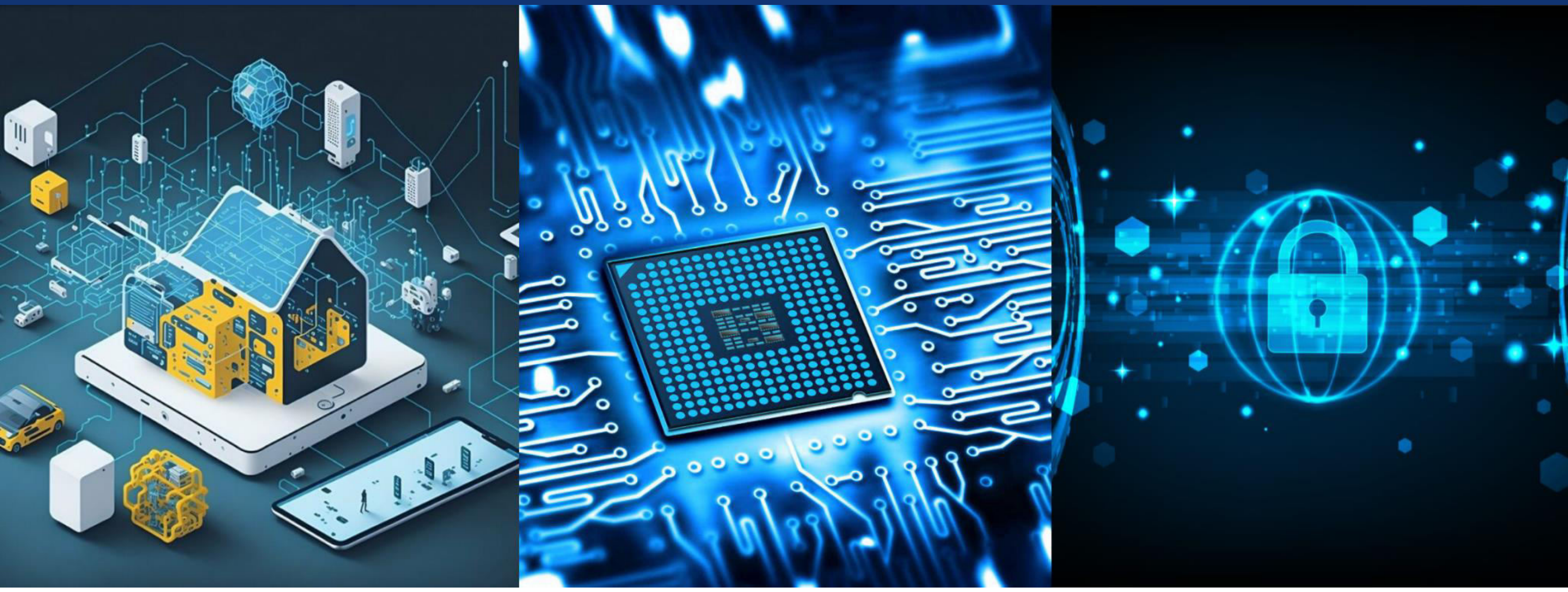
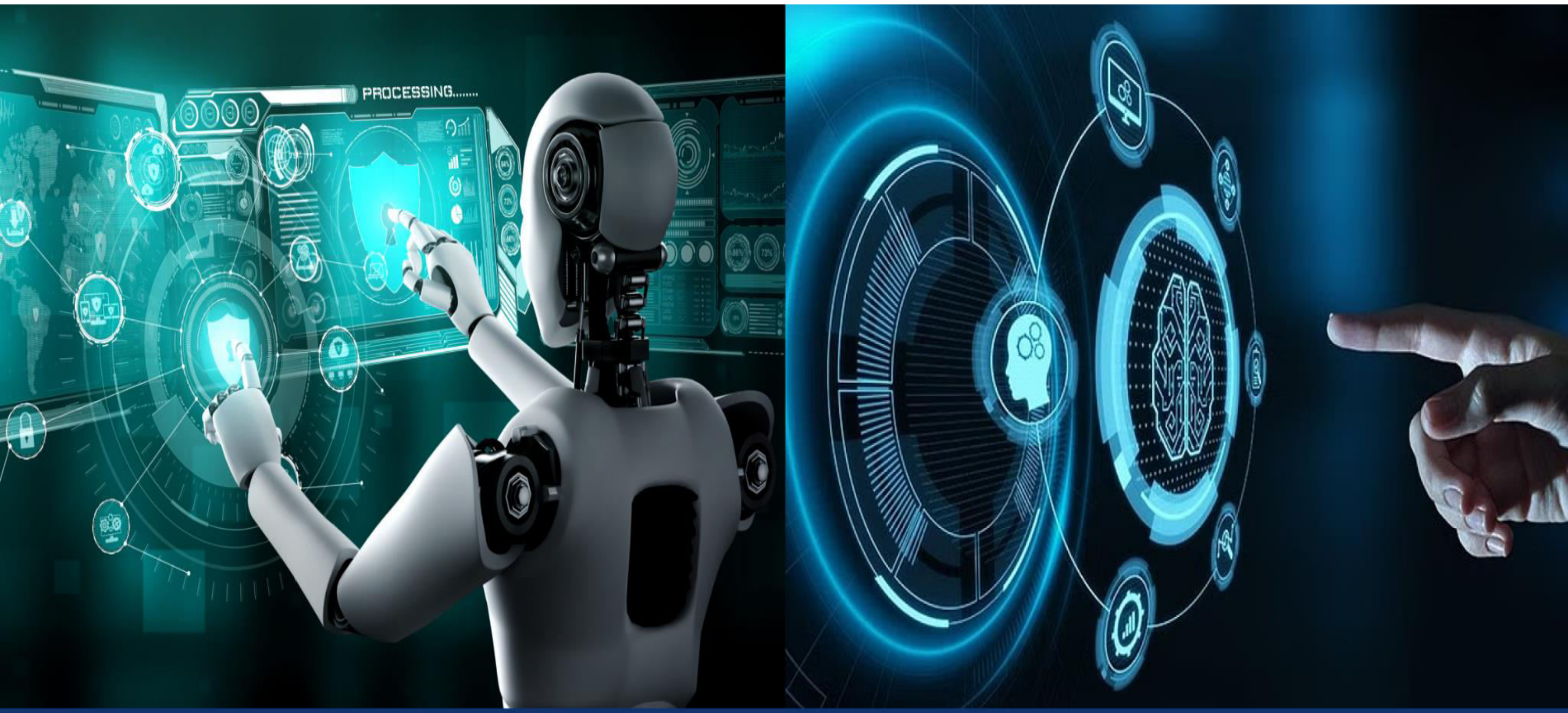
IJIRCCE

