International Journal of Engineering Trends and Technology
ISSN: 2231–5381 / https://doi.org/10.14445/22315381/IJETT-V74I2P118

Volume 74 Issue 2, 245-265, February 2026

Original Article

Improved Adaptive Kernel-Based SVM Ensemble for Enhanced Heart Disease Diagnosis: A Feature Optimization Approach

G. Amalorpavam[1], N. Rajkumar[2]

[1]*Department of Computer and Information Science, Annamalai University, Annamalainagar, Tamil Nadu, India.*
[2]*Department of Computer Science, Manbumigu Dr Purachithalivar M.G.R. Government Arts & Science College, Kattumannarkoil, Tamil Nadu, India.*

[1]*Corresponding Author : amalphdcisau@gmail.com*

Received: 08 August 2025 Revised: 22 January 2026 Accepted: 27 January 2026 Published: 14 February 2026

Abstract *- Since cardiovascular disease continues to be the world's leading cause of death, precise, data-driven diagnostic systems must be developed. By combining multi-phase feature selection, adaptive model training, and sophisticated preprocessing, this study suggests an intelligent classification framework for the diagnosis of heart disease. Using a novel hybrid kernel function for dynamic feature space adaptation, the Improved Adaptive Support Vector Machine (IASVM) is an improved version of the Random Forest (RF), Neural Network (NN), and Support Vector Machine (SVM) classifiers. The dataset is first normalized for consistency and cleaned using outlier detection (Isolation Forest). A comprehensive method that combines correlation analysis, ANOVA F-test, Random Forest Importance (RFI), and SHAP value analysis is used to select features. These complementary methods reduce dimensional complexity while identifying a small, highly impactful subset of features that maintain diagnostic significance. To assess how feature reduction affects performance, all four models are trained on both the full feature set and the optimized subset for classification. The IASVM uses an adaptive kernel function that dynamically scales according to the geometric properties of the dataset, integrating the Manhattan and Euclidean distances. Because of this, it can more effectively differentiate between overlapping classes in nonlinear spaces, especially in clinical settings where feature distributions are unbalanced or skewed. To fine-tune classification boundaries, grid search and cross-validation are used in the IASVM's hyperparameter tuning process. A real-world dataset of heart disease is used for experimental evaluations, and metrics like accuracy, precision, recall, F1-score, and AUC are used to compare the models. The findings highlight the IASVM's capacity to generalise in high-dimensional and noisy domains by showing that, even though traditional models function well, it invariably performs better than the others, particularly when using the chosen feature set. Additionally, to improve clinical interpretability and usability, a graphical user interface (GUI) is created to display feature selection results, classification metrics, and accuracy comparisons. This study demonstrates how well feature optimisation and adaptive kernel-based classification work together, offering a scalable and understandable method for improving cardiovascular healthcare decision support.*

Keywords *- Heart Disease Diagnosis, Random Forest, Neural Network, Support Vector Machine, Adaptive Support Vector Machine, Grid search, Feature Selection, SHAP, Ensemble Learning, Medical Classification, ROC Curve.*

1. Introduction

The Cardiovascular Diseases (CVDs) have proven to be among the primary reasons for human deaths across the globe [1]. Among these diseases, Coronary Artery Disease (CAD) has been identified as a life-threatening disease caused by the obstruction or narrowing of the coronary arteries. The diagnosis of a human cardiac disease is an important factor in reducing human mortality rates and providing ample time for proper treatment [2]. The current methods of diagnosis involve a lot of manual analysis of various tests and have proven to cause delays in diagnosis. Due to the recent acceleration in the development of artificial intelligence and machine learning, automated heart disease diagnosis tools using artificial intelligence and machine learning techniques have received considerable interest in recent years [3]. Various artificial intelligence and machine learning algorithms, including Logistic Regression, Decision Trees, Random Forest, Support Vector Machines, and Neural Networks, have been widely used to interpret clinical data and help doctors in heart disease prediction. These algorithms have shown promising results in disease pattern detection using relevant clinical features like age, blood pressure, cholesterol, ECG, and type of chest pain. However, the accuracy and robustness of automated heart disease diagnosis

