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HYBRID ENSEMBLE LEARNING MODEL WITH BALD EAGLE SEARCH FEATURE OPTIMIZATION FOR HEART DISEASE DIAGNOSIS

N. SENTHILSELVAN¹, B. KARTHIKEYAN², P.S. SUPRAJA³, H. SAMIHA⁴, B. ELANGO VAN⁵,
R. VIJAY SAI¹, G. MANIKANDAN^{1,*}

¹School of Computing, SASTRA Deemed To Be University, Thanjavur, India

²Department of CSE, KPR Institute of Engineering and Technology, Coimbatore, India

³Tata Consultancy Services, Bangalore, India

⁴Cognizant Technology Solutions, Chennai, India

⁵Department of CSE, Koneru Lakshmaiah Education Foundation, Vijayawada, India

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Abstract. Heart disease is a wide phrase that covers a variety of disorders affecting the heart and blood arteries. It's one of the leading causes of death globally. In some cases, heart disease develops silently over years, showing no symptoms until a major event like heart attack or stroke occurs. It results from a complex interplay of lifestyle, genetic, metabolic, and environmental factors. The growing prevalence and complexity of heart disease highlight the urgent need for intelligent, data driven early prediction systems. Healthcare, which has been transformed by machine learning, a branch of Artificial Intelligence, allows computers to learn and make precise predictions. Unlike traditional statistical techniques, Machine learning algorithms can model complex, non-linear relationships and capture subtle patterns in medical data, making them highly suitable for heart disease prediction. These models exposed to more data, so they improve over time, this makes them more accurate with continuous retaining. This work uses Bald Eagle Search optimization, a metaheuristic algorithm for feature selection. For classification, ensemble methods such as Random Forest, Voting, Bagging, Stacking, and various boosting techniques are used.

*Corresponding author

E-mail address: manikandan@it.sastra.edu

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The dataset for this work has 1025 instances and 14 features which is obtained from Kaggle. The result shows that Stacking has achieved highest accuracy of 95.61%.

Keywords: bald eagle search optimization; ensemble methods; heart disease; machine learning; metaheuristic algorithm; stacking.

2020 AMS Subject Classification: 68T09.

1. INTRODUCTION

Heart disease is one of the major causes of death in many countries, with risk factors such as elevated cholesterol, diabetes, high blood pressure, smoking, obesity, insufficient physical activity, and family with CVD history [1]. Symptoms associated with heart disease can include shortness of breath, fatigue, chest pain, and irregular heartbeats. Coronary artery disease is the most prevalent type, resulting from the blockage of arteries due to plaque accumulation. Symptoms of heart disease can be chest pain, trouble breathing, tiredness, and irregular heartbeats. But in some cases, no symptoms are experienced till the occurrence of heart attack [2]. The most common type is coronary artery disease, which happens when arteries get blocked by plaque. Doctors use tests like electrocardiograms (ECG), echocardiograms, stress tests, and angiography to diagnose heart disease. To prevent it, people should eat better, exercise more, manage stress, quit smoking, and limit alcohol. Genetics can also play a role in the risk of developing heart disease.

Ongoing technology advancements in machine learning improve medical diagnosis capabilities which results in better patient and healthcare service outcomes. Machine Learning (ML) automates the diagnosis of cardiac illness thereby reducing the stress on healthcare professionals and improving efficiency. ML models can detect cardiac illness early by processing massive amounts of medical data, leading to early treatment and risk reduction. ML models improve with additional data and provide stronger diagnostic skills. ML simplifies diagnosis and eliminates superfluous testing, lowering healthcare expenditures and improving patient care. Advanced machine learning algorithms can identify deeper patterns in patient data, outperforming traditional diagnostic procedures. ML's scope is increasing rapidly in recent times [3].

To build ML models for the diagnosis of heart disease, patient specific variables, such as medical records, lifestyle factors, and clinical test outcomes, must be examined. By utilizing

ML models, doctors may make informed decisions that result in suitable treatment recommendations. With this it is clearer that doctors rely on ML tools [4]. While working with these models, it is crucial to avoid overfitting, and pruning can help with that. Ensemble classifiers combine independent classifier predictions using consensus-based prediction to increase performance. Adjusting hyperparameters like tree number, learning rate, and depth affects ensemble algorithm performance. These important characteristics must be tuned to maximize model system performance.

The dataset for this work is heart.csv which is obtained from Kaggle. It is a combination of data from four hospitals. This dataset totally has 1025 instances and 14 features. This work utilizes Bald Eagle Search optimization (BES) to select the important features. Various ensemble methods were also utilized in this work. The result shows that Stacking has achieved higher accuracy than other models.

