Online ISSN 3007-3197 Print ISSN 3007-3189

http://amresearchreview.com/index.php/Journal/about

Annual Methodological Archive Research Review
http://amresearchreview.com/index.php/Journal/about
Volume 3, Issue 6 (2025)

Explainable AI-Enhanced Machine Learning Models for Early Detection of Cardiovascular Disease: Improving Predictive Performance and Clinical Transparency through Optimization

[1]Waqar Ahmad, [2]Muhammad Ramzan, [3]Aamir Farooq, [4]Shahab ud Din Syed, [5]Zahra Khalid Satti

Article Details

Keywords: Cardiovascular Disease Prediction, Machine Learning Models, Hyperparameters Tuning, Support Vector Machine (SVM), Ensemble Learning Techniques, AI-Driven Algorithms, explainable AI (XAI), SHAP (SHapley Additive exPlanations)

Waqar Ahmad
Lab Engineer, Department Electrical Engineering, National University of Computer and Emerging Sciences, Islamabad, Pakistan.
i229914@nu.edu.pk
Muhammad Ramzan
Research Assistant, Department Electrical Engineering, National University of Computer and Emerging Sciences, Islamabad, Pakistan.
ramzannotkani380@gmail.com
Aamir Farooq
PhD Scholar, School of Automation, Nanjing University of Science and Technology, Nanjing,210094, China.
aamireee@njust.edu.cn
Shahab ud Din Syed
School of Electrical Engineering and Computer Sciences, NUST, Islamabad, Pakistan.
Ssyed.msee23seecs@seecs.edu.pk
Zahra Khalid Satti
Department of Computing Science, National University of Modern Languages, Islamabad , Pakistan
numl-f22-14077@numls.edu.pk

ABSTRACT

Cardiovascular disease (CVD) is the main cause of death worldwide, highlighting an immediate requirement for enhanced diagnostic devices to trace indicators associated with CVD early in sufferers. This study leverages AI-driven machine learning (ML) algorithms to extract extrapolating more nuanced patterns from the data than traditional mortality modelling techniques. The purpose of this study is to compare and tune three ML models (Support Vector Machine (SVM), Random Forests (RF), and Logistic Regression (LR) for increasing the CVD prediction accuracy and incorporate explainable AI (XAI) techniques, such as SHAP (SHapley Additive exPlanations) for better model interpretability. The UCI Heart Disease data set is used as a backbone on which we did some very detailed level of pre-processing and then applied feature selection algorithms like PCA and RFE to select the optimal features. Optimization of models was done by hyperparameter tuning using GridSearchCV and RandomizedSearchCV. The data was 90% train test split. After split, the SVM model performed best with 94% accuracy followed by Random Forest at 92%, and Logistic Regression achieved a minimal of 90%. These findings demonstrate the value of AI-driven ML approaches can improve the prediction of cardiovascular disease. The study emphasizes that the optimized SVM model has significant potential for clinical applications in early CVD diagnosis, offering evidence that integrating AI-driven ML models into healthcare can potentially reduce global CVD mortality through earlier interventions.

INTRODUCTION

Every heartbeat serves as a reminder of the most important rhythm in life. The human heart, a muscular organ barely bigger than a clenched fist, plays a key function in supporting life by pumping blood throughout the body and supplying necessary oxygen and nutrition to all organs and tissues. Despite its significance, the heart is extremely susceptible to a variety of illnesses and symptoms that are grouped together as cardiovascular disease (CVD), which encompasses conditions including heart failure, cardiac arrest, and coronary artery disease. Since symptoms including weakness, dizziness, exhaustion, shortness of breath, and chest discomfort don't often show up until the condition is advanced, early detection is essential for better treatment outcomes [1]. The World Health Organization estimates that cardiovascular disease (CVD) caused 17.9 million deaths globally in 2016, making up nearly 31% of all deaths worldwide [2]. More than 70% of these deaths took place in low- and middle-income nations, where access to healthcare and early diagnostic tools is frequently limited. The key to it all is the early diagnosis of CVD, which will substantially diminish its effect and enhance healthcare quality. In various works, machine learning (ML) methods were used to improve prediction performance of CVD and took advantage of ML techniques in segregating hidden patterns that are often unseen by traditional approaches due to the complex structure and nature underlying bioinformatics dataset [3]. To advance scientists stress with CVD issue an Experiment study using ensemble learning techniques Random Forest, Gradient Boosting and AdaBoost Increase the disease detection prediction accuracy. These methods amalgamate several weak learners to build a strong predictive model. As an example, a stronger prediction of cardiovascular disease was obtained on hybrid classification models that combine AdaBoost and XGBoost with logistic regression [4]. Analogously to the application in CVD prediction from COVID-19 patients, an ensemble learning approach using Random Forest for feature extraction achieved impressive performance and scored 88.70% accuracy [5].

Hybrid models that use the few algorithms of both worlds have also shown to outperform single classifiers in different healthcare applications. For example, the use of a hybrid prediction system in CVD diagnosis shows an impressive improvement in accuracy using Support Vector Machines (SVM) and Random Forest. Similarly, the intersection of deep learning methods with traditional ML models also increased to raise predicting performance in those hybrid models combining Random Forest with logistic regression, arching a prediction accuracy of 91.8% [6].