systems heavily rely on data quality, relevance, and adaptability. Feature selection has been recognized as a crucial step to improve the classification accuracy, interpretability, and computational efficiency [4]. Most of the current studies use one single strategy of statistical, wrapper, or embedded feature selection techniques independently, such as the Chi-square test, ANOVA, Recursive Feature Elimination, and tree-based importance measures. However, a single-strategy feature selection cannot capture complementary information from different perspectives, which usually incurs either redundant feature retention or loss of discriminative attributes. Moreover, recently explainable artificial intelligence tools, such as SHAP, have also attracted much more emphasis to improve the transparency and trust in the clinical decision-making system [5]. SVM is still one of the best classifiers for medical diagnosis because of its solid theoretical fundamentals and generalization capability [6]. However, it traditionally depends upon fixed kernel functions such as radial basis functions, polynomials, and sigmoid functions. These kernels are inherently fixed and usually fail to be adapted to the heterogeneous and nonlinear distributions of clinical data. Thus, their classification performance deteriorates in high-dimensional, imbalanced, and noisy medical datasets. Although many methods of kernel optimization have been proposed up till now, most of them lack adaptability and distance-aware learning capability.

Recent research trends indicate an increasing need for adaptive kernel learning mechanisms that may adapt dynamically to the intrinsic geometry of medical data [7]. Simultaneously, ensemble learning and hybrid feature optimization strategies have shown superior performance compared to single-model frameworks. However, only a few studies have tried to integrate adaptive kernel learning with multi-strategy feature optimization in a unified diagnostic framework. Moreover, most existing works mainly focus on accuracy and offer very limited interpretability and practical clinical usability. Despite these advances, several important gaps persist in the current literature: First, fixed kernel SVM models cannot adapt to complex clinical feature distributions. Second, most existing feature selection frameworks mainly rely on isolated techniques other than synergistic multi-strategy optimization. Third, interpretability-driven feature validation is often not considered. Finally, very few studies have provided comprehensive comparisons supported by statistical significance testing and clinical-oriented visualization.

In an attempt to address these challenges, an improved adaptive kernel-based SVM ensemble solution combined with an extensive feature optimization technique is proposed to facilitate better heart disease prediction. The proposed solution presents an Improved Adaptive Support Vector Machine (IASVM) solution that uses an innovative distance-aware kernel through Manhattan and Euclidean distance scaling. The adaptive kernel is used to facilitate better margins between heart disease and non-heart disease to qualify better adaptability and learning capabilities. In the subsequent step, an extensive feature optimization flow chain involving ANOVA F-Test, Recursive Feature Elimination, RF Importance, and SHAP Values is established to detect the most crucial feature. The extracted feature set is then utilized to train and test the models of RF, Neural Network, SVM, and IASVM.

The key takeaways or contributions of this work are as follows:

- Formulation of a new adaptive hybrid kernel-based IASVM approach to classify heart disease patients.
- Multi-strategy features optimization framework design, including statistical methods. Add wrapper and embedded approaches. Use explainability.
- Detailed comparative analysis based on various performance criteria, ROC analysis, and validation tests.
- Integration of graphical interface support for real-time clinical decision assistance and comparison of models.

Various experimental analyses have validated that the designed IASVM model with chosen features performs much better than conventional machine learning models concerning their accuracy, precision, recall, and F1-score values. The designed framework is, thus, a reliable, interpretable, and practical solution for early-stage heart disease analysis.

2. Related Works

R. Raniya et al. [8] presented a new and more comprehensive way to improve the diagnosis of heart disease by using machine learning algorithms and statistical methods for feature selection. In particular, the authors used the Chi-square (χ^2) test using clinical characteristics that affect the outcomes of heart disease to identify the features that were most relevant to providing a significant improvement in the prediction of heart disease. By doing so, the algorithm not only provided increased accuracy but also helped in the efficiency and effectiveness of the model by reducing the dimensionality of the problem. Mohsen Dorraki et al. [9] investigated the potential of improving Cardiovascular Disease (CVD) risk prediction by incorporating psychological factors into machine learning (ML) models. The initial model using only CVD risk factors had an accuracy of 71.31%. The authors then built a model that included psychological variables, including depression, anxiety, and stress. The accuracy of the model improved remarkably to 85.13%. Narendra Kumar Sharma et al. [10] reported a noteworthy and innovative approach to improving heart disease prediction through ensemble machine learning strategies. The authors suggest and support an iterative ensemble learning strategy that aggregates multiple classifiers, even if they perform at low levels as classifiers, to develop a predictive model. An evolution of different algorithms through an ensemble assists in combining multiple