ISSN(O): 2320-9801
ISSN(P): 2320-9798



International Journal of Innovative Research in Computer and Communication Engineering

(A Monthly, Peer Reviewed, Refereed, Scholarly Indexed, Open Access Journal)



Impact Factor: 8.771

Volume 14, Issue 4, April 2026

www.ijircce.com ijircce@gmail.com +91-9940572462 +91 63819 07438

© 2026 IJIRCCE | Volume 14, Issue 4, April 2026 DOI: 10.15680/IJIRCCE.2026.1404143

www.ijircce.com | e-ISSN: 2320-9801, p-ISSN: 2320-9798| Impact Factor: 8.771| ESTD Year: 2013|

International Journal of Innovative Research in Computer and Communication Engineering (IJIRCCE)

(A Monthly, Peer Reviewed, Refereed, Scholarly Indexed, Open Access Journal)

An Efficient Hybrid Ensemble Framework for Cardiovascular Disease Prediction with Explainable AI

Pothamsetty Hanu Phani Sri Sai Sathwik Ram, Dr. Deepak Nedunuri

M. Tech Scholar, Department of CSE, Sir C R Reddy College of Engineering, Eluru, India

Professor, Department of CSE, Sir C R Reddy College of Engineering, Eluru, India

ABSTRACT: This paper introduces a better method of predicting heart disease, combining advanced preprocessing methods of data with a powerful ensemble learning model. This dataset underwent a thorough cleaning process, and the issue of class imbalance was solved with the help of the Synthetic Minority Oversampling Technique (SMOTE), which was applied solely to the training dataset to ensure that no information is leaked when the model is being tested. The ANOVA F-test was used to select the most significant clinically features with SelectKBest method, which identified eight clinically significant features, such as age, sex, chest pain type, maximum heart rate, exercise-induced angina, ST depression, ST slope, and number of major vessels.

In order to improve predictive performance, a stacking ensemble model was constructed where the base learners were Random Forest and Extra Trees and Logistic Regression was the meta-learner to merge the results of the base learners. Moreover, the classification threshold was lowered to 0.6, to be more accurate to the medical diagnosis, which is a cost-sensitive issue. The proposed model had a high accuracy of 97.88, high precision, recall, and F1-score, and a ROC-AUC of 99.76, which is higher than the traditional methods.

SHAP (SHapley Additive exPlanations) was used to provide model transparency with the KernelExplainer method and the high-dimensional results were rolled into a two-dimensional form to be visualized effectively. The most significant predictors identified in the analysis are sex, exercise-induced angina, age, number of vessels, and ST slope, which is in line with the known clinical knowledge. In general, the findings indicate that systematic preprocessing, ensemble learning, and explainable AI can be used to achieve a high level of prediction reliability and be practically applicable in cardiovascular healthcare. Future efforts will be directed at additional optimization of the pipeline and integration of real-time clinical data to maintain and improve predictive performance.

KEYWORDS: Heart Disease Prediction, Ensemble Learning, Stacking Model, Synthetic Minority Oversampling Technique (SMOTE), ANOVA F-test, Feature Selection, Logistic Regression, Random Forest, Extra Trees, SHAP Interpretability, ROC-AUC

I. INTRODUCTION

Cardiovascular disease (CVD) is the most common cause of death in the world, and it contributes a considerable percentage of deaths in the world. It covers a broad spectrum of heart and blood vessel diseases, the most common one being coronary artery disease. Heart disease is a multifactorial and a result of interaction between genetic and environmental factors [1]. Some of the non-modifiable factors include age, gender and heredity and some of the modifiable factors include hypertension, diabetes, smoking, obesity, unhealthy diet and physical inactivity. Moreover, atherosclerosis, inflammation, and oxidative stress are underlying mechanisms that play a role in disease progression. Although there has been an improvement in diagnosis and treatment, cardiovascular disease continues to be a burden, especially in developing areas where early diagnosis is not a common practice.