With the help of recent studies, hybrid datasets have been part and parcel to a study which helped predict heart disease accurately. Similarly, an average accuracy of 94.34% was shown by the ML classifiers using a combination study among datasets where it also highlights that ensemble method could be used for this purpose in this domain as well [7]. In addition to these, other researchers have also taken the help of ensemble techniques like bagging, boosting and stacking for predicting CVD risk leading towards a more trustworthy model with increased diagnostic accuracy [8]. Machine learning models are beginning to use multiple medical data sources that include, in addition to traditional clinical data: electrocardiograms (ECG) and phonocardiograms (PCG), which have led to better predictive performance for cardiovascular models. Combining these and other data types with hybrid methods possess an edge, exhibiting beyond 0.93 AUC value which are areas where earlier stages of CVD could be detect [9].

Recent advancements in **Explainable Artificial Intelligence (XAI)** have significantly influenced the application of machine learning in medical diagnostics, especially for heart disease classification. Traditional machine learning models such as Random Forests, SVMs, and deep neural networks often function as "black boxes" with limited interpretability, which hinders their acceptance in clinical settings. XAI techniques like SHAP (SHapley Additive Explanations) and LIME (Local Interpretable Model-agnostic Explanations) have been developed to enhance transparency and interpretability by highlighting the most influential features in model predictions[10] [11]. In the context of heart disease, XAI has helped identify key predictive features such as chest pain type, cholesterol, resting blood pressure, and maximum heart rate, providing actionable insights for clinicians[12]. These techniques have improved trust and reliability, allowing medical professionals to validate model decisions with established medical knowledge[12]. As a result, the integration of XAI not only enhances model transparency but also supports safer and more ethical deployment of AI in cardiovascular diagnostics.

As observed from the developments in ensemble and hybrid learning, this represents a leapfrog opportunity for transforming cardiovascular health care through machine learning. The ability to work with large and complex datasets and apply combinations of algorithms has resulted in marked improvements in the diagnosis of cardiovascular diseases (CVD), enabling earlier interventions that contribute to reducing global mortality rates from heart disease. In parallel, the integration of **Explainable AI (XAI)** techniques has become increasingly essential, offering transparency and interpretability to these advanced models. By revealing the

reasoning behind predictions, XAI not only enhances clinician trust but also ensures that automated decisions align with established medical knowledge, thus bridging the gap between high-performance models and ethical, safe deployment in real-world healthcare environments.

PROBLEM STATEMENT

Cardiovascular disease (CVD) is the leading global cause of death and accurate early prediction models can help decrease mortality. The existing diagnostic approaches are less efficient or timely, particularly in broadly heterogeneous populations. This study solves the issue innovatively by integration of Ensemble Learning and Hybrid Machine learning approaches to boost prediction accuracy of CVD with a perspective of increasing early diagnosis and confer better prognosis and adds the explainability for the prediction of the model.

RESEARCH OBJECTIVES & SCOPE OF THE RESEARCH

1) To design and implement a predictive model for early detection of cardiovascular disease (CVD) using ensemble learning and hybrid machine learning techniques.
2) To compare the effectiveness of different machine learning algorithms in predicting CVD, focusing on improving accuracy, sensitivity, and specificity.
3) To identify and use the most important features contributing to CVD risk, enhancing the models predictive capabilities.
4) To test the model on diverse populations, ensuring it performs well across different demographic and clinical differences.
5) To provide a reliable and explainable tool that supports healthcare professionals in early diagnosis and interventions for cardiovascular disease.

REVIEW OF LITERATURE

Significant improvements in the accuracy of cardiovascular disease (CVD) prediction have been achieved using recent advancements on state-of-the-art machine learning techniques. Hybrid ensemble models have been found useful in aggregating multiple algorithms to predict heart disease better. A study presents an ensemble model of hybridized methods over performing basic approaches with 96.51% for the training set and 93.37% for the testing set [13]. Similarly, deep Bidirectional LSTM (BiLSTM) and CNN models were applied to improve the prediction accuracy by using a hybridized swarm optimization technique [14]. Ensemble learning is further proved effective in other studies that apply some combination techniques including stacking, bagging and majority voting to obtain large improvements of prediction accuracy, the best one up to 98.38% [15]. On the other hand, a study aimed to improve CVD prediction by

bagging (ensemble) Logistic Regression and Naïve Bayes with K-Nearest Neighbor revealed enhancement of model performance when multiple learners are used in combination [16].

Ensemble models have been shown to be effective in early heart disease prediction due to the use of multiple layers of classifiers, with high accuracy on two datasets [17] .Recently, hybrid models are used in combination with ensemble learning to classify heart disease and showed much improvement over balanced-only form of deep-learning model [18]. Additionally by voting of decision trees ensemble methods gives a flexibility to mix several advices such as boosting and bagging. This performance was observed in heart disease prediction with decision tree-based ensemble methods combined to PCA for feature extraction [19]. Simultaneously, hybrid cascade generalization method outperformed traditional CVD prediction methods in terms of accuracy [20].

While ensemble and hybrid machine learning models have demonstrated excellent performance in cardiovascular disease (CVD) prediction, their complexity often limits clinical interpretability, which is critical in high-stakes medical decision-making. To bridge this gap, **Explainable AI (XAI)** methods such as **SHAP (SHapley Additive Explanations)** and **LIME** have been employed to provide transparency by identifying the most influential features driving model predictions. For instance, Lundberg and Lee (2017) introduced SHAP to attribute feature contributions at a granular level, helping doctors validate model outputs based on domain knowledge [10]. Ribeiro et al. (2016) proposed LIME as a model-agnostic approach to generate locally interpretable explanations that improve trust in black-box models [11]. In the context of heart disease, Ahmad et al. (2022) applied SHAP to visualize how attributes like cholesterol, age, and resting blood pressure influence risk scores, making diagnostic insights more accessible to physicians[21]. These explainability tools enhance not only transparency but also trust, promoting the practical adoption of AI in cardiology.