kinds of classifiers to improve prediction accuracy and thus, empower more informed healthcare decisions. Ahmad Hammoud et al. [11] provide an extensive assessment of multiple machine learning models to predict Coronary Heart Disease (CHD). They examine seven algorithms with a dataset of 1,189 instances and 12 attributes. Feature selection was done to reduce it to seven correlated features. Hyperparameter tuning was performed using Grid Search, Random Search, and Bayesian Search. The performance of the Random Forest model stood out from the other algorithms as it performed with an average accuracy of 92.85%, which improved to 94.96% using ensemble methods. Govardhan Logabiraman et al. [12] observed how several machine learning techniques can be applied to improve the prediction for heart disease. The authors used a hybrid model that combined the use of learning algorithms, for example, Artificial Neural Networks (ANN), Gradient Boosting, Decision Trees, SVM, Random Forests, and Logistic Regression, to set up a full-fledged forecasting with different learning algorithms and techniques.

Neeraja Joshi et al. [13] present a holistic strategy in the early detection of heart disease using machine learning. They focus on the classification of heart disease using essential parameters: age, sex, chest pain type, fasting blood sugar, and resting ECG, with data sourced from the Cleveland dataset. The authors applied different machine learning algorithms, such as linear regression, backpropagation neural networks, SVM, and k-Nearest Neighbors (KNN), to formulate a system that can diagnose heart conditions prior to a patient meeting with the doctor. Vankamamidi S. Naresh et al. [14] present a new framework that uses Fully Homomorphic Encryption (FHE) coupled with logistic regression to ensure privacy in predictive heart disease. The authors implemented the Cheon-Kim-Kim-Song (CKKS) encryption scheme and built a Homomorphic Encryption-Driven Logistic Regression (HELR) model that performed computations on encrypted data, preserving patient data without decryption. This research creates a substantial contribution to the development of privacy-preserving predictive models in the healthcare domain. The authors of [15], Rasool Reddy Kamireddy et al., proposed an inclusive framework for the early detection of CVDs through supervised Machine Learning approaches. This article emphasizes the potential of integrating substantial preprocessing and hyperparameter tuning for building advanced ML-derived diagnostic strategies for CVD prediction. A. Pandey et al. [16] indicated the serious issue of class imbalance (the dataset with more data points from some classes and fewer from others, often misleading the predictive model performance), which is a significant factor that can hinder the modeling process. The authors applied four sampling methods (Synthetic Minority Oversampling Technique (SMOTE), Random Oversampling (ROS), Random Undersampling (RUS), and cost-sensitive learning) for addressing data imbalance to define the reliability of machine learning models and, in return, clinical testing procedures in medical diagnosis. B. Ramesh et al. [17] describe a framework that combines deep learning and neuro-fuzzy inference systems for the early detection and prevention of CHD. The proposed model is described as a hybrid deep learning structure and a neural fuzzy inference, combining two approaches to provide better accuracy.