2. RELATED WORKS

A framework was suggested by Patro, S. P. et al. [5] to predict heart disease. This framework was built on various classifier algorithms, such as NB, KNN, SVM, and Ridge regression. The researcher utilized PCA and LDA to classify the data. They took advantage of a data set that was open source. All fourteen characteristics from an open-source data set were utilized in this method. The research concludes that the support vector machine offers an accuracy of 92%. Khan, M. A., et al. [6] studied wearable devices in the Internet of Medical Things health monitoring system. This study examined machine learning based heart disease prediction properties. Researchers utilized modified salp swarm optimization an adaptive neuro fuzzy inference method to enhance the accuracy of the IoMT framework. The MSSO-ANFIS prediction model outperforms others with 99.45 accuracy and 96.54 precision.

Wang, J., et al. [7] developed a two-level stacking architecture consisting of a base and a meta level. The outputs of base classifiers are utilized as inputs for the meta classifier processing. For Experimentation Z-Alizadeh Sani CHD dataset comprising 2020 cases of coronary artery disease (CAG) is used. The results of this model demonstrated an accuracy of 95.3%, specificity of 94.44%, and sensitivity of 95.84%. A filter approach utilizing a multi objective differential evolution algorithm was presented by Subrat Kumar Nayak et al. [8] for feature selection. This

algorithm handles duplicate and undesirable dataset features. They tested feature subsets of 23 needed datasets using 10-fold cross validation in this innovative approach. This study tests 23 benchmark datasets using 10-fold cross validation and four popular classifiers.

A new healthcare architecture using Swarm-ANN to forecast cardiac disease was created by Nandy et al. [9]. This approach randomly creates a number of NNs for training and framework assessment based on their consistency. A new heuristic formulation controlled the weight of the NN populations using two weight adjustment periods throughout training. The proposed Swarm-ANN technique predicted cardiovascular illness 95.78% of the time using a benchmark dataset. Nagarajan et al. (2022) [10] developed an ML-based cardiac detection approach that was successful and accurate.

The GCSA model outperformed earlier feature selection methods in classification accuracy with 94% accuracy. Al-Yarimi et al. (2021) [11] proposed a model developed through machine learning techniques to predict cardiac disease. Optimal feature selection and an appropriate initial data corpus were essential for achieving the primary objective of determining predictive analytics while minimizing false alerts. The investigation illustrated the efficacy of the proposed model relative to existing feature selection methods for predicting HD.

Tiwari, A., et al. [12] devised a framework leveraging stacked ensemble classifier to predict cardiovascular disease. Algorithms such as Extra Trees Classifier, RF and XGBoost were employed. The study used an extensive dataset, a blend of Hungarian, Switzerland, Cleveland, Statlog, and Long Beach VA datasets. The model's evaluation was done using performance metrics like ROC, specificity, F1-score, accuracy, AUC, sensitivity, and MCC. The proposed framework was reportedly able to achieve the accuracy of 92.34% which is greater than that mentioned in the literature. Zhang, J., et al. [13] introduced a framework employing ensemble ML techniques to predict coronary heart disease (CHD). This method applied different classifiers to this model in a two-level stacked generalization. They made use of sixty-four 2D speckle tracking echocardiographic (2D-STE) features and seven clinical features. Their ensemble model reportedly achieved an accuracy of 87.7%, Sensitivity of 90.3%, Specificity is 84.3% and AUC of 90.4%.

A framework based ESNN model to predict heart diseases was proposed by Imran et al. [14]. Classifiers like LR, DT, GB, RF, XGBoost, AdaBoost, SVM, KNN, and Naive Bayes were used to combine machine learning and deep learning in this framework. Combined datasets from Cleveland, Long Beach VA, Statlog, Hungarian, and Switzerland were used for the analysis. Data preprocessing involved handling missing values (imputation), outlier removal, normalization, and feature reduction using PCA. The ESNN model was found to have an accuracy of 95%. A study [15] proposed an ensemble ML framework for predicting disease. Various models such as LDA, CART, SVM, KNN and Naive Bayes were used with Random Forest functioning as meta classifier. They used patient data from a dataset and applied preprocessing techniques. It was shown in the study that the ensemble model accuracy rose from 85.53% to 87.64%. The authors of [16] introduced a framework incorporating a stacked classifier model for disease prediction. A two-tier stacking approach was used to merge several heterogeneous learners. They utilized the UCI dataset. The study found that the stacking model reached an accuracy of 92%.

An accuracy-based stacked ensemble learning model to predict heart disease was presented by Bhutia, S., et al. [17]. The method relied on LR, RF, and AdaBoost classifiers. Logistic Regression Recursive Feature Elimination method was employed for feature selection; Normal Scalar to scale the data. Hyperparameter tuning was achieved through random and grid search techniques. Kaggle's Cleveland dataset mentioned in this study. According to the study, AB-SEL model achieved 90.16% accuracy with an AUC of 0.892 and computation time was 0.2 secs. The authors of [18] proposed a heart disease prediction framework using ensemble algorithms. RF, XGBoost, and LR were used with a Voting Classifier in the framework to boost prediction accuracy. Three Kaggle datasets were used with 5-fold cross validation. The study reported that the ensemble model achieved 99.4% training accuracy and 91.7% testing accuracy. Table 1 summarizes the various works conducted by other authors.

