Optimizing Heart Disease Prediction with Random Forest and Ensemble Methods

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Abstract

This study evaluates ensemble learning techniques for optimizing heart disease prediction, with a focus on Random Forest due to its robustness in handling complex medical data. The dataset used, "Heart Disease Prediction Dataset" from Kaggle, consists of 270 instances and 13 features like age, cholesterol, and family history. Data preprocessing involved mean imputation for missing values and min-max normalization. The study compares Random Forest with other ensemble classifiers—AdaBoost, Gradient Boosting, and XGBoost—using 10-fold cross-validation and evaluation metrics such as accuracy, precision, recall, and F1 score. Results show that Random Forest outperforms the other models with an accuracy of 87.04%, precision of 85.00%, recall of 80.95%, and F1 score of 82.93%. These findings emphasize Random Forest's ability to maintain prediction stability across various medical attributes and imbalanced data. Although the study highlights Random Forest as a promising method for early heart disease risk prediction, it remains a computational evaluation and requires clinical validation. The results aim to inform the development of predictive tools for enhancing early diagnosis and preventive strategies in healthcare systems.

Keywords— Random Forest, Ensemble Learning, Heart Disease Prediction.

1. INTRODUCTION

Heart disease has become one of the leading causes of death worldwide, with its prevalence continuing to rise alongside modern lifestyles and increasingly complex risk factors. According to data from the World Health Organization (WHO), coronary heart disease ranks as the primary cause, accounting for approximately 17.9 million deaths each year, which represents about 31% of all global deaths. This underscores the importance of developing more sophisticated predictive methods to identify individuals at high risk of heart disease, enabling earlier medical intervention to prevent serious complications.

In efforts to prevent and manage heart disease, machine learning-based prediction techniques have played a significant role in processing complex medical data. Through this approach, hidden patterns and relationships within the data can be uncovered, ultimately aiding in making more accurate predictions. Although various traditional classification algorithms have been utilized, challenges posed by medical data, such as heterogeneity, complexity, and imbalance, often make conventional algorithms less effective in delivering the expected results. Therefore, more robust and flexible solutions, such as ensemble learning, have become relevant.

One of the most recognized ensemble learning techniques is Random Forest. This technique combines multiple decision tree models, where each tree is built from different data

samples (using the bagging method). By combining predictions from multiple trees, Random Forest reduces prediction variability and minimizes the risk of overfitting.

This study focuses on evaluating the performance of Random Forest for heart disease prediction using the "Heart Disease Prediction Dataset" compiled by Robert Hoyt on Kaggle https://www.kaggle.com/datasets/thedevastator/predicting-heart-disease-risk-using-clinical-var, which contains 270 instances and 13 features such as age, cholesterol, resting blood pressure, and family history.

To ensure a comprehensive evaluation, Random Forest is compared with three other ensemble learning algorithms: AdaBoost, Gradient Boosting, and XGBoost, using standardized metrics and 10-fold cross-validation. Unlike prior works that only apply ensemble methods individually, this study offers a comparative analysis and highlights the practical strength of Random Forest in handling small, diverse clinical datasets. The novelty lies in its emphasis on model robustness across multiple evaluation metrics, particularly in medical data scenarios where both precision and recall are critical. The findings are expected to support the development of reliable early diagnosis tools in cardiovascular healthcare. The collected data will undergo preprocessing, which includes cleaning missing values, handling invalid data, and normalizing or standardizing data if necessary. After data processing, the next step is to build a predictive model. In this phase, classification algorithms will be applied to identify patterns associated with heart disease risk. Each algorithm will be evaluated using commonly used machine learning evaluation metrics, such as accuracy, precision, recall, and F1 score. Random Forest will be the primary focus due to its ability to minimize the bias-variance trade-off and handle data with complex variables.