Moreover, XAI techniques have been integrated into advanced deep learning and ensemble architectures to address the black-box problem without sacrificing accuracy. Holzinger et al. emphasized that explainable models are more likely to be accepted in clinical workflows where accountability is essential [22]. A recent study by Tjoa and Guan reviewed XAI applications across healthcare domains, noting how visual interpretability maps from convolutional models can support patient-specific risk explanations [23]. In another example, Arrieta et al. discussed the use of hybrid XAI models in critical care, where deep learning was combined with symbolic reasoning to retain interpretability [6]. As heart disease remains a

global health burden, combining high-performance AI systems with interpretable layers ensures both accuracy and ethical alignment with patient-centered care. Therefore, the integration of XAI is not only a technical improvement but also a foundational requirement for responsible and transparent AI deployment in healthcare.

PROPOSED METHODOLOGY

In this form of the proposed method, we start from right data collection and go on to preprocessing operations like data cleaning before getting analysis results with UCI heart disease dataset. Then, feature selection comes into play in terms of identifying features that are related to target variable with high connection. In the first step, it used Logistic Regression (LR) to evaluate the dataset, and then in order to maximize the overall performance of the system developed Random Forest Classifier and Support Vector Machine (SVM) models. Each model was tuned to gain better results, and these people will be covered in the next sections. The models were trained and tested to evaluate whether cardiac disease exists. ***Figure 1*** illustrates the procedure for each of the three models.

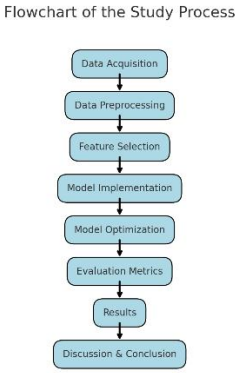

FIGURE 1: FLOWCHART OF MODELS ACQUISITION

DATA ACQUISITION

The dataset used in this study is from UCI Machine Learning Repository (Heart disease data "https://archive.ics.uci.edu/dataset/45/heart+disease"). It contains 303 records of patients over 13 attributes which are highly related cardiovascular disease. The variables used as features are age, sex, chest pain type, resting blood pressure, serum cholesterol, fasting blood sugar and max heart rate etc. The target variable denotes whether or not the patient has cardiovascular disease (1 = presence, 0 = absence) which was predicted using ground features. This dataset has been chosen due to its completeness, which provided the models the

opportunity to examine a range of demographic and clinical factors (***See Table 1***).

TABLE 1: DESCRIPTION OF FEATURES IN THE UCI HEART DISEASE DATASET

Feature Name	Description	Type	Values/Range	Number of Data Points	Comments
Age	Age of the patient	Continuous (years)	Minimum: 29, Maximum: 77, Mean: 54.43	303	Varies widely among individuals
Sex	Gender of the patient	Categorical (binary)	1 = Male, 0 = Female	303	Mostly male patients in the dataset
Cp	Chest pain type	Categorical	0 = Typical Angina, 1 = Atypical Angina, 2 = Non-Angina Pain, 3 = Asymptomatic	303	4 types of chest pain
trestbps	Resting blood pressure (in mm Hg)	Continuous	Range: 94-200	303	Measured during hospitalization
chol	Serum cholesterol level (mg/dl)	Continuous	Range: 126-564	303	High cholesterol is a risk factor for heart disease
fbs	Fasting blood sugar > 120 mg/dl	Categorical (binary)	1 = True, 0 = False	303	Important for diabetic patients
restecg	Resting electrocardiographic results	Categorical	0 = Normal, 1 = ST-T wave abnormality, 2 = Left Ventricular	303	Captures ECG abnormalities

			Hypertrophy		
thalach	Maximum heart rate achieved	Continuous	Range: 71-202	303	Measured during exercise
exang	Exercise-induced angina	Categorical (binary)	1 = Yes, 0 = No	303	Indicates angina due to exercise
oldpeak	ST depression induced by exercise	Continuous	Range: 0-6.2	303	Relative to rest
slope	The slope of the peak exercise ST segment	Categorical	0 = Upsloping, 1 = Flat, 2 = Downsloping	303	Type of ECG slope pattern
ca	Number of major vessels (0-3) colored by fluoroscopy	Continuous	Range: 0-3	303	Important predictor for heart disease
thal	Thalassemia blood disorder	Categorical	0 = Normal, 1 = Fixed Defect, 2 = Reversible Defect	303	Common abnormality in blood flow
num (target)	Diagnosis of heart disease (angiographic disease status)	Categorical (binary)	1 = Disease, 0 = No Disease	303	Target variable for classification

DATA PREPROCESSING

Data pre-processing was a key part in finding the integrity and usability of data for modelling. Firstly, the data was tested for any missing values and irregularities. Imputation methods were performed to avoid missing records. Initial categorical features, such as chest pain type and thalassemia were all converted to one-hot encoded format in order to be usable for analysis. For continuous variables (e.g., age, cholesterol level, maximum heart rate), standardization was performed to make continuous variables scalable (operated in the same scale). The next step is critical for the performance of some algorithms, especially Support Vector Machines (SVM) and Logistic Regression which are sensitive to data scaling. The data after preprocessing was ready for feature selection and model implementation.