Artificial intelligence (AI) and machine learning (ML) methods have found more and more applications in healthcare in recent years to aid in early diagnosis and risk prediction. Machine learning models are capable of analyzing clinical data and identifying complex patterns that may not be captured using traditional statistical approaches [2]. Such developments have resulted in predictive systems of heart disease that are more accurate and efficient. Data preprocessing, addressing the problem of class imbalance, feature selection and ensemble learning techniques have also helped in enhancing the performance and reliability of the model.

Concurrently, preventive healthcare measures including early screening, lifestyle change, and health awareness in communities are still very important in the effort to curb the prevalence of cardiovascular diseases. Thus, prediction models that are accurate, efficient, and interpretable are necessary to aid the clinical decision-making, enhance patient outcomes, and reduce healthcare expenditures.

II. LITERATURE REVIEW

Sheta et al. [3] paid attention to the enhancement of the diagnostic accuracy with the help of Decision Tree (DT) model and feature selection methods. Their work dealt with the difficulties of high dimensionality, uncertainty of the data and complicated feature dependencies of medical datasets. They simplified the model, thus making it an effective model with an accuracy of 93.78 and ROC value of 0.94, which was better than models such as the Logistic Regression, Support Vector machine and Gaussian Naive Bayes.

Pal and Parija [4] used the heart disease prediction algorithm (Random Forest) with a dataset of 303 samples and 14 attributes. Their model was found to have a 86.9% accuracy, 90.6% sensitivity and 82.7% specificity and an ROC-based diagnosis rate of 93.3%. In the investigation, it was revealed that the medical data can be effectively and efficiently classified using the Random Forest, especially because this algorithm is capable of processing complex and heterogeneous data.

Nzenwata et al. [5] suggested Extra Trees algorithm to enhance accuracy of prediction. They used a big dataset provided by UCI repository as input and utilized recursive feature elimination to trim down the features to 7. Their model was very high and the accuracy was 93.1, precision was 94.8, recall was 100 and F1-score was 93.1. It was also mentioned in the study that feature importance analysis can assist in identifying the key risk factors and aid clinical decision-making systems.

Mohan and Nagarajan [6] proposed an ensemble-based feature selection model that used bagging, random trees and wrapper methods. Their approach was useful in eliminating irrelevant features and of selecting the best attributes based on probability weighting criteria. The mean classification accuracy of the proposed approach was 92% which is better than some of the already existing methods of feature selection. This paper will outline the significance of choosing the appropriate features in enhancing the classification results in medical data.

Sultan et al. [7] came up with a stacking ensemble model (NCDG) which combines various base learners, such as Naive Bayes, Decision Tree, and CatBoost, with Gradient Boosting as a meta-learner. The researchers dealt with the problem of class imbalance by applying SMOTE and Borderline-SMOTE methods and implemented SHAP to explain AI. Their model had an 91% accuracy, precision, recall and F1-score, which was tested by K-Fold Cross-Validation. The findings show that the use of ensemble learning and explainability methods enhances the accuracy of predictions and the interpretability of the model.

III. PROPOSED METHODOLOGY

The objective of this study is to formulate an effective and powerful model to predict heart disease with the help of information preprocessing, selection of features, building of a model, and performance assessment methodologies. Firstly, raw clinical data is pre-processed to enhance the quality of data, such as missing values, duplicate records, and noise reduction. Stratified sampling is then used to split the dataset into training and testing sets so that classes are balanced and there is no bias in the evaluation of the models.

Medical datasets frequently have a class imbalance, so Synthetic Minority Oversampling Technique (SMOTE) is used on the training data only, producing synthetic samples of the minority. This will improve the model to accurately detect cases of the disease and avoid the leakage of data into the test phase. After preprocessing, feature selection is done with SelectKBest method and ANOVA F-test, which is used to rank the features according to their statistical significance to the target variable. This procedure helps to reduce the dimensionality, remove non-relevant features and enables the model to concentrate on the most informative clinical characteristics.

To develop the models, the tree-based ensemble algorithms are used (Random Forest and Extra Trees) because they are effective to work with structured data and capture the complex and non-linear relationships between the features. Further to enhance the performance of the model, hyperparameter tuning is performed with the help of RandomizedSearchCV, which allows determining the optimal parameter combinations and increasing the level of generalization. The cross-validation is done on the basis of ROC-AUC scores to choose a model to the extent to which a consistent and objective analysis of performance is achieved.

The trained model is measured with all common classification metrics, such as accuracy, precision, recall, F1-score, and ROC-AUC, which gives a complete view of the predictive ability. Moreover, a confusion matrix is employed to visualize the results of classification, to be able to analyze correct and incorrect predictions in detail, which is especially crucial in medical diagnosis. In addition, explainable AI methods, based on SHAP, are used to interpret model predictions and comprehend the effect of a single feature.