3. PROPOSED METHODOLOGY

The main objective of this work is diagnosing heart disease using various ML models. This work is structured as follows: obtaining the heart disease dataset and scaling it, then feature selection using BES and classification using various ensemble models, and using various metrics for model evaluation. Figure 1 shows this in detail.

TABLE 1. Summary of Various Works

References	Methodology Used	Feature Selection	Dataset	Accuracy (%)
Biswas et al. [19]	SVM, LR, DT, RF, NB, KNN	ANOVA F-value, Chi-Square, Mutual Information	UCI Cleveland	94.51
Ahmad et al. [20]	LR, Neural Networks, RF, SVM, Naive Bayes, KNN	Mutual Information, ANOVA, Chi-Square	Clinical indicators dataset	82.3
Theerthagiri et al. [21]	Gradient Boosting	Recursive Feature Elimination (RFE)	Cardiovascular disease dataset	89.7
Sowmiya et al. [22]	Stacking classifier	Improved BSSA	Cleveland and Statlog	95
Elsedimy et al. [23]	Quantum-behaved Particle Swarm Optimization with SVM	QPSO-based feature selection	Cleveland Heart Disease Dataset	96.31
Nourah et al. [24]	SVM, KNN, C4.5, RF, Adaboost, LR, NB	Chi-squared	UCI Cleveland	87.91

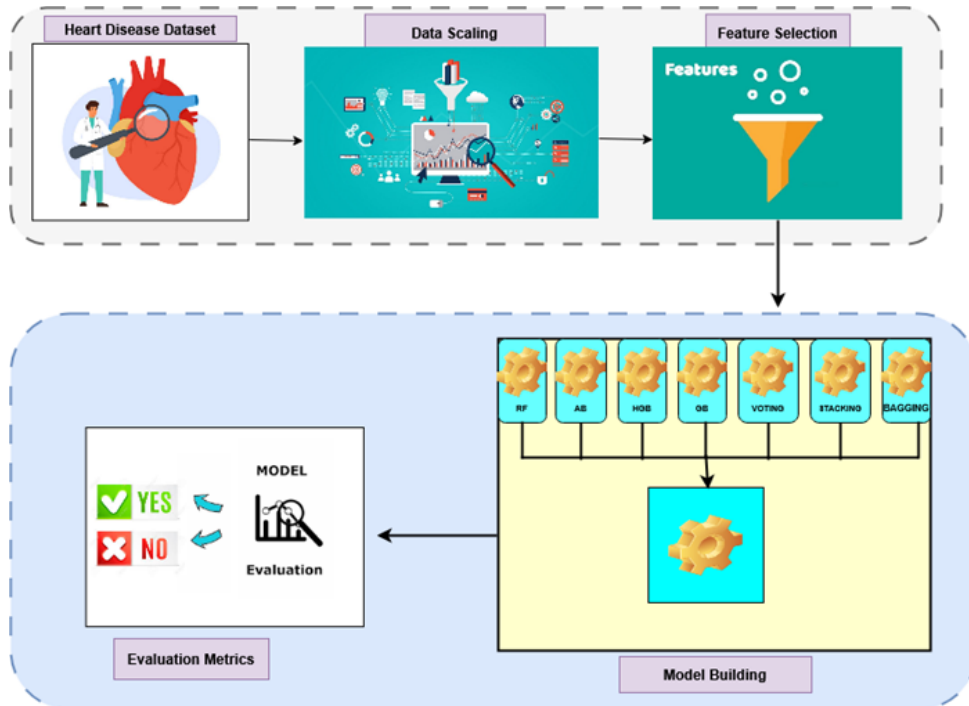


FIGURE 1. Proposed Methodology

3.1. Feature selection using BES optimization. Feature selection is the process of choosing the most relevant from the dataset to build a more efficient, accurate and interpretable model.

Irrelevant or redundant features can introduce noise and reduce prediction performance. So, in this work BES used for feature selection. BES is a metaheuristic optimization method inspired by nature. It is based on bald eagle hunting behavior [25]. This algorithm is divided into three parts, they are Select space (Exploration), Search within space (Exploitation), Swooping (Final decision) [26]. The steps in BES are as follows:

Step 1: Initialization

- A subset of features is represented by each candidate solution (1 – selected, 0 – not selected).
- Eagles, a population of these solutions, are created at random.