S. Kanimozhi et al. [18] conduct a comparative study of machine learning models for heart prediction. The authors discuss the importance of early detection in lowering the risk of heart attack, and propose a prediction model that finds the optimal algorithm in a systematic manner for precise predictions. Songze Li [19] also conducts a comparative study of many machine learning algorithms to predict heart disease. The study emphasizes the importance of early detection of heart disease and provides personalized treatment recommendations, and provides rapid results to the patient to avoid heart disease. Ankit Garg et al. [20] describe a framework that integrates machine learning and smart health systems in order to improve Cardiovascular Disease (CVD) prevention. The authors emphasize the use of the newest algorithms to utilize patient data that allows for early detection and for patients to take action prior to CVD. Their solution emphasizes real-time monitoring and personalized healthcare, which is consistent with the evolution of digital health. In "Multi-Objective Multi-Verse Optimizer Fused with a Firefly Algorithm and Deep Learning for Cardiac Disease," A. Mehmood et al. [21] proposed an innovative approach to improve heart disease prediction by enhancing feature selection and classification through advanced ensemble learning and selection methods. They describe a method for Integrated Filter-Evolutionary Search-based Feature Selection (iFES-FS), which combines adaptive Threshold Information Gain-based Feature Selection (aTIG-FS) with Evolutionary Gravity-Search-based Feature Selection (EGS-FS). The hybrid filtering and search components proposed in this study allow for the identification of the most significant features in the dataset. They then improve classification by offering an Intelligent Multi-Layer Perceptron Neural Network-based Ensemble Classifier (IMLP-NN-EC) where multi-objective hyper-parameters are optimized using a Firefly-driven Multi-Objective Multi-Verse Optimizer (FF-MOMVO) algorithm to assess the best parameter ranges for maximizing the classifier's performance. In "Predicting Cardiovascular Disease Risk: A New Option Using Deep Learning and Feature Augmentation," María Teresa García-Ordás et al. [22] described a new approach to predicting cardiovascular disease (CVD) risk in patients using the techniques of deep learning and feature augmentation to refine prediction. The authors recognized the complexity and many interacting variables that influence heart disease, and suggested a two-pronged contribution of deep learning and feature augmentation to enhance predictive capability.

S.N. Netra et al. [23] present an adaptive deep SVM framework for early heart disease detection among cardiac patients. Their study combines deep feature learning with

adaptive SVM classification to enhance diagnostic accuracy. The authors demonstrate that adaptive kernel tuning significantly improves class separation, particularly in complex clinical datasets. The work highlights the potential of hybrid deep learning and SVM integration for early-stage cardiovascular risk prediction. A. E. A. Alowaidi and M. Cevik [24] introduce the Adaptive Volcano Support Vector Machine (AVSVM) for efficient classification. The proposed model dynamically adjusts its kernel behavior based on data distribution, enabling improved robustness and classification stability. Their experimental results confirm that AVSVM outperforms conventional SVM variants across multiple benchmark datasets. This study emphasizes the importance of adaptive kernel strategies for handling heterogeneous data patterns. An author focus on explainable machine learning techniques for heart disease detection, emphasizing interpretability and robust evaluation. Their framework integrates explainability mechanisms to enhance clinical trust and transparency in decision-making. The authors demonstrate that explainable models can achieve competitive accuracy while providing meaningful insights into feature contributions. This work reinforces the necessity of interpretability in clinical AI systems. J. Y. Jang [25] proposes an explainable AI-based clinical signal analysis framework for the prevention and management of heart disease. The study highlights the role of XAI techniques in improving model transparency and supporting early intervention strategies. The author shows that explainable models can effectively assist clinicians in understanding risk patterns from physiological signals.

This research aligns with the growing demand for trustworthy and interpretable AI in healthcare applications. Although many machine learning and deep learning techniques have been proposed for the diagnosis of heart disease, many existing methods have the following drawbacks. Conventional machine learning methods heavily depend on fixed kernel functions, single-step feature selection techniques, or non-transparent/black-box deep learning techniques. Many existing studies have proposed methods to increase the accuracy of classification or the effectiveness of feature selection independently. However, a unified and adaptive solution for both has not been pursued. Most existing research studies on this topic have not been equipped with distance-aware adaptability for the kernel functions, statistical validation, or the relevance of the features obtained. This proposed work seeks to combine the feature optimization process with the improved adaptive hybrid kernel function-based Support Vector Machine ensemble technique for better discrimination and interpretability. The proposed research work is therefore novel and unique for its ability to provide improved adaptability, accuracy, and applicability.

3. The Proposed Model

The proposed model for heart disease diagnosis involves a systematic procedure. In the beginning, preprocessing of clinical datasets will be performed to clean, normalize, and standardize the features. As a next step, important feature-based selection will be performed from the multi-strategy optimization method.