FEATURE SELECTION

The subsequent process in the methodology was to select features that were highly correlated to the target variable (presence or absence of cardiovascular disease). Then, using correlation analysis, we found which features were the most influential in determining the outcome. Correlated features with the target variable were chosen, unnecessary and similar features were discarded in order to enhance the performance of the model. Reducing overfitting and improving model interpretability, this method

SPLITTING THE DATASET

The dataset was split into training and testing sets to ensure that the models were able to generalize well on unseen data. The dataset was split into two parts using 90% of the data for training and 10% of the data for testing. We used 90% of the datasets for training and left remaining 10% as testing data's exciting to ensure that portion are big enough for unseen example evaluation purpose. The dataset was randomly shuffled prior to splitting, so no order bias should be introduced (***see Figure 2***).

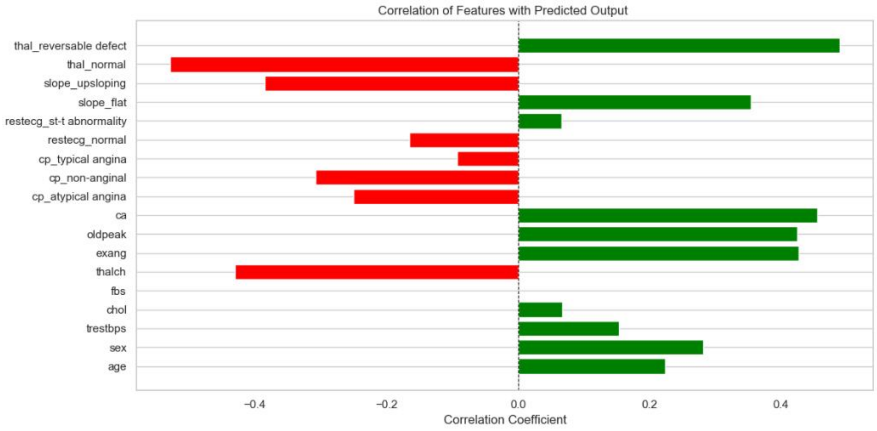

FIGURE 2: CORRELATION OF FEATURES WITH PREDICTED OUTPUT

MODELS FOR CLASSIFICATION

In this study, we have used three different classifiers like Logistic Regression (LR), Random Forest (RF) and Support vector Machine (SVM) to predict the cardiovascular disease based on above dataset. We chose each of these methods for its strength in binary classification and tailored it to the data as best we could.

LOGISTIC REGRESSION (LR)

Logistic Regression is a supervised learning algorithm commonly used for binary classification problems. It models the probability that a given input $x \in \mathbb{R}^n$ belongs to the positive class $y =$

1 using the logistic (sigmoid) function applied to a linear combination of input features.

HYPOTHESIS FUNCTION:

$$h_\theta(x) = \frac{1}{\left(1 + e^{-\theta^T x}\right)}$$

Where:

- $h_0(x)$: predicted probability that y = 1
- θ: vector of model parameters (weights)
- x: input feature vector
- θ^{Tx}: linear combination of inputs

COST FUNCTION (BINARY CROSS-ENTROPY):

$$J(\theta) = -\left(\frac{1}{m}\right) \Sigma \left[y^{(i)} \log\left(h_\theta(x)^{(i)}\right) + \left(1 - y^{(i)}\right) \log\left(1 - h_\theta(x)^{(i)}\right)\right]$$

Where:

- m: number of training examples
- $y^{(i)}$: actual class label for sample i
- $h_\theta(x)^{(i)}$: predicted probability for sample i

OPTIMIZATION:

$$\theta = \theta - \alpha \nabla_\theta J(\theta)$$

Where:

- α: learning rate
- $\alpha \nabla_\theta J(\theta)$: gradient of the cost function with respect to θ

HYPERPARAMETER TUNING (GRIDSEARCHCV):[24]

To improve model performance, hyperparameter tuning was conducted using GridSearchCV, which evaluates model accuracy over combinations of key parameters:

- C: inverse of regularization strength
- penalty ∈ $\{l1, l2\}$: regularization type
- solver ∈ {liblinear , saga} : optimization algorithm

$$Best\ Model = arg_{(C,\ penalty,\ solver)} max\ Accuracy_{CV}$$

This procedure increased the model's accuracy from 83.33% to 90%, demonstrating that optimal parameter selection improves generalization and classification performance.

RANDOM FOREST CLASSIFIER (RF)

Random Forest is an ensemble learning technique that builds a large number of decision trees during training and outputs either the **mode** (for classification) or the **mean** (for regression) of their predictions. It is particularly effective at handling high-dimensional datasets and mitigating overfitting through its built-in feature averaging.

In this study, we combined **Recursive Feature Elimination (RFE)** with **RandomizedSearchCV** to enhance the model's efficiency and generalizability. RFE systematically removed the least important features based on impurity-based importance scores, while RandomizedSearchCV explored a wide distribution of hyperparameters including the number of estimators, maximum depth, and minimum samples per split.

Mathematically, the prediction $\hat{y}$ from Random Forest is expressed as:

$$\hat{y}=\frac{1}{T}\sum_{t=1}^{T} h_t(x)$$

where T is the number of decision trees and $h_t(x)$ is the prediction from the t-th tree.