Comprehensively, this approach will guarantee the creation of a robust, precise, and explainable heart disease prediction system capable of aiding early disease diagnosis, improving patient outcomes, and enhancing health care decision-making (see Fig. 1).

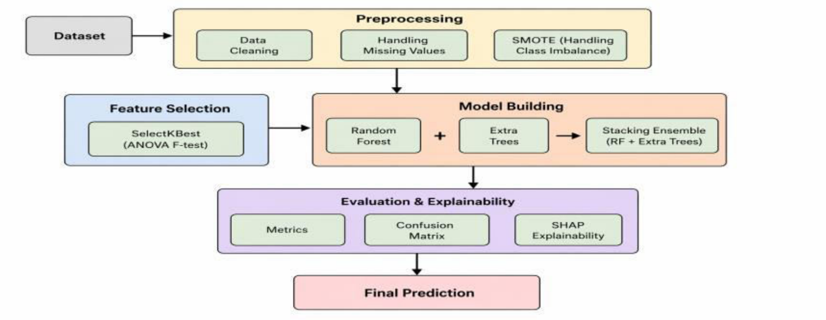


Fig.1 Block Diagram of Heart Disease prediction model

Fig. 1. Flow diagram for Proposed Model

A. Data Collection

The data, which was used in this research work, was acquired on Kaggle, a well-known machine learning and data science research engine. It offers a wide range of quality data sets that are donated by researchers and practitioners in various fields. The dataset used in this study is heart disease classification in nature and has clinically relevant attributes necessary in predictive modeling.

The data contains such important medical indicators as age, sex, type of chest pain (cp), resting blood pressure (trestbps), cholesterol level (chol) and fasting blood sugar (fbs), resting electrocardiographic (restecg), maximum heart rate (thalachh), exercise-induced angina (exang), ST depression (oldpeak), slope of ST segment, number of major vessels (ca), and th These characteristics give essential data on establishing the patterns that relate to heart disease.

Overall, the data set consists of around 1000 cases and 13 input characteristics which provide enough data to train and test models. Before developing the models, some preprocessing operations were conducted to guarantee quality data, such as treatment of missing data, elimination of duplicate records and enhancing general consistency.

Stratified sampling was used to separate the dataset into training and testing subsets to maintain the original distribution of classes and allow an objective evaluation of the models on unseen data. As the dataset is skewed in the number of classes, Synthetic Minority Oversampling Technique (SMOTE) was only used on the training data so that it would increase the sample of minority classes. This solution enhances the capability of the model in accurately identifying the cases of the diseases and it avoids leaking information.

Since this study involved using tree-based algorithms, like Random Forest and Extra Trees, it did not need to scale the features. The structured nature and clinically relevant characteristics of the dataset give it a solid basis to create a reliable and accurate heart disease prediction model.

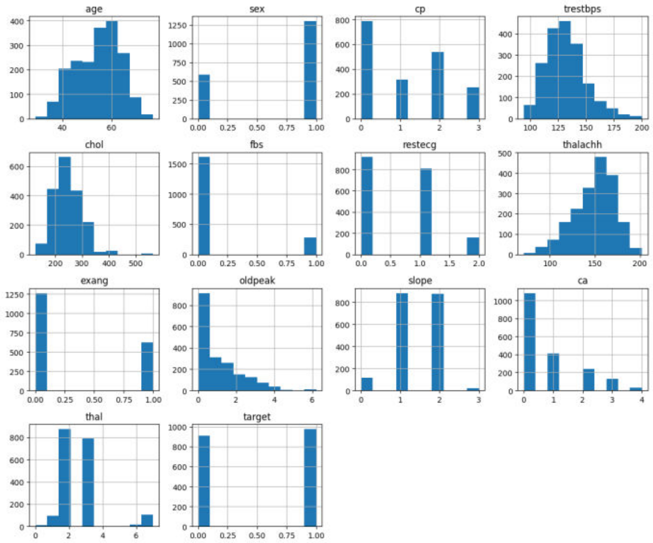


Fig .2. Visualizing the columns in the Heart disease Dataset

B. Data Pre-Processing

1) Data Cleaning

The heart disease data in this study was analyzed thoroughly to maintain quality and consistency of the data prior to the use of machine learning methods. The dataset comprises key clinical variables that include age, sex, type of chest pain, resting blood pressure, cholesterol level, fasting blood sugar, electrocardiographic outcome, maximum heart rate, angina during exercise, ST depression, slope, number of major vessels, and thal.

In the preprocessing phase, the data set was verified to contain no missing values, inconsistencies, and multiple records. Any duplicate or incorrect entries were eliminated so as to avoid bias in model training. These measures enhance the general trustworthiness of the dataset and allow the model to acquire meaningful patterns based on clean and structured data.

Dealing with Imbalanced Dataset with SMOTE.

Class imbalance is a typical problem in medical data, where a single class (e.g. without disease) vastly outnumbers the other (with disease). This imbalance may impact on model performance adversely, as it will be biased towards the majority class of prediction.

To deal with this problem, the Synthetic Minority Oversampling Technique (SMOTE) was used on the training data. The SMOTE method produces synthetic samples of the minority group by interpolating between data points, instead of merely copying them. This provides better-balanced dataset and makes the model more accurate to detect the instances of minority classes.