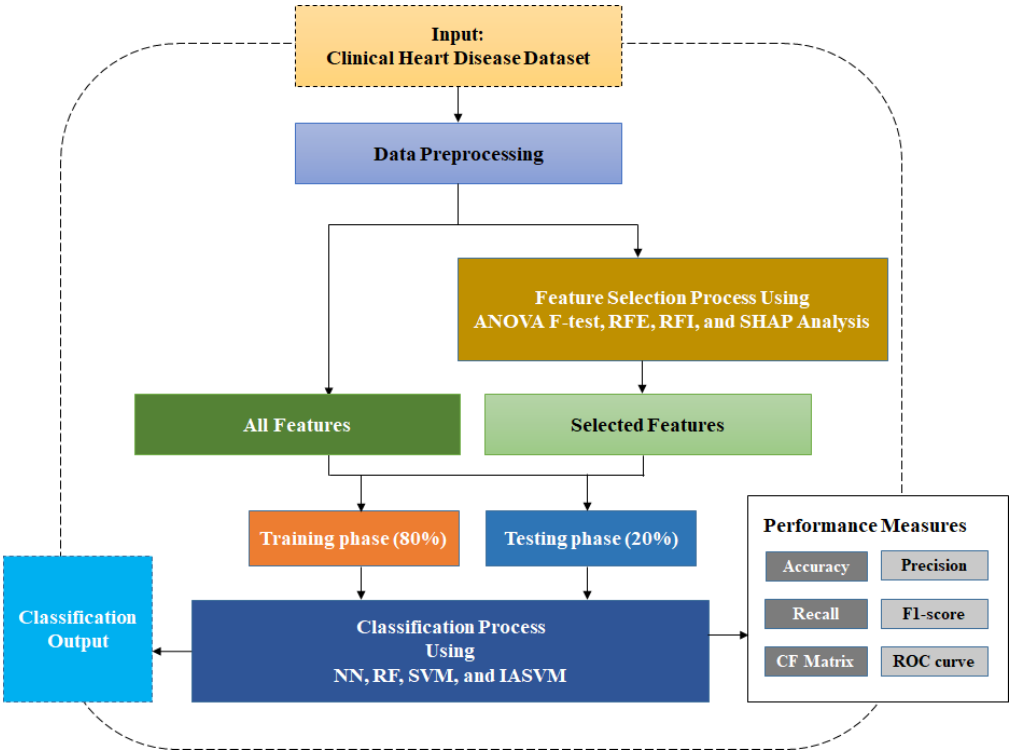

Fig. 1 Block diagram of proposed framework

The SMOTE method, which can create synthetic instances for samples from minority classes, will also help address the class imbalance. Following that, to establish a basis for our comparisons, we will first train a baseline SVM model using a standard RBF kernel.

The model can then be adapted and improved upon in our Adaptive Kernel-Based SVM, which introduces both Manhattan and Euclidean distances to model the correct structure of the underlying data. Finally, the models can be completely evaluated with an assortment of evaluation metrics (accuracy, precision, recall, F1-score, confusion matrices, and ROC curves) that will ensure the proposed framework's credibility. The block diagram of the proposed approach is shown in Figure 1.

3.1. Data Preprocessing

The quality of the input data is incredibly important to the performance of any machine learning model, especially in sensitive domains such as heart disease diagnosis.

Therefore, a thorough preprocessing phase is crucial to prepare a dataset for feature selection and classification. The preprocessing phase consists of handling missing values, data normalization, handling outliers, and correcting class imbalances. Each of these steps is described in detail below:

3.1.1. Missing Value Handling

In actual clinical datasets, missing values due to erroneous measurement or recording are often present. In the current work, mean imputation is used to handle any missing values. Each missing value $x_{missing}$ in feature j is replaced by the mean of the observed values:

$$x_{missing}^{(j)} = \frac{1}{n} \sum_{i=1}^{n} x_i^{(j)} \quad (1)$$

Where n is the number of observed (non-missing) samples.