Step 2: Select Space (Exploration)

- Eagles explore the feature space by flying randomly over a wide area.
- This simulates searching for regions in the feature space that are likely to contain high-quality feature subsets.
- Positions (feature subsets) are updated using the mathematical equation:

$$(1) \quad Z_{\text{new}} = Z_{\text{current}} + r \cdot (Z_{\text{best}} - Z_{\text{current}})$$

where r is a random value, and Z_{best} is the current best feature subset.

Step 3: Search within Space (Exploitation)

- Eagles focus their search after identifying a promising area.
- This focuses the search on refining and enhancing the best solutions found during the exploration phase.
- Exploitation strategies use spiral or curved paths to simulate bald eagles gliding and analyzing their prey area.

Step 4: Swooping (Final Decision)

- The ideal solution, or the best feature subset, is captured by the best candidate (eagle) who dives (swoops).
- This involves intensifying the search around the current best solution using fine-tuned movements.

Step 5: Fitness Evaluation

- For each subset, a fitness function is calculated as:

$$(2) \quad \text{Fitness} = \alpha \cdot (1 - \text{Accuracy}) + \beta \cdot \frac{\text{No. of selected features}}{\text{Total features}}$$

where α and β are weights that balance accuracy and simplicity.

Step 6: Iteration Until Convergence

- The algorithm runs for several iterations (generations), continuously updating and improving the feature subset until convergence or a stopping condition is met.

3.2. Random Forest (RF). RF is a bagging technique, meaning each decision tree trains from a bootstrapped sample and also uses a random set of features. This additional randomness decreases the correlation between trees and hence increases generalities. Random Forest uses data and feature randomness, thereby diversifying model and reducing overfitting. It handles noise well, scales to large datasets and easily takes care of missing values.

3.3. Bagging. Bagging (Bootstrap Aggregating) refers to training of number of models on random subsets, that have been bootstrapped of the original dataset. By sampling with replacement, a subset is created: some samples may be repeated and some samples may not be present at all. The basic idea is to average the base models, typically decision trees predictions, in order reduce variance. In regression, predictions from all models are averaged to obtain the final prediction; in classification, it is obtained by majority voting. Mathematically, the prediction for a new input x is represented as,

$$(3) \quad Y = \frac{1}{N} \sum_{a=1}^N f_a(x)$$

3.4. AdaBoost. AdaBoost (Adaptive Boosting) trains weak learners in a sequential manner, with each subsequent learner focusing more on the errors of its predecessor. All instances in the training data initially have equal weight. The weights of misclassified instances are boosted after each round, forcing next learner to pay more attention. The final prediction is a weighted majority vote/sum of all learners - where weights are assigned to each learner based on its accuracy. To significantly modify the data distribution for AdaBoost, in order that weak learners convert strong learner.

3.5. Gradient Boosting (GB). Gradient Boosting is a sequential modelling method which is similar to AdaBoost but in contrast to AdaBoost, it does not optimize for the error rate. Instead, a new model is added that fits to the residuals (errors) of existing ones and a loss function is optimized. At each iteration, a model is fitted to the negative gradient of the loss function which becomes a pseudo-residual. This approach corrects errors without resampling the data.

3.6. Histogram-Based Gradient Boosting (HistGB). HistGB is a faster variant of GB, it buckets continuous features into discrete bins (histograms) thus making it more efficient to train on large datasets. Computation expense is reduced, yet accuracy maintained by considering histogram bins (rather than every possible split point). It naturally handles large data, high dimensions and missing values: HistGB is fast due to data compression and speeding up split finding without losing much accuracy.

3.7. Stacking. In stacking, multiple models are trained, called base learners, on the same dataset and a meta-model aggregates their predictions. The base learners may capture different aspects of the data and the meta-model learns to effectively combine them. Out-of-fold predictions are utilized to avoid leakage during training. Stacking is very powerful as it takes advantage of the diversity in multiple learning algorithms instead of depending on a single one.

3.8. Voting. Voting is an ensemble classification method that uses predictions from several models, aggregating them with either hard voting or soft voting. In hard voting, the class label predicted by the majority of the models is selected, while in soft voting the average of the predicted probabilities is calculated. Voting works best when individual models are accurate and diverse: specifically, it can be useful to join models of different strengths.

4. EXPERIMENTAL ANALYSIS AND RESULTS

4.1. Dataset Description. As mentioned earlier, it is Kaggle obtained dataset. The URL for the dataset is given in [27]. This dataset has data collected from the hospitals of Cleveland, Switzerland, Hungary, and Long beach.

4.2. Data Scaling. Data scaling involves standardizing or normalizing attributes in the dataset to a specific scale, thereby ensuring that all of them contribute equally to a machine learning

model. This work used “StandardScaler” to normalize numerical features, ensuring they have zero mean.

4.3. Feature Selection and Classification. Using BES optimization algorithm, top 6 important features were selected. They are ['cp', 'thalach', 'exang', 'oldpeak', 'ca', 'thal']. These features are then classified using different ensemble models. Figure 2 Shows the correlation matrix of the selected features.