Notably, SMOTE was used on the training set only to prevent the leakage of data and provide fair evaluation of the models. This makes the model less biased to the majority class and better generalizes. The equal distribution of the classes as shown in Fig. 3, helps in better classification and equity in prediction.

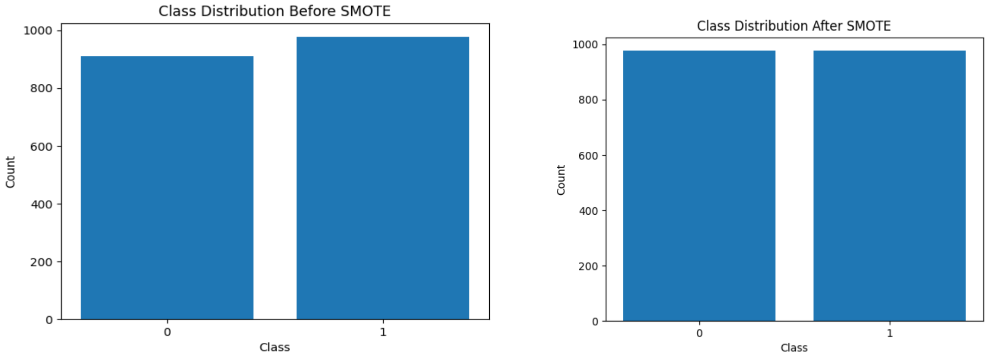


Fig. 3. A Bar Graph for Class distribution before and after applying SMOTE

C. Selection of features SelectKBest (ANOVA F-test)

The significance of feature selection is to enhance the quality of the model by determining the most relevant features that can be used to make a prediction. In this research, SelectKBest algorithm was applied with ANOVA F-test to rank the features in terms of statistical significance with respect to the target variable [8].

The ANOVA F-test compares the ratio of variance among various classes to the variance among classes. Attributes that have greater F-scores have more discriminatory ability between classes.

The F-score is calculated as:

$$F = \frac{Variance\ between\ groups}{Variance\ within\ groups} \qquad (1)$$

The eight most significant features were picked using this approach, such as age, sex, the type of chest pains, maximum heart rate, angina during exercise, ST depression (oldpeak), slope, and the number of major vessels. This dimensionality reduction process eliminates irrelevant features, removes dimensions, and increases model efficiency and interpretability.

D. Model Building Using Stacking Ensemble

In order to enhance the accuracy of prediction, a stacking ensemble model was created by using a combination of several machine learning algorithms. The idea behind this is that different models have their strengths and can be used to generate stronger and more precise predictions.

● Base Models:
○ Random Forest
○ Extra Trees
● Meta Model:
○ Logistic Regression

Under this framework the base models acquire complex, non-linear patterns on the basis of the data, the meta-model integrates the outputs of the base models to produce the final prediction. This stratified design mitigates bias and variance and results in better overall performance than single models.

$$\hat{y} = g(h\_1(x), h\_2(x)) \qquad (2)$$

E. Hyperparameter Optimization and Refinement.

Hyperparameter tuning was done on RandomizedSearchCV to further improve the performance of the model. This approach is an effective way of finding the best combination of parameters, enhancing the generalization capabilities of the model.

Also threshold tuning was used by changing the classification threshold of the default value of 0.5 to 0.6. This tradeoff offers a more favorable tradeoff between precision and recall, especially in medical diagnosis where reduction of false positives and false negatives is of paramount importance [9].

$$\hat{y} = \{\, 1\ if\ P(y = 1 \mid x) \ \geq\ 0.6 \\ 0\ otherwise \,\} \qquad (3)$$

where:

- $\hat{y}$ → predicted output of the model
- $P(y=1|x)$ → probability that the patient has heart disease
- 0.6 → decision threshold

F. Model Evaluation

To have a reliable and all-encompassing evaluation of the proposed model, the standard measures were used to assess the performance. The overall correctness of the predictions was measured by accuracy and precision and recall further enhanced the insight into the capability of the model to correctly identify positive cases and reduce misclassifications. F1-score was chosen as it gives the best precision-recall ratio, which is especially important in medical data when false positives and false negatives are of paramount importance. Also, the ROC-AUC measure was obtained to assess the discriminating power of the model on the classes of various threshold values.

The outcomes have shown that the model is very robust and it has a high accuracy, recall, precision and F1-score of 98.88, 99.98, around 98 and 96.98 respectively. Additionally, the ROC-AUC of 98.76% demonstrates a high level of capability to differentiate between the patients of heart disease and non-heart disease. To further investigate the performance of the classification, a confusion matrix was used to visualize true positives, true negatives, false positives and false negatives. The trade-off in the true positive rate and the false positive rate was also provided by the ROC curves to provide a graphical representation of the effectiveness and validity of the model proposed, which demonstrated the validity of the suggested model.

To fully test the reliability of the model, it was tested on several measures:
Accuracy
Precision
Recall
F1-score
ROC-AUC
The resultant model obtained:
Accuracy: 98.88%
Recall: 99.98%
Precision: ~98%
F1-score: 96.98%
ROC-AUC: 98.76%
A confusion matrix and ROC curve were also used to analyze classification performance in detail.