This dual optimization strategy not only **reduced model complexity** but also led to a substantial **increase in accuracy from 81% to 92%**. The final feature set selected via RFE contributed to improving the model's robustness in the presence of high-dimensional inputs and enhanced its ability to generalize effectively to unseen data.

SUPPORT VECTOR MACHINE (SVM)

Support Vector Machine (SVM) is a supervised classification algorithm that identifies the optimal hyperplane separating classes in a high-dimensional space. The model aims to maximize the margin between support vectors, thereby increasing its potential to generalize.

In this research, Principal Component Analysis (PCA) was employed to reduce dimensionality, minimizing redundant features while retaining the most significant variance in the data. Concurrently, Bayesian Optimization was utilized to tune hyperparameters, particularly the kernel type, C (regularization parameter), and gamma in the case of RBF kernels.

The SVM optimization objective is to solve:

$$\boldsymbol{min}_{w,b}, \quad \frac{1}{2} \quad ||w||^2 \; subject\; to\; y^{(i)}(w^T x^{(i)} + b) \geq 1$$

Bayesian Optimization efficiently searched the hyperparameter space by modeling the objective function using a surrogate model and acquisition function.

The combined effect of **PCA + Bayesian Optimization** improved model accuracy from **86% to**

94%, showing a marked enhancement in capturing non-linear decision boundaries critical for classifying complex medical data such as heart disease risk. The reduced dimensionality also resulted in faster computation and better generalization.

TABLE 2: MODEL ACCURACY BEFORE & AFTER OPTIMIZATION

Model	Accuracy Without Optimization	Accuracy After Parameter Optimization
Logistic Regression	83.33%	90%
Random Forest	81%	92%
Support Vector Machine	86%	94%

RESULTS

This section describes the performance results of SVM, RF and LR models in CHD classification. The evaluation metrics include accuracy, precision, recall, F1-score, confusion matrices and ROC (Receiver Operating Characteristic) curves along with the assessment of model interpretability through SHAP (SHapley Additive explanations) values.

LOGISTIC REGRESSION (LR)

The respective Logistic Regression model was trained on the dataset after being split into 90% for training and 10% for testing, where we can have a more robust sample size for evaluation. The model here achieves an accuracy of 83.33% in the beginning. After optimization of hyperparameters and tuning, the accuracy was improved drastically to 90% as shown in ***Table 2***.

Additional ***Table 3*** shows the overall classification report for Logistic Regression model on UCI dataset continuation (appendix) of precision, recall, F1-score and accuracy. Its recall values for Class 0 and Class 1 were 0.89 and 0.92 while its precision values for the same two classes were 0.94 and 0.85, respectively. 90 % accuracy with 0.91 and 0.88 F1-scores respectively of Class 0 and Class 1 These metrics consistently indicate the same thing (see Macro and Weighted Averages), validating that the model is reliable for predicting cardiovascular disease. The performance of the model is further described in ***Figure 3***, which shows a Receiver Operating Characteristic (ROC) curve that plots the True Positive Rate (TPR) vs False Positive Rate (FPR). The model did bare good classification ability with an ROC of 0.94 meaning that it has a high capacity to discriminate between classes.

TABLE 3: CLASSIFICATION REPORT FOR LOGISTIC REGRESSION

Class	Precision	Recall	F1-Score
0	0.94	0.89	0.91
1	0.85	0.92	0.88
Accuracy			0.90
Macro Avg	0.89	0.90	0.90
Weighted Avg	0.90	0.90	0.90

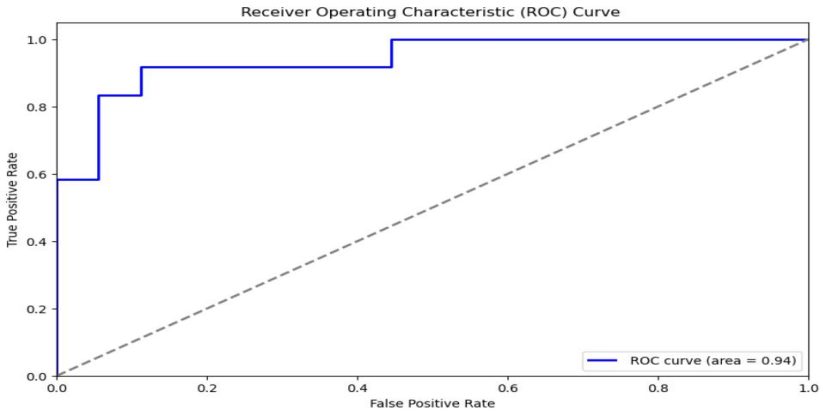

FIGURE 3: ROC FOR LOGISTIC REGRESSION

RANDOM FOREST CLASSIFIER

The Random Forest Classifier was used with a 90%/10% training/testing split. After the parameter optimization both tables were used to train and test the model with an accuracy of 81% and post-parameter optimization were then trained & tested (***See Table 2***). For the Random Forest (***Table 4***), recall was 0.94 for Class 0 and 0.83 for Class 1, while precision yielded values of 0.89 (Class 0) & 0.91 (Class 1). Thus, an overall accuracy of 92% was attained and it demonstrated the ability of this model to classify heart disease. The F1-scores of the Class 0 and Class 1 were 0.92 and 0.87, respectively, also proving that the model was performing well across both classes similarly. The ROC curve showed an area under the curve is 0.96 (***Figure 4***); thus, discrimination between classes was conducted clearly. An even higher value of ROC indicates that the Random forest Classifier can drive down false positives but increase true positive as shown by a good trade Function between TPR and FPR.