3.1.2. Data Normalization

Medical data features often exist at different scales, which can bias model training. Standardization (Z-score normalization) can help put all features on the same scale:

$$z_i^{(j)} = \frac{x_i^{(j)} - \mu_j}{\sigma_j} \quad (2)$$

Where, $x_i^{(j)}$ is the value of the i^{th} sample in the j^{th} feature, μ_j is the mean of feature j, and σ_j standard deviation of feature j.

Standardization transforms the features so every feature has a mean of 0 and a standard deviation of 1. It allows for faster convergence and more reliable, stable model training.

3.1.3 Outlier Handling

The process of outlier handling is an essential step of the preprocessing stage because, in medical datasets, extreme values can skew the machine learning model's learning process. In this research, outliers are identified using the Interquartile Range (IQR) method, which is a strong and commonly used method in statistics. The first quartile (Q1) and the third quartile (Q3) of each feature are calculated, and the interquartile range is calculated as:

$$IQR_j = Q3_j - Q1_j \quad (3)$$

Data points are considered outliers if:

$$x_i^{(j)} < Q1_j - 1.5 \times IQR_j \ (or)\ x_i^{(j)} > Q3_j + 1.5 \times IQR_j \quad (4)$$

These extreme values, when not addressed, can cause feature distributions to be skewed, which could lead to poor generalization across the model. Once outliers are detected, they can either be excluded from the dataset or "capped" to the closest threshold value of an acceptable range. Outlier capping ensures the data distribution maintains statistical consistency and reduces overfitting, ultimately leading to a more accurate and less variable classification model.

3.1.4 Class Imbalance Handling

In several heart disease datasets, there can be more 'Normal' records than 'CAD' records. To prevent the model from being biased towards the majority class, the Synthetic Minority Oversampling Technique (SMOTE) is included. SMOTE creates synthetic samples for the minority class by interpolating between minority samples. For a minority sample x and one of its $k - nearest$ neighbors $x_{neighbor}$, the synthetic sample x_{new} is generated as:

$$x_{new} = x + \lambda \times (x_{neighbor} - x) \quad (5)$$

Where, $\lambda \sim U(0,1)$ is a random number between 0 and 1. By doing this, new data points are created on the line segments representing the samples of the minority classes. This increases the diversity of the samples belonging to the minority classes without repeating the data. This helps SMOTE to remove the imbalance existing within the classes.

To evaluate the effect of SMOTE, the performance is measured on both occasions, without SMOTE and with SMOTE. Without SMOTE, the classifiers had increased bias values towards the majority class, because of which the recall and F1-score values decreased along with the rise in the number of false negatives for CAD samples. When SMOTE is employed, it results in unbiased classes, and there is an improvement in recall scores and ROC-AUC scores. The IASVM model performs better because of SMOTE, as it raises

the sensitivity towards CAD cases without fluctuating the precision values. This shows that SMOTE is an important factor in increasing the detection capability of the proposed system.

3.2. Multi-Strategy Feature Selection Pipeline

Feature selection is a crucial process that improves the performance and interpretability of the machine learning model through the discovery of the most valuable and pertinent features. In this paper, a multi-strategy feature selection pipeline was used to iteratively diminish the dimensionality of the dataset and remove any redundant or irrelevant features. The initial step included applying an ANOVA F-test to statistically measure the degree of relationship between each feature and the target variable by keeping those features that remain with significant variance across classes. The next step incorporated Recursive Feature Elimination (RFE) using a linear Support Vector Machine (SVM) estimator, resulting in the sequential management of features in order of importance and their impact on classification. We combined the RFE results with the results of Random Forest Impurity (RFI) scores that capture possible nonlinear interactions amongst features. As a more transparent metric, we also calculated SHAP values to derive each feature's individual contribution to the model's predicted outcome. The final list of selected features was determined by combining the highly ranked features from each feature selection algorithm, ensuring training the model on the most relevant features in the downstream analysis. Taken together, this feature selection process improved the classification accuracy of the model and minimized overfitting, training time, and computational burden.