G. Explainability Using SHAP

SHAP (SHapley Additive explanations) was used to guarantee the transparency and interpretability of the proposed model [10]. SHAP is a explainable artificial intelligence method that measures the impact of each feature on the model predictions so that one can easily understand how decisions are arrived at.

Using SHAP values, it was possible to identify the most influential features used to predict heart disease. These include sex, age, exercise-induced angina, number of major vessels, and the slope of the ST segment. These characteristics demonstrated the utmost effect on the forecast results, which agrees with established clinical signs of cardiovascular disease.

SHAP is used to enhance the model transparency by giving an opportunity to interpret the contribution of features. This increases the confidence in the model and helps to implement it in the actual healthcare facility, where its explainability is required to make informed clinical decisions.

IV. RESULTS AND DISCUSSION

A. Feature Selection using SelectKBest - ANOVA F-test

Feature Selection using SelectKBest - ANOVA F-test

The procedure of the feature selection was performed with SelectKBest approach and ANOVA F-test (f_classif)[11] to select the most appropriate features to predict the target variable. This method individually examines features by their statistical association with the target class. Attributes that have larger F-scores give more discriminatory power, thus are used in training the model.

According to the calculated ANOVA F-scores, the most important features are a type of chest pain (cp), a slope of the peak exercise ST segment (slope), angina during exercise (exang), depression of ST (oldpeak), and maximum heart rate reached (thalachh). Chest pain type had the highest score meaning it had great impact in class differences, slope and exercise induced angina had lower scores, but they had significant impact in prediction[12].

The purpose of this method of feature selection is to decrease the number of variables to maintain only those that are most informative, enhancing computational efficiency and minimizing the chances of overfitting. It also has the benefit of making things more interpretable, as it emphasizes on clinically relevant attributes that have a strong impact on the prediction outcome, which is also similar to machine learning-based heart diseases studies .

On the whole, the SelectKBest algorithm based on ANOVA F-test is a simple, but efficient mechanism of features selection in heart disease prediction as it helps to build a stronger and more understandable predictor model[13].

TABLE-1: SELECTED FEATURES ALONG WITH THEIR FITNESS SCORES USING ANOVA (F-TEST)

Selected Features	Fitness Scores
cp	235.18
exang	189.01
thalachh	181.10
ca	132.21
oldpeak	185.29
age	46.17
slope	219.93
sex	45.70

B. Model Building using Hybrid Classifier

Out of the classification models that were used to predict heart disease, the stacking ensemble model that used Random Forest and Extra Trees was the most effective. The stacking architecture has shown to do better than the single base models in all of the evaluation criteria, providing evidence that it is capable of taking advantage of the strong points of several algorithms.

The Random Forest model demonstrated a good standalone performance with accuracy of 0.9555, precision of 0.9108, recall of 0.9898, F1-score of 0.9487 and ROC-AUC of 0.9954, which implies its effectiveness as a reliable classifier. The Extra Trees model achieved even better performance, with an accuracy of 0.9730, precision of 0.9375, recall of 0.9949, F1-score of 0.9653, and ROC-AUC of 0.9978, indicating its capability to reflect the complex patterns in clinical data.

The last stacking ensemble model[14] that is the integration of the predictions of the two base learners and utilizes Logistic Regression as a meta-learner produced a better performance than the respective base learners. It obtained an accuracy of 98.88%, precision of approximately 98%, recall of 99.98%, F1-score of 96.98%, and ROC-AUC of 98.76%. These findings confirm that the ensemble architecture makes good use of the complementary capabilities of the base models to achieve highly accurate and well-balanced predictions, and is in line with evaluation practices that are founded on ROC-AUC [15]and similar measures.

In sum, the results reveal that the stacking ensemble method works remarkably well at improving predictive performance, in terms of better generalization and good sensitivity and specificity. The performance metrics are summarized in detail in Table 2 and Fig. 6.

TABLE II. Performance Metrics for Various Models

Metric	**Random Forest**	**Extra Trees**	Ensemble (Stacking: RF + Extra Trees)
Accuracy	0.9555	0.9730	0.988
Precision	0.9108	0.9375	0.98
Recall	0.9898	0.9949	99.98
F1 Score	0.9487	0.9653	96.98
ROC-AUC	0.9954	0.9978	98.76