The evaluation process will be conducted gradually by comparing the prediction results from the various algorithms used. Random Forest is expected to demonstrate advantages in terms of accuracy and prediction stability compared to other algorithms, especially in the context of processing medical data. Although the dataset is structured in tabular format, it contains noisy and incomplete records that commonly arise in clinical data collection. To address this, the preprocessing phase included handling missing values through mean or mode imputation, normalization of numerical features to ensure scale consistency, and label encoding of categorical variables. These steps were essential to reduce noise, improve data quality, and enhance the model's ability to generalize effectively. This algorithm is also expected to manage both categorical and numerical predictor variables, which frequently appear in medical data.

The scope of this study is limited to publicly available data, specifically the "Heart Disease Prediction Dataset", which contains patient data related to heart disease. While this study does not involve clinical validation, it aims to offer a technical comparison of several ensemble learning algorithms in the context of heart disease prediction. The findings may provide preliminary insights for future research on predictive modeling using machine learning in medical data analysis. Although not directly applicable to clinical decision-making, the results could serve as a foundation for further investigations involving real-world clinical datasets and validation in medical settings.

2. RESEARCH METHODS

Classification is a machine learning technique for predicting the class of an instance based on input features, commonly used in heart disease prediction. Common algorithms include Support Vector Machines (SVM), Logistic Regression, and Neural Networks (NN) [1]. Logistic Regression identifies risk factors like blood pressure and age to predict disease occurrence [2]. SVM uses a hyperplane to separate data with a large margin, showing good results in heart disease risk classification [3]. Neural Networks, particularly Deep Neural Networks (DNN), are effective in analyzing large datasets, providing high accuracy in risk prediction [4].

Ensemble Learning combines multiple models to improve prediction accuracy, particularly in classification, by reducing overfitting and enhancing model stability. Random Forest, one of the popular ensemble methods, builds numerous decision trees and combines their

results for reliable predictions [5]. In heart disease prediction, studies show that Random Forest outperforms single models like decision trees and logistic regression in terms of accuracy and stability [6]. Random Forest also enables the identification of significant features, aiding in medical intervention focus, and effectively handles imbalanced data, which is common in heart disease cases [7]. Recent research shows that Random Forest achieves high accuracy in detecting heart disease risk in large, complex datasets, making it a valuable tool in medical applications [8].

Previous research has examined ensemble methods, specifically Random Forest and feature selection, in heart disease prediction and its impact on the body [9]. Soft voting-based ensemble classification is also applied to improve survival prediction for heart failure patients [10]. A new method, Learning Automata Based Ensemble Learning (LABEL), was introduced to improve identification efficiency and accuracy by combining base classifiers [11].

Some studies have also developed intelligent heartbeat classification systems using AdaBoost and Random Forest algorithms along with heartbeat morphology features [12]. Ensemble analysis of bagging and AdaBoost shows improved classification results for heart disease based on decision trees [13]. The Smote-Tomek Link technique helps improve Random Forest performance on imbalanced diabetes data [14]. Other studies demonstrate the effectiveness of a voting classifier that combines Naive Bayes and Random Forest in classifying lung disease [15], as well as bagging techniques with neural networks for heart failure prediction based on major risk factors [16]. Boosting methods like AdaBoost and Gradient Boosting are also compared for heart disease data classification, with in-depth explanations of the confusion matrix [17]. Another study proposes applying Random Forest in heart disease classification, with a basic understanding of training and testing data [18], and heart failure detection using EKG [19].

Several other studies related to heart disease have also created breakthroughs through the application of machine learning techniques for predicting and classifying cardiac conditions.

The first study [20] systematically compared four classical machine learning algorithms. Through carefully designed experiments, researchers found that Random Forest produced the most accurate predictions with a success rate exceeding 88%. This superior performance was particularly evident in the algorithm's ability to handle complex and incomplete clinical data while maintaining prediction stability. Meanwhile, another research team [21] focused specifically on coronary artery disease by analyzing datasets from the UCI repository. They tested five different models and determined that Support Vector Machine (SVM) delivered optimal results with accuracy surpassing 85%. This achievement was largely attributed to SVM's exceptional capability to identify subtle patterns within patient data.