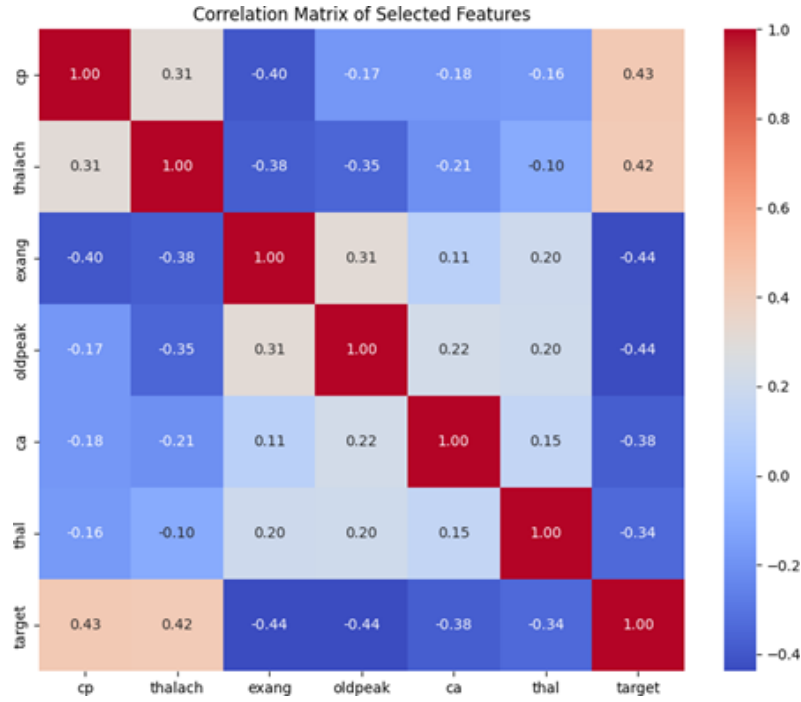


FIGURE 2. Correlation Matrix of Selected Features

4.4. Results and Discussion. To evaluate model performance various key metrics such as accuracy, recall, f1-score, and precision are used. Accuracy: It shows the overall effectiveness of the model by calculating the ratio of correctly predicted instances to the total number of instances.

$$(4) \quad \text{Accuracy} = \frac{T_p + T_n}{T_p + T_n + F_p + F_n}$$

Precision: It shows how many of the instances that were predicted as positive are actually positive.

$$(5) \quad \text{Precision} = \frac{T_p}{T_p + F_p}$$

Recall: It tells how many of the actual positive instances the model successfully identified.

$$(6) \quad \text{Recall} = \frac{T_p}{T_p + F_n}$$

F1 score: It is a performance metric that combines precision and recall into a single value by calculating their harmonic mean.

$$(7) \quad \text{F1-Score} = \frac{2 \cdot \text{Precision} \cdot \text{Recall}}{\text{Precision} + \text{Recall}}$$

A confusion matrix (CM) provides a detailed overview of a classification model's performance on test data with known labels. It helps in visualizing the types of errors the model makes. Confusion Matrix obtained for various ensemble model is given from Figure 3 to Figure 9. Table 2 shows the results of various ensemble models. The ROC curve obtained is given in Figure 10. The bar plot for the accuracy of each model is given in Figure 11. From the Table 2 and Figure 12, it's clear that stacking performed best compared to other models with an accuracy of 95.61%. The bar plot for each model's precision is shown in Figure 12. The graph for recall of each model is shown in Figure 13. The graph for F1-score of each model is shown in Figure 14.