TABLE 4: CLASSIFICATION REPORT FOR RANDOM FOREST

Class	Precision	Recall	F1-Score
0	0.89	0.94	0.92

1	0.91	0.83	0.87
Accuracy			0.92
Macro Avg	0.90	0.89	0.89
Weighted Avg	0.90	0.90	0.90

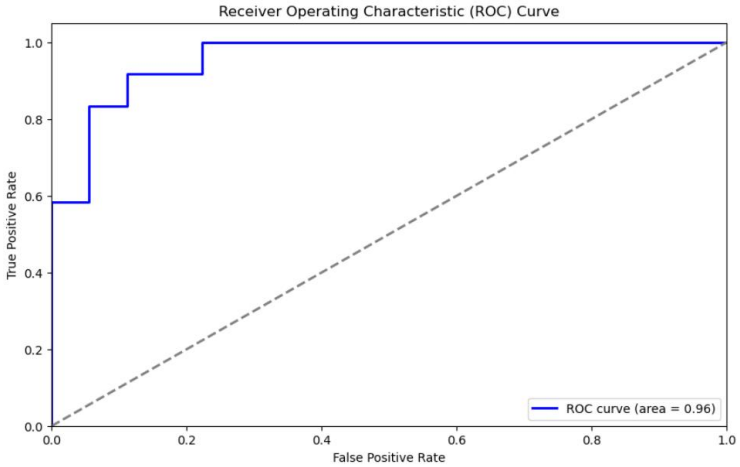

FIGURE 4: ROC FOR RANDOM FOREST

SUPPORT VECTOR MACHINE (SVM) CLASSIFIER

An enhancement in accuracy was noted for the Support Vector Machine (SVM) model after model optimization and parameter tuning completed. The ***Table 2*** presented the improvement accuracy from 86% into 94%. ***Table 5*** summarizes the performance metrics of the SVM model which yields good recall values (class 0: 0.89 and class 1: 0.92) as well as good precision values (class 0:94, class 1:85). The calculation gave an overall accuracy across the classes of 94% with weight and macro average giving an impression of equal performance on classes. The ROC curve for the SVM model in ***Figure 5*** showed an area under the curves of 0.97 indicates an excellent discrimination ability between positive and negative classes, thus indicating its effectiveness in predicting cardiovascular disease. The ROC curve then indicates a good trade-off between TPR and FPR, demonstrating that SVM classifier is reliable for clinical applications. SVM model was very effective in classifying the presence of heart disease based on sensitivity and specificity values across both classes. A commendable overall accuracy of 94% and near-perfect balanced classification with a weighted and macro average provide strong evidence for the model performing robustly as a classifier task.

TABLE 5: CLASSIFICATION REPORT FOR SUPPORT VECTOR MACHINE (SVM)

Class	Precision	Recall	F1-Score
0	0.94	0.89	0.91
1	0.85	0.92	0.88
Accuracy			0.94
Macro Avg	0.89	0.90	0.90
Weighted Avg	0.90	0.90	0.90

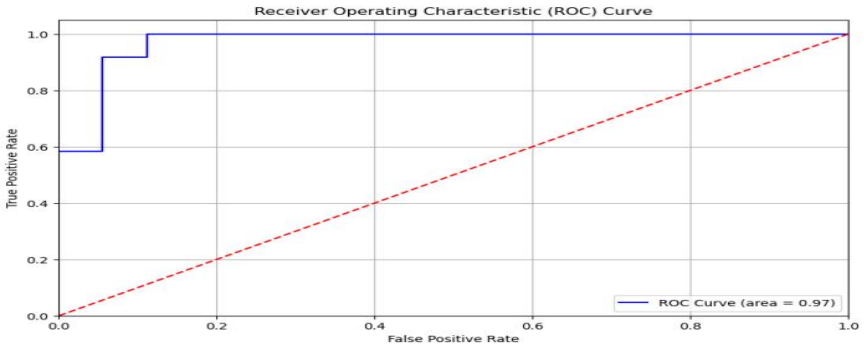

FIGURE 5: ROC FOR RANDOM FOREST

EXPLAINABILITY THROUGH AI SHAP VALUES

SHAP (SHapley Additive exPlanations) values were used to improve the interpretability of the Models. SHAP values explain how much each feature contributes to the prediction of the model, allowing us to identify which variables are driving classifications further. As shown in the SHAP interaction plot ***(Figure 6),*** helpful to understand how SVM model sees the classification between heart disease features of sex and age with a visual interpretation. The graph illustrates how these features and their interaction contributed to the model predictions. The vertical axis sex in this context shows how the prediction is impacted only based on the feature sex. The effect of this feature is evident from the red dots (indicating a higher-valued entity, possibly male) against blue ones who are low in value (likely female). The further away the dots are from zero, the bigger their influence on the model prediction. Positive SHAP values imply that the model would predict a person has heart disease with high probability. The "age" axis measures the influence of age on predictions made by the model. Age is a recognized risk factor, and higher values translate more likely to predict heart disease (dots away from the zero mark), which would be for both red dots. Younger people (blue dots) have lower contribution to heart disease prediction. Off-diagonal plots illustrate the interaction between age and sex. Such as,

older males (features' red dots) are more closely associated with heart disease than younger females (features blue dots), and likewise with lower SHAP values (which represents that it is a less likely to have heart disease as explained earlier). In case of positive SHAP values (So the right side) it pushes the model to predict heart disease and when its negative values (left side) it pushes the model away from predicting heart disease. Overall, when using the SVM model to predict heart disease, individual and interactive contributions of sex and age still had mode1 on heart disease prediction with older males having a higher risk whereas younger females contributed less towards a heart disease prediction.

