figure 1).

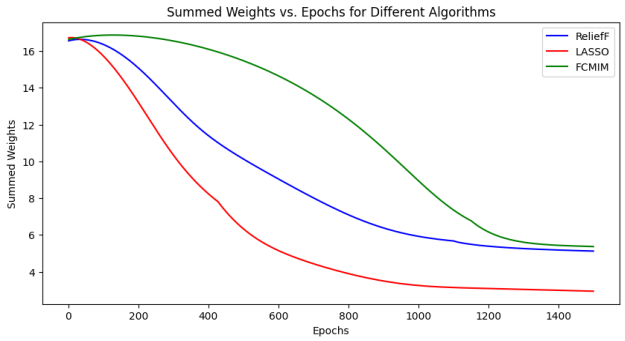

Figure 1 Graphical Representation of Weight Analysis of Different Algorithms

4.5.Error Analysis

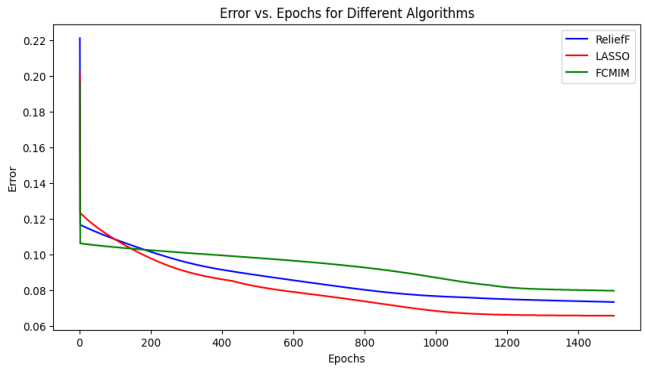

Figure 2 Graphical Representation of Error Analysis of Different Algorithms

In ANN training, the loss function measures the error between predicted and actual outputs. Relief, LASSO, and FCMIM affect error trends, with Relief causing fluctuations and LASSO ensuring steady error reduction through sparsity. Below is the graph of summed weights vs. epochs for three algorithms (Figure 2).

Confusion Matrix Comparison: - Table 2 presents the classification performance of three feature selection algorithms Relief, LASSO, and FCMIM on the WBC dataset. Each algorithm's ability to classify instances as either "benign (0)" or "malignant (1)" is evaluated. The table shows the number of correctly and incorrectly classified samples for both classes, with "Classified as Benign (0)" indicating the benign predictions and "Classified as Malignant (1)" showing the malignant predictions. Relief correctly identified 100 benign cases but misclassified 8, and accurately classified 57 malignant cases with 6 misclassifications. LASSO performed slightly better, correctly classifying 101 benign cases with 7 misclassifications and detecting 57 malignant cases correctly with 6 misclassifications. FCMIM showed strong performance, correctly identifying 93 benign cases (15 misclassified) and detecting 62 malignant cases with only 1 misclassification. Table 1 provides a comparative evaluation of classification performance using Relief, LASSO, and FCMIM, based on specificity, sensitivity, and Matthews Correlation Coefficient (MCC), assessing the effectiveness of each algorithm with selected feature subsets.

Table 1 Performance Result of Model with Different Algorithm

Fs Algorithm	Specificity (%)	Sensitivity (%)	MCC (%)
Relief	89.81	95.24	83.26
LASSO	93.52	90.48	83.72
FCMIM	86.11	89.00	81.95

Table 2 Confusion Matrix Result of Model with Different Algorithm

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Dataset	Algorithm	Class	Classified as Benign (0)	Classified as Malignant (1)	Classification
WBC	Relief	Benign (0)	100	8	91.81
		Malignant (1)	6	57	
	LASSO	Benign (0)	101	7	92.40
		Malignant (1)	6	57	
	FCMIM	Benign (0)	93	15	90.64
		Malignant (1)	1	62	

Relief based feature selection demonstrates strong performance, with 89.81% specificity for benign tumors, 95.24% sensitivity for malignant cases, and an MCC of 83.26%, reflecting balanced classification across both classes. LASSO-selected features improve predictive performance with 93.52% specificity, surpassing Relief in classifying benign cases. While sensitivity is 90.48%, the MCC of 83.72% indicates balanced performance and greater prediction stability. FCMIM-elected features show competitive performance with 86.11% specificity, indicating a higher false-positive rate. Sensitivity at 89.00% is the lowest, and the MCC of 81.95% reflects balanced but slightly weaker performance compared to Relief and LASSO. LASSO excels in classifying benign cases with high precision, while Relief is better at detecting malignant cases. Bar charts compare Relief, LASSO, and FCMIM with ANN model, highlighting LASSO's superior overall performance (Figure 3).

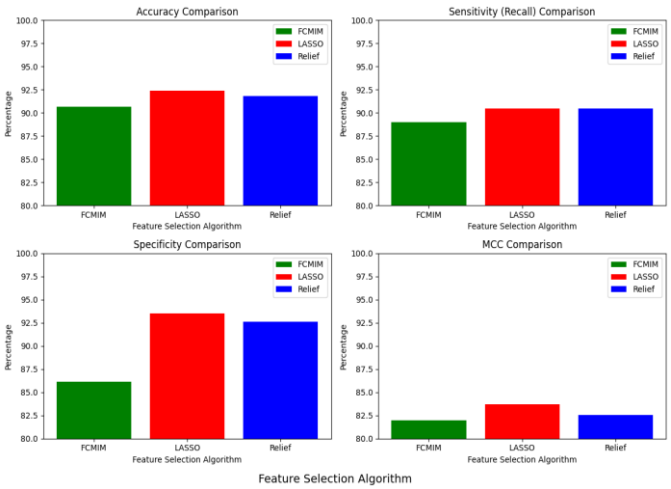

Figure 3 Comparison of Different Feature Selection Algorithms ANN Model

5. Comparison of Breast Cancer Prediction Model

This section reviews, compares breast cancer classification models and accuracy to identify the most effective diagnostic approaches. Below is the comparative table (3):

Table 3 Comparative Analysis of Existing Studies

Paper Name	Method Used	Accuracy (%)
Enhancing Breast Cancer Detection and Classification Using Advanced Multi-Model Features and Ensemble Machine Learning Techniques [28]	DTC (Decision Tree Classifier) under the Stacking (Base Layer) category	91.6 ± 1.7
Breast Cancer Prediction Based on Neural Networks and Extra Tree Classifier Using Feature Ensemble Learning [29]	Quadratic SVM [Quadratic Kernel]	81.9
A Least Absolute Shrinkage and Selection Operator based Artificial Neural Network for Breast Cancer Identification LASSO-based Artificial Neural Network (ANN)	LASSO feature selection algorithm with Artificial Neural Network (ANN) model	92.40

Conclusion

This study explored the impact of feature selection

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techniques Relief, LASSO, and FCMIM on breast cancer identification model performance. The results show that selecting relevant features significantly improved accuracy, specificity, sensitivity and MCC. LASSO outperformed the others, effectively retaining key features while minimizing redundancy. This research advances machine learning based diagnostic methods in healthcare**.**

Future Scope: Future work may involve using more diverse datasets, applying ensemble-based feature selection and optimizing hyper parameters to enhance model robustness. Incorporating explainable AI can further improve transparency by clarifying feature importance.

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