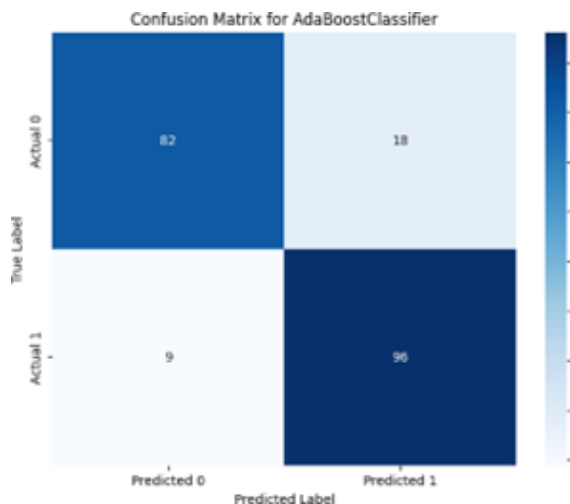


FIGURE 3. CM for AdaBoost

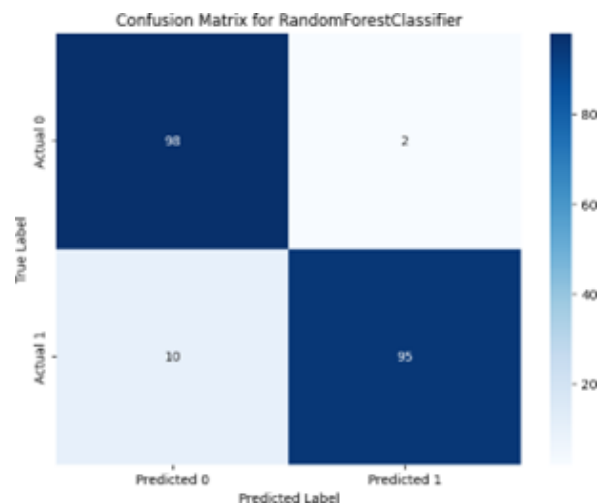


FIGURE 4. CM for RF

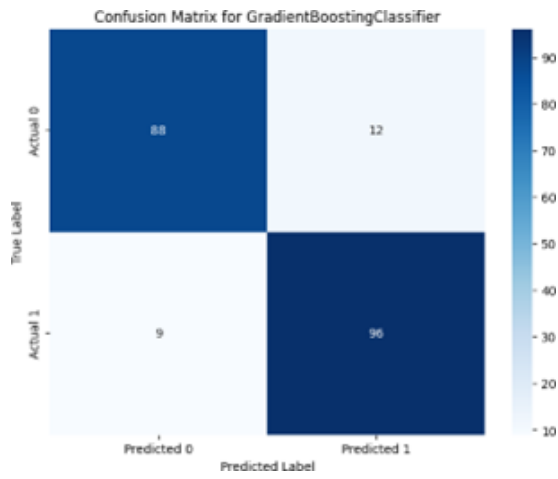


FIGURE 5. CM for GB

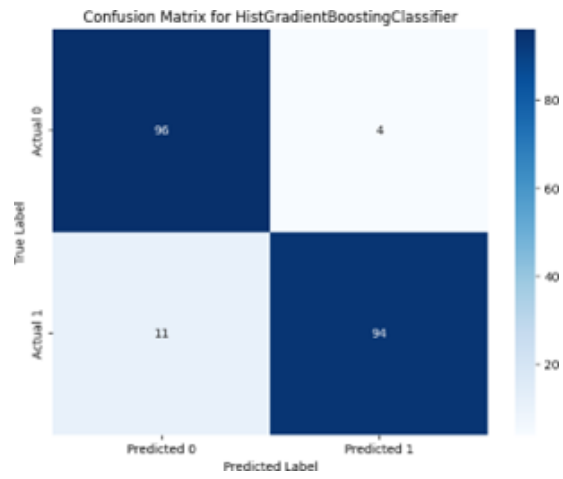


FIGURE 6. CM for HistGB

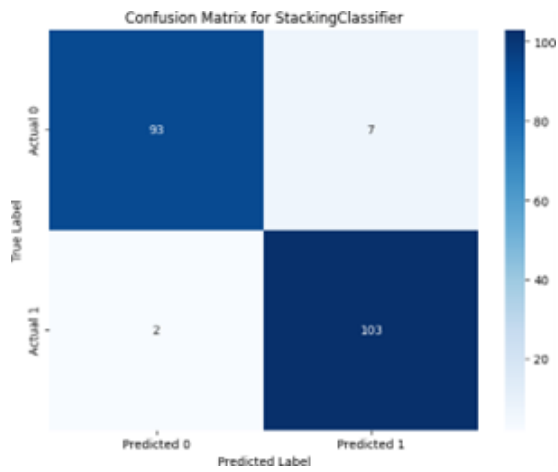


FIGURE 7. CM for Stacking

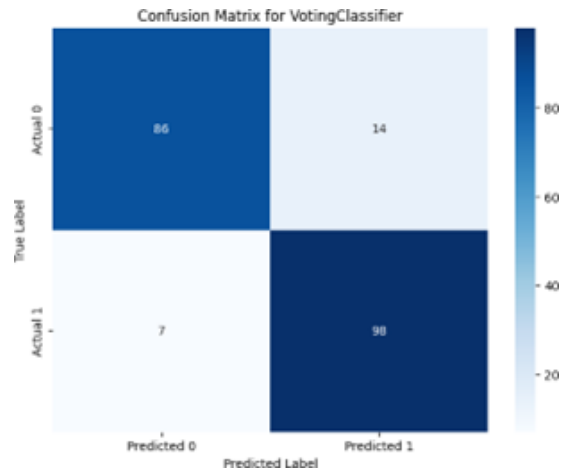


FIGURE 8. CM for Voting

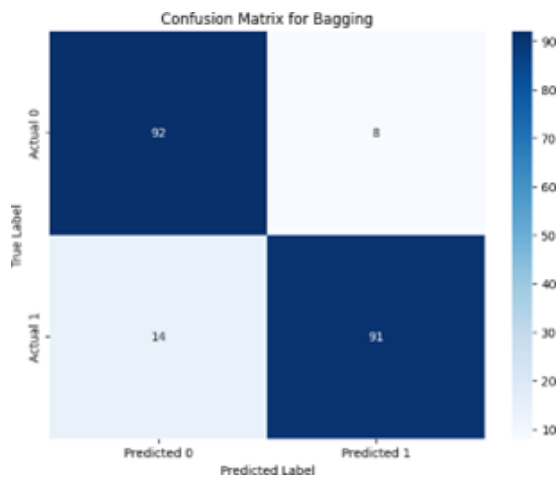