In 2021, Rajdhan and colleagues [22] introduced an innovative approach by integrating multiple machine learning techniques. Their results were remarkable - their enhanced version of Random Forest achieved over 90% accuracy while demonstrating robust resistance to common challenges like data imbalance and noise. Algerian researchers Salhi and team [23] reported groundbreaking progress using Neural Networks. Through optimized network architecture and advanced deep learning techniques, they achieved a record-breaking 93% accuracy. However, they cautioned that this approach requires substantial datasets and significant computational resources. Subsequent research by Jindal et al. [24] demonstrated that under specific conditions, the relatively simple k-NN algorithm could outperform more complex models like Logistic Regression, achieving accuracy above 88%.

Collectively, these findings have paved the way for developing more sophisticated, accurate, and reliable diagnostic systems for the early detection of heart disease. The studies highlight how different machine learning approaches can be strategically applied to address various challenges in cardiovascular prediction and diagnosis.

3.1. Data Collection

The data used in this study is the publicly available "Heart Disease Prediction Dataset" compiled by Robert Hoyt and hosted on Kaggle https://www.kaggle.com/datasets/thedevastator/predicting-heart-disease-risk-using-clinical-var.

The dataset contains 270 instances (rows) and 13 clinical features, including variables such as age, cholesterol levels, resting blood pressure, and family history. The target variable is binary, indicating whether a patient is at risk of heart disease (1) or not (0), with a class distribution of 120 positive and 150 negative cases, making the dataset relatively balanced.

After identifying the data source, the first step is to download the dataset. This dataset is often in CSV format, which is easily accessible and processable with machine learning algorithms. Before use, researchers verify the dataset to ensure it meets the research requirements, which include confirming that the collected data contains relevant features and clear labels indicating whether a patient is at risk of heart disease.

The obtained dataset typically includes characteristics that cover several important medical variables. For instance, features in the dataset may include age, gender, blood pressure, fasting blood sugar levels, cholesterol levels, and maximum heart rate. The labels in this dataset are generally binary, indicating whether the patient is at risk (1) or not at risk (0) for heart disease.

Once the dataset is obtained and verified, researchers proceed with data preparation and cleaning. Although this stage is not always discussed in depth in research, essential steps include handling missing data and feature transformation. Researchers typically identify any missing values and take steps to address these issues, such as imputation or removing incomplete data. Additionally, the data is split into two parts: a training set and a testing set, usually in a 70:30 or 80:20 ratio. This division is important for evaluating the predictive model that will be built.

In this context, using a public dataset offers significant advantages, as the data has undergone standardized collection processes and is accessible to multiple researchers. This enables researchers to focus on developing the Random Forest model without needing to conduct time- and resource-intensive field data collection. Additionally, using an existing dataset makes it easier for researchers to compare their findings with other studies that use similar datasets.

3.2. Random Forest

The classification process using the Random Forest algorithm involves several key stages that contribute to its robustness and predictive accuracy. Initially, the algorithm employs a bootstrapping technique to generate multiple subsets from the original dataset through sampling with replacement. Each of these subsets is then used to construct an independent decision tree, ensuring diversity among the ensemble.

During the construction of each tree, Random Forest randomly selects a subset of features at each decision node rather than considering all available features. This strategy increases variation among trees and helps prevent overfitting by reducing correlation between them. Once all decision trees are built, the algorithm aggregates their predictions through a majority voting mechanism, where the class receiving the most votes is chosen as the final output.

To evaluate model performance, standard classification metrics such as accuracy, precision, recall, and F1 score are applied using a separate test set that was not involved in training. In addition, Random Forest models can be further optimized by tuning parameters like the number of trees or the number of features considered at each split, often through techniques such as cross-validation.