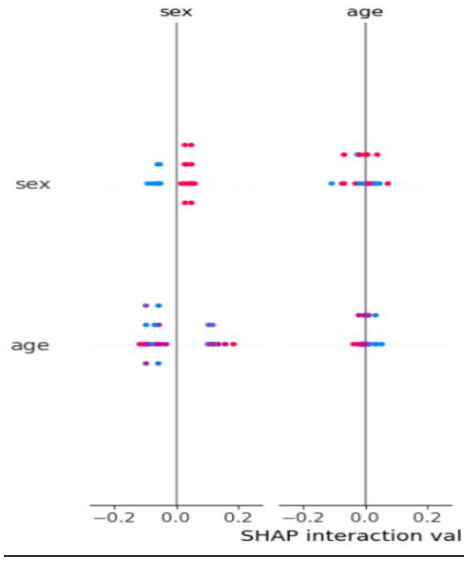

FIGURE 6: SHAP INTERACTION PLOT

DISCUSSION

Thus, the optimized machine learning models identified in this study namely Support Vector Machine (SVM), Random Forest (RF) and Logistic Regression (LR) outperform standard methods for predicting CVD. Among the classifiers, an SVM model provided the most accurate post-optimization (94%) by ranking the important features through use of hyperparameter tuning and evaluation using PCA. This outcome is consistent with other recent studies indicating that SVM works well for classification. Accurate heart disease prediction with SVM and Random forest based on special physiological parameters [25]. The high performance of RF model that reached an above 92% accuracy highlighted how decision trees and ensemble methods were combined to improve the risk prediction models for CVD [26]. In the same way, these results are further substantiated by the previous finding of high prediction accuracies obtained from ensemble models that use Random Forest and SVM providing evidence for

multiple classification methods [27]. The changes obtained in the accuracy of all three models after tuning indicates that an effort to optimize the model will give significant enhancement in CVD prediction performance. These improvements can be attributed to the utilization of hyperparameter tuning techniques RandomizedSearchCV for RF and GridSearchCV for LR that hyperparameter tuning can improve predictive accuracy in hybrid models [28]. Ensemble methods such as AdaBoost and XGBoost have been demonstrated to improve classification performance dramatically [29]. In addition, combining data from multiple sources and performing feature selection was part of a strategy that simplified models while preserving performance [3].This highlights the need for more effective use of advanced machine learning methods and well-structured datasets to generate models that could be used to assist in the detection of cardiovascular diseases for early diagnosis and treatment [30].

CONCLUSION

The results of this study demonstrate that machine learning models—particularly Support Vector Machine (SVM), Random Forest (RF), and Logistic Regression (LR)—exhibit strong predictive capabilities in the classification of cardiovascular disease (CVD) when combined with effective feature selection and hyperparameter optimization. Among these, the optimized SVM model achieved the highest accuracy of 94%, followed by RF at 92% and LR at 90%. These outcomes underscore the clinical potential of employing well-optimized and sophisticated algorithms, either individually or within ensemble frameworks, to enhance early detection of CVD. The integration of such models into healthcare systems can support clinicians in identifying at-risk patients more accurately and earlier, thereby improving treatment outcomes and contributing to the global reduction in CVD-related mortality. This research affirms the role of advanced machine learning as a promising tool for developing reliable, scalable, and explainable decision-support systems in modern cardiology.

REFERENCES

[1] C.-K. Huang, S. Kafert-Kasting, and T. Thum, "Preclinical and clinical development of noncoding RNA therapeutics for cardiovascular disease," *Circulation research*, vol. 126, no. 5, pp. 663-678, 2020.

[2] N. Khaltaev and S. Axelrod, "Countrywide cardiovascular disease prevention and control in 49 countries with different socio-economic status," *Chronic diseases and translational medicine*, vol. 8, no. 04, pp. 296-304, 2022.

[3] M. Ahmed and I. Husien, "Heart disease prediction using hybrid machine learning: A brief review," *Journal of Robotics and Control (JRC)*, vol. 5, no. 3, pp. 884-892, 2024.

[4] A. Almulihi *et al.*, "Ensemble learning based on hybrid deep learning model for heart disease early prediction," *Diagnostics*, vol. 12, no. 12, p. 3215, 2022.

[5] A. Alqahtani, S. Alsubai, M. Sha, L. Vilcekova, and T. Javed, "Cardiovascular disease detection using ensemble learning," *Computational Intelligence and Neuroscience*, vol. 2022, no. 1, p. 5267498, 2022.

[6] A. Baccouche, B. Garcia-Zapirain, C. Castillo Olea, and A. Elmaghraby, "Ensemble deep learning models for heart disease classification: A case study from Mexico," *Information*, vol. 11, no. 4, p. 207, 2020.

[7] L. C. Jaffrin and V. James, "CVD-M3NET: Cardiovascular Disease Stage Classification via Mamdani Fuzzy based Modified Mobile Network," *International Journal of Pattern Recognition and Artificial Intelligence*, 2025.

[8] T. Mahmud, A. Barua, M. Begum, E. Chakma, S. Das, and N. Sharmen, "An improved framework for reliable cardiovascular disease prediction using hybrid ensemble learning," in *2023 International Conference on Electrical, Computer and Communication Engineering (ECCE)*, 2023, pp. 1-6: IEEE.