FIGURE 9. CM for Bagging

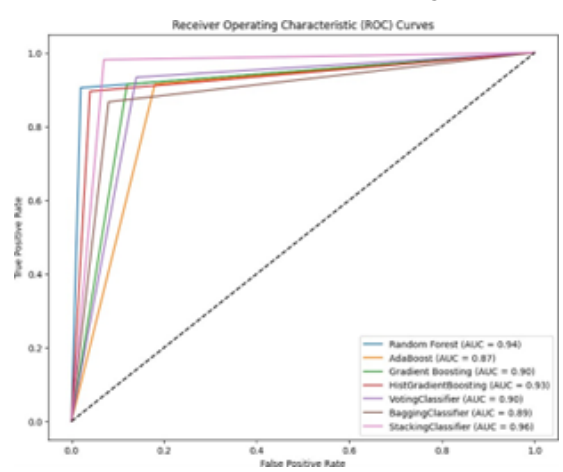


FIGURE 10. ROC Curve

TABLE 2. Result of Ensemble Models

Model	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)
Random Forest	94.146	97.938	90.476	94.059
AdaBoost	86.829	84.211	91.429	87.671
HistGB	92.683	95.918	89.524	92.611
Gradient Boosting	89.756	88.889	91.429	90.141
Voting	89.756	87.500	93.333	90.323
Bagging	89.268	91.919	86.667	89.216
Stacking	95.610	93.636	98.095	95.814