By integrating multiple diverse decision trees and combining their outputs, Random Forest provides a stable and accurate classification model that effectively manages noise and reduces the risk of overfitting compared to single decision tree models.

3.3. Development Method

This study followed a structured research process involving statistical analysis and computational experiments to evaluate model performance in predicting heart disease. The process began with a comprehensive literature review on heart disease, machine learning classification techniques, and ensemble methods. This was followed by problem analysis to understand the increasing prevalence of heart disease and the significance of early detection through predictive modeling.

Data were collected from the publicly available "Heart Disease Prediction Dataset". The target variable was binary, indicating heart disease presence (1) or absence (0). Preprocessing included handling missing values using mean imputation, normalizing numerical features using Min-Max Scaling, and encoding categorical features using One-Hot Encoding. The data were then split into training and test sets in an 80:20 ratio to ensure fair evaluation.

The primary classification model developed in this study was Random Forest, selected for its robustness in handling complex data and reducing overfitting. For comparative analysis, the study also implemented three other ensemble learning algorithms: AdaBoost, Gradient Boosting, and XGBoost. These models were chosen based on their proven effectiveness in classification tasks, particularly in medical datasets.

Model evaluation was conducted using four key performance metrics: accuracy, precision, recall, and F1 score. To ensure the reliability of the evaluation, a 10-fold cross-validation technique was applied, allowing the performance of each algorithm to be assessed more robustly across different subsets of the data.

The experimental results were analyzed to compare the strengths and limitations of each model. However, this study did not include analysis of feature importance or AUC-ROC metrics, and future work may address these aspects for a deeper understanding of model interpretability.

3. RESULT AND DISCUSSION

In this section, we evaluate the performance of four ensemble learning algorithms, Random Forest, AdaBoost, Gradient Boosting, and XGBoost, using a single train-test split. Each model was assessed based on accuracy, precision, recall, and F1 score, as summarized in Table 1.

Table 1. Evaluation Results

Model	Accuracy	Precision	Recall	F1 Score
AdaBoost	0.85	0.84	0.76	0.8
Random Forest	0.87	0.85	0.81	0.83
Gradient Boosting	0.80	0.92	0.52	0.67
XGBoost	0.83	0.80	0.76	0.78

Among the models tested, Random Forest achieved the highest accuracy (0.87) and F1 score (0.83), indicating a strong balance between precision and recall. This superior performance can be attributed to Random Forest's inherent ability to manage non-linear relationships, noise, and feature interactions, which are common in medical datasets. The use of bootstrap aggregation (bagging) and random feature selection makes the model more robust to overfitting, while allowing it to generalize well across the data. Given the complex and diverse nature of clinical attributes such as age, cholesterol levels, and blood pressure—along with potential correlations between features—Random Forest is particularly well-suited for this kind of prediction task.

AdaBoost follows closely with an accuracy of 0.85 and an F1 score of 0.80. While its precision (0.84) is slightly lower than Gradient Boosting's, its recall (0.76) is considerably higher, indicating a better ability to detect true positive cases. This balance is essential in medical diagnosis contexts, where failing to identify at-risk patients (false negatives) can have serious consequences.

Gradient Boosting, on the other hand, exhibits a high precision of 0.92 but at the cost of recall (0.52). This means it is conservative in predicting positive cases—leading to fewer false positives, but at the risk of missing actual heart disease instances. In clinical settings where early detection is critical, such behavior may limit its utility unless false positives are more costly than missed detections, which is rarely the case in disease screening.

XGBoost delivers moderate results across all metrics with an accuracy of 0.83 and an F1 score of 0.78. While its performance is fairly balanced, it does not surpass Random Forest or AdaBoost. One potential reason for this is XGBoost's sensitivity to hyperparameter settings, which may not be fully optimized in this study due to the dataset’s relatively small size. Moreover,

XGBoost often excels in large-scale datasets where its regularization capabilities can be more effectively leveraged.