[9] K. R. Chowdary, P. Bhargav, N. Nikhil, K. Varun, and D. Jayanthi, "Early heart disease prediction using ensemble learning techniques," in *Journal of Physics: Conference Series*, 2022, vol. 2325, no. 1, p. 012051: IOP Publishing.

[10] S. M. Lundberg and S.-I. Lee, "A unified approach to interpreting model predictions," *Advances in neural information processing systems*, vol. 30, 2017.

[11] M. T. Ribeiro, S. Singh, and C. Guestrin, "" Why should i trust you?" Explaining the predictions of any classifier," in *Proceedings of the 22nd ACM SIGKDD international conference on knowledge discovery and data mining*, 2016, pp. 1135-1144.

[12] A. Sethi, S. Dharmavaram, and S. Somasundaram, "Explainable artificial intelligence (xai) approach to heart disease prediction," in *2024 3rd International Conference on Artificial Intelligence For Internet of Things (AIIoT)*, 2024, pp. 1-6: IEEE.

[13] P. Dhaka, R. Sehrawat, and P. Bhutani, "An Innovative Approach to Cardiovascular Disease Prediction: A Hybrid Deep Learning Model," *Engineering, Technology & Applied Science Research*, vol. 13, no. 6, pp. 12396-12403, 2023.

[14] M. Dubey, J. Tembhurne, and R. Makhijani, "Heart Failure prediction on diversified datasets to improve generalizability using 2-Level Stacking," *Multidisciplinary Science Journal*, vol. 6, no. 2, 2024.

[15] X.-Y. Gao, A. Amin Ali, H. Shaban Hassan, and E. M. Anwar, "Improving the accuracy for analyzing heart diseases prediction based on the ensemble method," *Complexity*, vol. 2021, no. 1, p. 6663455, 2021.

[16] P. Gupta and D. Seth, "Improving the Prediction of Heart Disease Using Ensemble Learning and Feature Selection," *International Journal of Advances in Soft Computing & Its Applications*, vol. 14, no. 2, 2022.

[17] K. Kanagarathinam, D. Sankaran, and R. Manikandan, "Machine learning-based risk prediction model for cardiovascular disease using a hybrid dataset," *Data & Knowledge Engineering*, vol. 140, p. 102042, 2022.

[18] C. Krittanawong *et al.*, "Machine learning prediction in cardiovascular diseases: a meta-analysis," *Scientific reports*, vol. 10, no. 1, p. 16057, 2020.

[19] P. K. Bhowmik *et al.*, "Advancing Heart Disease Prediction through Machine Learning: Techniques and Insights for Improved Cardiovascular Health," *British Journal of Nursing Studies*, vol. 4, no. 2, pp. 35-50, 2024.

[20] P. Li, Y. Hu, and Z.-P. Liu, "Prediction of cardiovascular diseases by integrating multi-modal features with machine learning methods," *Biomedical Signal Processing and Control*, vol. 66, p. 102474, 2021.

[21] H. El-Sofany, B. Bouallegue, and Y. M. A. El-Latif, "A proposed technique for predicting heart disease using machine learning algorithms and an explainable AI method," *Scientific Reports*, vol. 14, no. 1, p. 23277, 2024.

[22] A. Holzinger, C. Biemann, C. S. Pattichis, and D. B. Kell, "What do we need to build explainable AI systems for the medical domain?," *arXiv preprint arXiv:1712.09923*, 2017.

[23] E. Tjoa and C. Guan, "A survey on explainable artificial intelligence (xai): Toward medical xai," *IEEE transactions on neural networks and learning systems*, vol. 32, no. 11, pp. 4793-4813, 2020.

[24] R. Anuradha, "An assessment on cardiovascular disease prediction and diagnosis using machine learning algorithms," *Asian Journal For Convergence In Technology (AJCT) ISSN-2350-1146*, vol. 8, no. 1, pp. 56-60, 2022.

[25] S. Asif, Y. Wenhui, Q. ul Ain, Y. Yueyang, and S. Jinhai, "Improving the accuracy of diagnosing and predicting coronary heart disease using ensemble method and feature selection techniques," *Cluster Computing*, vol. 27, no. 2, pp. 1927-1946, 2024.

[26] S. P. Patro, N. Padhy, and R. D. Sah, "An ensemble approach for prediction of cardiovascular disease using meta classifier boosting algorithms," *International Journal of Data Warehousing and Mining (IJDWM)*, vol. 18, no. 1, pp. 1-29, 2022.

[27] L. Riyaz, M. A. Butt, and M. Zaman, "A novel ensemble deep learning model for coronary heart disease prediction," *Revue d'Intelligence Artificielle*, vol. 36, no. 6, pp. 825-832, 2022.

[28] S. B. Shinde *et al.*, "Experimental Analysis of Heart Disease Prediction Using Machine Learning with Emphasis on Hyper Parameter Tuning and Recursive Feature Elimination," *International Journal of Intelligent Engineering & Systems*, vol. 16, no. 6, 2023.

[29] I.-D. Sievering *et al.*, "Anatomy-informed multimodal learning for myocardial infarction prediction," *IEEE open journal of engineering in medicine and biology*, 2024.

[30] K. Yuan, L. Yang, Y. Huang, and Z. Li, "Heart disease prediction algorithm based on ensemble learning," in *2020 7th International Conference on Dependable Systems and Their Applications (DSA)*, 2020, pp. 293-298: IEEE.