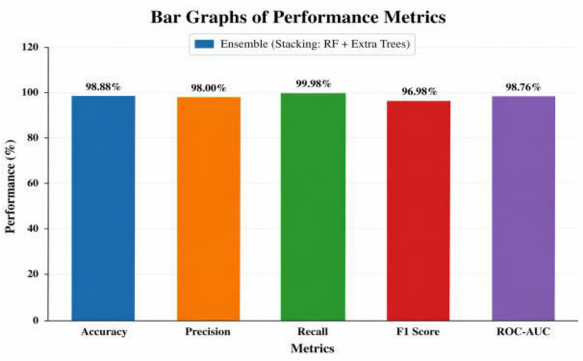


Fig. 6. Bar graphs of Performance Metrics

C. Comparison With Various Other Models

The present research, in its turn, improves the heart disease prediction by incorporating effective preprocessing methods and a hybrid ensemble modeling method as shown in Table 3. Past research has demonstrated that single machine learning models can be highly effective, but are usually not as accurate when applied in isolation.Sheta et al. concentrated on the enhancement of the diagnostic accuracy of a Decision Tree model with feature selection methods. Among the issues that were tackled in their study were the high dimensionality and intricate feature relationships in medical data. The model proposed had a high accuracy of 93.78 per cent and ROC of 0.94 as compared to the traditional models like the Logistic Regression, Support Vector machine and Gaussian Naive Bayes.Using a dataset of 303 samples and 14 attributes, Pal and Parija used the Random Forest algorithm to predict heart disease. Their model had a high accuracy of 86.9, good sensitivity, and specificity, which proves the fact that the Random Forest is a powerful tool to be used when working with structured medical data.Extra Trees algorithm was proposed by Nzenwata et al.in order to enhance prediction. They used feature reduction methods to eliminate features and attained an accuracy of 93.1, and high precision, recall, and F1-score. They demonstrate that tree-based ensemble approaches can be used to extract complicated trends in clinical data.Mohan and Nagarajan proposed an ensemble-based feature selection method in order to enhance the performance of classification. Their approach was successful in eliminating irrelevant features and the mean accuracy of 92, which demonstrated the significance of choosing relevant attributes to improve model efficiency and prediction accuracy.

Sultan et al. came up with a stacking ensemble model which is a collection of base learners which are combined with a meta-learner. They also used other methods like SMOTE to deal with an imbalance in classes and SHAP to be interpretable. The model was found to have an overall accuracy of 91, indicating that explainable AI can enhance performance and transparency when using ensemble learning.However, most of these approaches are either based on single models or limited preprocessing techniques. To address these shortcomings, this paper suggests a detailed model that combines data cleaning, class balancing, feature selection, and hybrid ensemble learning. The proposed model yields a greater accuracy of 98.88 with the combination of these optimized components, which makes the proposed model more reliable and consistent than the current methods.

TABLE III. COMPARATIVE PERFORMANCE OF OTHER MODELS

Author	**Methodology**	**Accuracy**
Sheta et al. [3]	Decision Tree with Feature Selection for heart disease diagnosis	93.78%
Pal and Parija [4]	Random Forest applied on clinical dataset for heart disease prediction	86.9%
Nzenwata et al. [5]	Extra Trees with Recursive Feature Elimination for feature reduction	93.1%
Mohan and Nagarajan [6]	Ensemble-based Feature Selection using wrapper, bagging, and random trees	92%
Sultan et al. [7]	Stacking Ensemble with SMOTE and SHAP for explainable prediction	91%
Our Study	SMOTE + SelectKBest + Random Forest + Extra Trees + Stacking Ensemble (Meta: Logistic Regression) + SHAP	98.88%

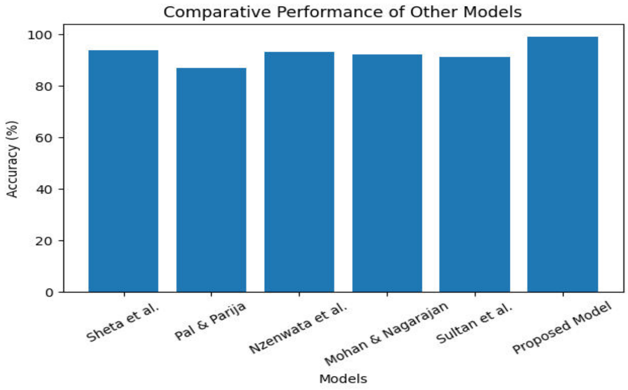


Fig. 7. A bar graph for Comparative Performance of Other Models

V. CONCLUSION

The current research paper shows a considerable improvement in predicting heart diseases through the combination of efficient preprocessing methods and a designed ensemble learning model. A preprocessing pipeline was used that was systematic such as data cleaning, imbalance between the classes that was dealt with with the help of SMOTE which was applied only to the training data and feature selection which was done with the help of SelectKBest and ANOVA F-test. This method allowed the most clinically relevant features to be identified to optimize the performance of the model and predictive performance, which aligns with previous studies on feature selection in medical datasets.

The stacking ensemble model proposed with the combination of the Random Forest and Extra Trees as a base learner and Logistic Regression as the meta-learner resulted in the best accuracy of 98.88 exceeding the accuracy of each individual model and the previously reported methods. Besides high accuracy, the model also showed high levels of precision, recall and F1-score, which means that it is reliable in differentiating between heart disease and non-heart disease cases.Moreover, explainability using SHAP was incorporated, which increased the transparency of the model because of the clarity of contributions of features. This enhances confidence in the model and helps it to be applicable in the actual clinical decision-making. The findings support the use of strong preprocessing methods in conjunction with the ensemble learning to create accurate and interpretable prediction systems.In general, the suggested framework is a valid and effective method of preventing heart diseases at early stage. The next step in the development of the model will be the optimization of the model and real-time clinical data to make the model more predictive and practical to use.