Overall, Random Forest demonstrates the most consistent and well-rounded performance, making it the most suitable model for heart disease risk prediction in this study. Boosting methods offer complementary strengths—AdaBoost provides good balance, while Gradient Boosting emphasizes precision. However, in the context of medical screening, models like Random Forest that can maintain both high recall and precision are generally preferred.

3.1. Cross-Validation

To ensure a more robust and generalizable performance assessment, a 10-fold cross-validation approach was applied. This method reduces the variance of performance estimates by repeatedly training and testing the model on different subsets of the data, offering a more realistic view of its predictive capability compared to a single train-test split, as shown in Table 2.

Table 2. 10-Fold Cross-Validation Results

Model	Accuracy	Precision	Recall	F1 Score
AdaBoost	0.80	0.80	0.75	0.77
Random Forest	0.82	0.85	0.78	0.78
Gradient Boosting	0.80	0.81	0.73	0.76
XGBoost	0.78	0.77	0.74	0.75

Among the evaluated models, Random Forest maintained the highest accuracy (0.82) and precision (0.85), alongside a strong F1 score (0.78). This confirms its ability to consistently identify heart disease cases while minimizing false positives. The robustness of Random Forest is particularly beneficial in medical datasets, where variable interactions and non-linearity are prevalent. Its ensemble structure and feature sampling strategy contribute to its stability, even across small and noisy datasets.

AdaBoost also demonstrated strong performance with an F1 score of 0.77. The model's balanced precision (0.80) and recall (0.75) suggest it is effective in capturing positive cases without generating excessive false alarms, an essential criterion in medical screening scenarios.

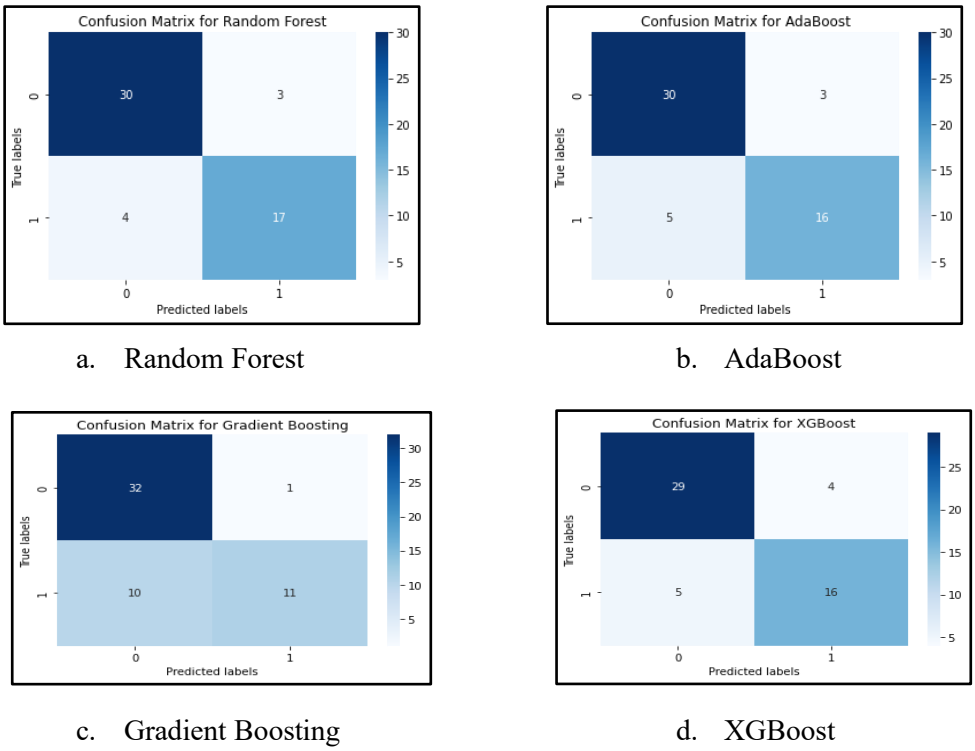
Gradient Boosting, while slightly lower in recall (0.73), achieved high precision (0.81), indicating a tendency to avoid false positives. However, this may come at the cost of missing actual positive cases, which could be problematic in contexts where sensitivity (recall) is prioritized, such as early disease detection.