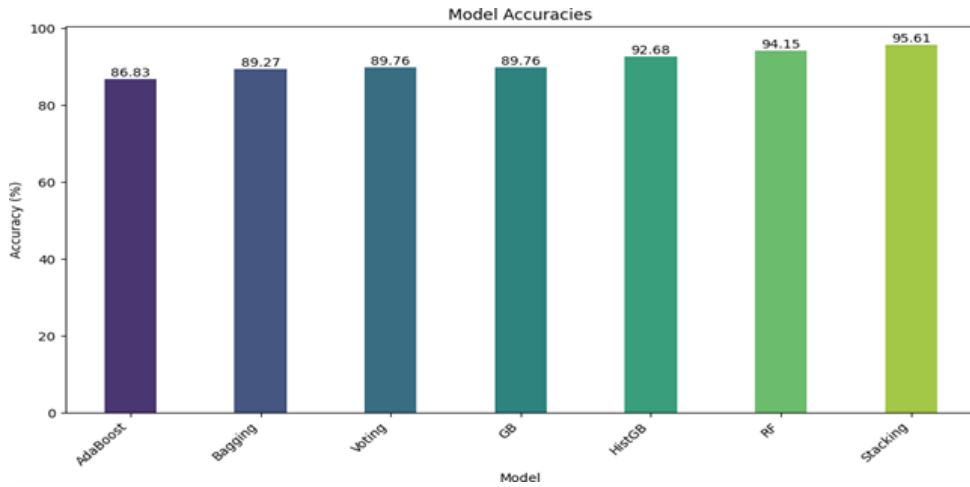


FIGURE 11. Accuracy Comparison

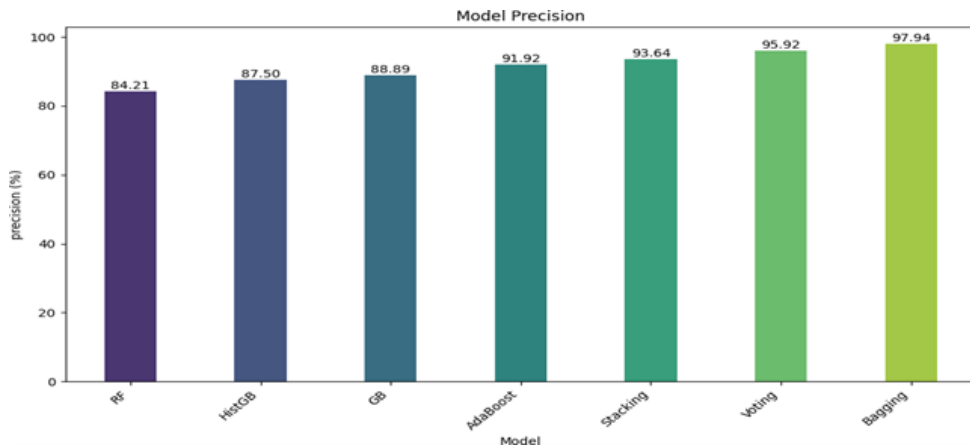


FIGURE 12. Precision Comparison

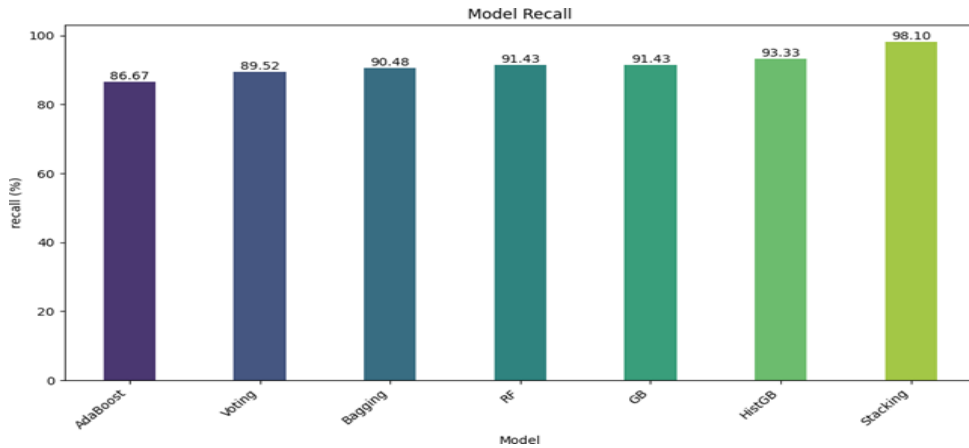


FIGURE 13. Recall Comparison

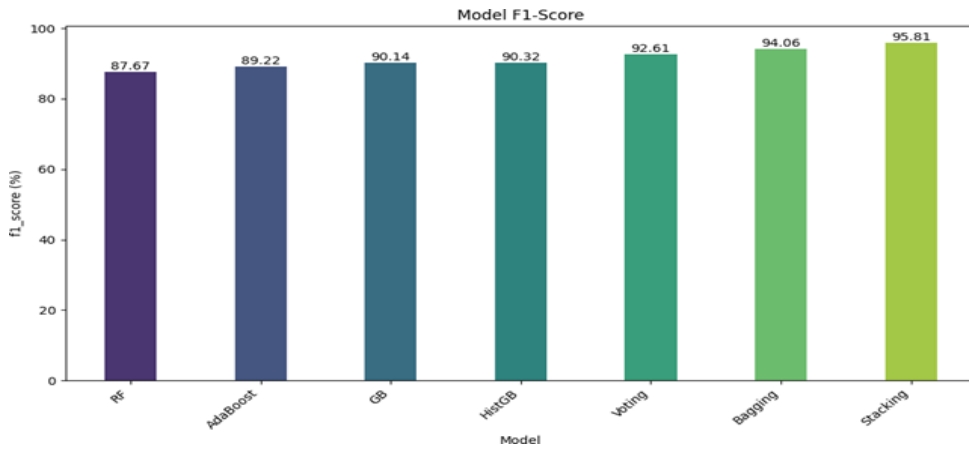


FIGURE 14. F1-Score Comparison

5. CONCLUSION

Heart disease covers a wide variety of heart and blood vessel conditions; usually this progresses without obvious symptoms for a while until followed by an event like heart attack. Due to factors such as unhealthy lifestyle, genetic predisposition and metabolic risks it remains a leading cause of mortality worldwide. Symptoms develop slowly and are complicated, so diagnosing them early is crucial but difficult. Machine learning ingests large and complex health data to uncover hidden risk patterns. The greater the availability of data, the more accurate these models become and allow faster reliable diagnosis. Machine learning supports early detection, thus assisting clinicians in decisions, and reducing burden on healthcare. This study demonstrates the effective use of machine learning and metaheuristic feature selection in predicting

heart disease. By applying the Bald Eagle Search algorithm and ensemble classifiers, the model achieved high accuracy, with stacking performing the best at 95.61%. These findings highlight the potential of advanced computational techniques in building reliable, data-driven tools for early heart disease diagnosis and prevention.

AUTHOR CONTRIBUTIONS

The authors confirm contribution to the paper as follows: study conception and design: Senthil-selvan N; data collection: Elangovan B; analysis: Karthikeyan B; Interpretation of results: Manikandan G; draft manuscript preparation: Supraja P.S and Samiha H. All authors reviewed the results and approved the final version of the manuscript.

DATA AVAILABILITY

The benchmark research materials used in this research can be downloaded from <https://www.kaggle.com/datasets/johnsmith88/heart-disease-dataset>.

CONFLICT OF INTERESTS

The authors declare that there is no conflict of interests.

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