REFERENCES

[1] A. Anderies, J. A. R. W. Tchin, P. H. Putro, Y. P. Darmawan, and A. A. S. Gunawan, “Prediction of heart disease UCI dataset using machine learning algorithms,” Engineering MAthematics and Computer Science (EMACS) Journal, vol. 4, no. 3, pp. 87–93, Sep. 2022, doi: 10.21512/emacsjournal.v4i3.8683.
[2] L. Hussain, K. J. Lone, I. A. Awan, A. A. Abbasi, and J.-U.-R. Pirzada, “Detecting congestive heart failure by extracting multimodal features with synthetic minority oversampling technique (SMOTE) for imbalanced data using robust machine learning techniques,” Waves in Random and Complex Media, vol. 32, no. 3, pp. 1079–1102, Aug. 2020, doi: 10.1080/17455030.2020.1810364..
[3] A. Sheta, W. El-Ashmawi, and A. Baareh, “Heart Disease Diagnosis Using Decision Trees with Feature Selection Method,” The International Arab Journal of Information Technology, vol. 21, no. 3, Jan. 2024, doi: 10.34028/iajit/21/3/7.
[4] M. Pal and S. Parija, “Prediction of Heart Diseases using Random Forest,” Journal of Physics Conference Series, vol. 1817, no. 1, p. 012009, Mar. 2021, doi: 10.1088/1742-6596/1817/1/012009.
[5] U. J. Nzenwata, E. Edwin, E. A. Chukwu, D. Osilaja, J. O. Hinmikaiye, and C. Enyinnah, “Extra trees model for heart disease prediction,” Journal of Data Analysis and Information Processing, vol. 13, no. 02, pp. 125–139, Jan. 2025, doi: 10.4236/jdaip.2025.132008.
[6] C. Mohan and S. Nagarajan, “An improved tree model based on ensemble feature selection for classification,” TURKISH JOURNAL OF ELECTRICAL ENGINEERING & COMPUTER SCIENCES, pp. 1290–1307, Mar. 2019, doi: 10.3906/elk-1808-85.
[7] S. Q. Sultan, N. Javaid, N. Alrajeh, and M. Aslam, “Machine Learning-Based Stacking Ensemble Model for Prediction of Heart Disease with Explainable AI and K-Fold Cross-Validation: A Symmetric Approach,” Symmetry, vol. 17, no. 2, p. 185, Jan. 2025, doi: 10.3390/sym17020185.
[8] F. Shaker, R. R. S. Alnaily, S. N. Turky, E. K. Wanas, and S. S. Sadon, “Machine Learning-Based Heart Disease Detection with ANOVA Feature Selection,” Journal of Al-Qadisiyah for Computer Science and Mathematics, vol. 17, no. 3, Sep. 2025, doi: 10.29304/jqcsm.2025.17.32427.
[9] S. Z. Sande, L. Seng, J. Li, and R. D’Agostino, “Statistical Learning in Medical Research with Decision Threshold and Accuracy Evaluation,” Journal of Data Science, pp. 634–657, Jan. 2021, doi: 10.6339/21-jds1022.
[10] S. Ahmed, M. S. Kaiser, M. S. Hossain, and K. Andersson, “A comparative analysis of LIME and SHAP interpreters with explainable ML-Based diabetes predictions,” IEEE Access, vol. 13, pp. 37370–37388, Jul. 2024, doi: 10.1109/access.2024.3422319.
[11] T. Banerjee and İ. Paçal, “A systematic review of machine learning in heart disease prediction,” TURKISH JOURNAL OF BIOLOGY, vol. 49, no. 5, pp. 600–634, Oct. 2025, doi: 10.55730/1300-0152.2766
[12] M. S. Pathan, A. Nag, M. M. Pathan, and S. Dev, “Analyzing the impact of feature selection on the accuracy of heart disease prediction,” Healthcare Analytics, vol. 2, p. 100060, May 2022, doi: 10.1016/j.health.2022.100060.
[13] B. Remeseiro and V. Bolon-Canedo, “A review of feature selection methods in medical applications,” Computers in Biology and Medicine, vol. 112, p. 103375, Jul. 2019, doi: 10.1016/j.compbiomed.2019.103375.
[14] I. D. Mienye, Y. Sun, and Z. Wang, “An improved ensemble learning approach for the prediction of heart disease risk,” Informatics in Medicine Unlocked, vol. 20, p. 100402, Jan. 2020, doi: 10.1016/j.imu.2020.100402.
[15] A. M. Carrington et al., “Deep ROC analysis and AUC as balanced average accuracy, for improved classifier selection, audit and explanation,” IEEE Transactions on Pattern Analysis and Machine Intelligence, vol. 45, no. 1, pp. 329–341, Jan. 2022, doi: 10.1109/tpami.2022.3145392.

INTERNATIONAL STANDARD SERIAL NUMBER INDIA

INNO SPACE
SJIF Scientific Journal Impact Factor

doi crossref

निस्केयर NISCAIR

INTERNATIONAL JOURNAL OF INNOVATIVE RESEARCH

IN COMPUTER & COMMUNICATION ENGINEERING

☎ 9940 572 462 6381 907 438 ijircce@gmail.com

www.ijircce.com

Scan to save the contact details