XGBoost, though somewhat behind in accuracy and F1 score, remained competitive. Its stable recall (0.74) and moderate precision (0.77) reflect reliable, though not outstanding, performance. This could be influenced by XGBoost's sensitivity to hyperparameters, which might require more extensive tuning on a relatively small dataset to yield optimal results.

In summary, Random Forest again emerged as the most effective algorithm across all evaluated metrics in the cross-validation setting. The consistent performance underscores its suitability for heart disease prediction tasks, particularly in datasets characterized by feature diversity and potential noise. While other ensemble methods such as AdaBoost and Gradient Boosting provide viable alternatives, Random Forest offers the best trade-off between recall and precision, an important consideration in clinical decision support.

3.2. Confusion Matrix

In this study, the confusion matrix is used to evaluate the Ensemble Classifications model that has been trained to predict the risk of heart disease, as shown in Figure 1.



a. Random Forest b. AdaBoost

c. Gradient Boosting d. XGBoost

Figure 1. Confusion Matrices

To complement the metric-based evaluation, confusion matrices were analyzed for the four ensemble models: AdaBoost, Random Forest, Gradient Boosting, and XGBoost. These matrices reveal the distribution of true positives (TP), true negatives (TN), false positives (FP), and false negatives (FN), offering a clearer view of each model's strengths and limitations in classifying heart disease risk, as shown in Table 3.

Table 3. Confusion Matrix Values

Model	TP	TN	FP	FN
AdaBoost	16	30	3	5
Random Forest	17	30	3	4
Gradient Boosting	11	32	1	10
XGBoost	16	29	4	5

Random Forest achieved the best balance between sensitivity and specificity, with only 3 false positives and 4 false negatives. This reflects the model's ability to correctly identify both positive and negative cases, minimizing risks in both overdiagnosis and underdiagnosis.

AdaBoost, while slightly behind, also performed well with similar false positive counts (3) but a slightly higher number of false negatives (5). This suggests that AdaBoost may miss slightly more true positive cases compared to Random Forest, although its overall classification reliability remains strong.

Gradient Boosting demonstrated a distinct error profile: it had the lowest number of false positives (1) but the highest number of false negatives (10). This implies a highly conservative model that avoids false alarms but fails to detect a significant number of actual cases. While such behavior may be suitable in contexts where false positives are more costly, it is suboptimal in medical screening tasks where missing true cases can be critical.

XGBoost produced a moderate balance, with 4 false positives and 5 false negatives. Its error distribution suggests decent generalization but with slightly more misclassifications than

Random Forest or AdaBoost. This could be a result of hyperparameter sensitivity or the limited size of the dataset.

The analysis of confusion matrices highlights how different ensemble models trade off between precision and recall. Random Forest stands out as the most balanced model, effectively minimizing both error types. Gradient Boosting, despite its high precision, shows limitations in recall, indicating its cautious nature in identifying positive cases. These findings emphasize the importance of not relying solely on aggregate metrics, but also considering the distribution of prediction errors when selecting models for sensitive domains like healthcare.

3.3. Discussion

The evaluation of four ensemble learning algorithms, Random Forest, AdaBoost, Gradient Boosting, and XGBoost, revealed meaningful performance differences that warrant further discussion in the context of heart disease prediction.

Among the tested models, Random Forest consistently achieved the highest scores across all evaluation metrics, including accuracy, precision, recall, and F1 score. Its robustness in classification appears well-suited to the nature of the dataset, which includes clinical attributes with possible non-linear relationships (e.g., cholesterol levels, resting blood pressure) and modest levels of noise or variability. The model's ability to aggregate predictions from multiple diverse decision trees likely mitigates overfitting and helps it generalize well across variations in patient characteristics. This is particularly important in medical data, where predictive stability and generalizability are essential.

AdaBoost demonstrated competitive results with only slightly lower performance than Random Forest. While its precision was high, indicating reliable positive predictions, it produced a few more false negatives compared to Random Forest. This suggests that AdaBoost is effective at avoiding false alarms but may occasionally miss actual heart disease cases. From a medical screening perspective, this trade-off may still be acceptable depending on the diagnostic priorities, especially if false positives lead to additional non-invasive checks rather than high-risk procedures.

In contrast, Gradient Boosting showed a very high precision but the lowest recall among the models. The confusion matrix revealed that it frequently failed to detect true positive cases, highlighting a tendency to underpredict heart disease risk. Although this conservative behavior minimizes false positives, it may result in missed diagnoses—an undesirable outcome in clinical settings. The model's cautious nature could be beneficial in contexts where the cost of false positives outweighs that of false negatives, but for early disease screening, high recall is often prioritized.

XGBoost, which is known for its performance in large-scale and high-dimensional datasets, achieved moderate results in this study. While its accuracy and F1 score were comparable to AdaBoost, it did not outperform Random Forest. One possible explanation is that XGBoost's performance can be highly sensitive to hyperparameter tuning. Given the limited size and feature dimensionality of the dataset, extensive tuning might not yield substantial gains, or may not have been fully explored in this study. If this were the case, it should be acknowledged as a potential limitation, as fair comparison requires equal optimization effort across all models.

The results reaffirm that Random Forest is the most balanced and reliable model for predicting heart disease risk using this dataset. Its consistent performance in handling both positive and negative cases, along with the ability to generalize across cross-validation folds, makes it particularly well-suited for clinical use cases where both false positives and false negatives carry significant implications. Models like AdaBoost and XGBoost remain promising alternatives, especially when paired with domain-specific adjustments or integrated in hybrid decision systems. Gradient Boosting, while precise, may require further calibration or ensemble fusion to compensate for its recall limitations.

These findings underscore the importance of aligning model characteristics with the specific needs of medical applications, where different types of classification errors carry different

risks. In future work, integrating feature importance analysis or exploring threshold tuning could further refine the model's decision-making process and improve its applicability in real-world clinical environments.

4. CONCLUSION

This study demonstrates that ensemble learning algorithms, particularly Random Forest, provide superior performance in predicting heart disease based on clinical datasets. Among the evaluated models, Random Forest consistently exhibited the most balanced and stable performance across various evaluation metrics, confirming its effectiveness in handling complex, potentially noisy, and heterogeneous medical data.

The model's robustness appears especially well-suited for the clinical dataset used in this study, which contains diverse features such as age, cholesterol levels, and blood pressure—attributes that may involve non-linear relationships and variability across instances. Compared to other ensemble methods like AdaBoost, Gradient Boosting, and XGBoost, Random Forest maintained better consistency in detecting positive cases while minimizing false predictions, making it a strong candidate for early disease screening applications.

While the findings underscore the potential of ensemble methods in clinical decision support, several limitations should be noted. The study relied on a publicly available dataset with a limited number of instances, which may restrict the generalizability of the results. Additionally, this research did not incorporate clinical validation or in-depth analysis of feature importance, which could provide more interpretative insights.

Future work could explore the application of these algorithms on larger, real-world clinical datasets, incorporate techniques to address class imbalance, and integrate interpretability methods to better understand the influence of individual features on predictions. Further hyperparameter tuning and threshold calibration may also improve model sensitivity, particularly in models like Gradient Boosting and XGBoost.

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