3.2.1. ANOVA F-Test

The ANOVA F-test (Analysis of Variance F-test) is one of the most commonly used statistical techniques to compare the mean differences in two or more groups. Regarding feature selection for heart disease diagnosis, the ANOVA F-test checks how well each feature can discriminate between classes (i.e., 'Normal' versus 'CAD'). The feature that is strongly correlated to the target variable will be kept for model training, while features that show weak comparisons will be discarded. The ANOVA F-test essentially checks two sources of variance: Between-group variance (which measures the separation between the individual groups/means) and Within-group variance (which measures the separation of means within the individual groups).

The F-statistic for each feature is computed as:

$$F = \frac{MS_{between}}{MS_{within}} \tag{6}$$

Where, $MS_{between}$ is the mean square between the groups, MS_{within} is the mean square within the groups. Each component is calculated as follows:

Between-Group Variance

Variability between the different class means is known as Between-group variance.

$$MS_{between} = \frac{SS_{between}}{k-1} \tag{7}$$

Where, $SS_{between}$ is the sum of squares between the groups, k is the number of classes.

The sum of squares between groups is:

$$SS_{between} = \sum_{j=1}^{k} n_j (\bar{x}_j - \bar{x})^2 \tag{8}$$

Where, n_j is the number of observations in class j, $\bar{x}_j$ is the mean of feature values in class j, $\bar{x}$ is the overall mean of the feature.

Within-Group Variance

Variability of data points within each class is known as Within-group variance.

$$MS_{within} = \frac{SS_{within}}{n-k} \tag{9}$$

Where, SS_{within} is the Sum of squares within the groups, n is the total number of samples.

The sum of squares within groups is:

$$SS_{within} = \sum_{j=1}^{k} \sum_{i=1}^{n_j} (x_{ij} - \bar{x}_j)^2 \tag{10}$$

Where, x_{ij} is the value of the feature for the i^{th} sample in class j.

Interpretation

- A higher F-value indicates that the feature has a substantial contribution toward discriminating between the classes, so it should be selected.
- A lower F-value suggests that the feature does not adequately discriminate between the classes, so it can be excluded.

Selection Strategy

After calculating the F-statistic for all features:

- The features are sorted according to their F-scores.
- A small subset of the best features is selected for future stages of model training.

In the proposed model, SelectKBest with score_func=f_classif from the scikit-learn library is implemented to perform this computation in an automated manner. The method evaluates the features independently of one another and keeps the features with the highest discriminative power, according to the F-statistic and related

top-tier features. By applying the ANOVA F-test in this methodical way, the classifier is guaranteed that all features used for training are statistically significant, improving overall time and heart disease classification accuracy.

3.2.2. Recursive Feature Elimination (RFE)

RFE is an iterative, efficient feature selection method that determines which features are most important by recursively learning from a model and eliminating the least important features at each iteration. After estimating the rank of the features in the proposed model for heart disease diagnosis, RFE was used to eliminate further features from the subset to improve classification performance. The basic procedure for RFE is as follows. First, a learning model is trained from data, and the important features are evaluated based on the coefficients of the model or the feature importance obtained. The least important features are removed from the dataset recursively through the procedure until the model has the desired number of features. The implementation details of RFE can be stated mathematically as follows:

Model Training

Initially, a machine learning model M is trained on the full feature set,

$$X \in R^{n \times d} \tag{11}$$

Where n is the number of samples, and d is the number of features. The model learns a weight vector $w \in R^{d}$ that defines the importance of each feature.

Feature Ranking

After training, each feature j is assigned an importance score. For a linear SVM, the importance score I_j for feature j is:

$$I_j = w_j^2 \tag{12}$$

Where, w_j is the coefficient corresponding to the j^{th} feature. The higher the value of I_j, the more important the feature is considered for the model.

3.2.3. Feature Elimination

The feature with the smallest importance score I_j is removed from the dataset. Thus, the feature set X is updated to X' with one less feature:

$$X' = X \setminus j_{min} \tag{13}$$

Where, j_{min} is the index of the feature with the minimum importance score.

Recursive Process

The model is retrained on the updated feature set X', and steps 2–3 are repeated recursively until the desired number of features k is retained, where $k \ll d$. Mathematically, after $d - k$ iterations:

$$|X'| = k \tag{14}$$

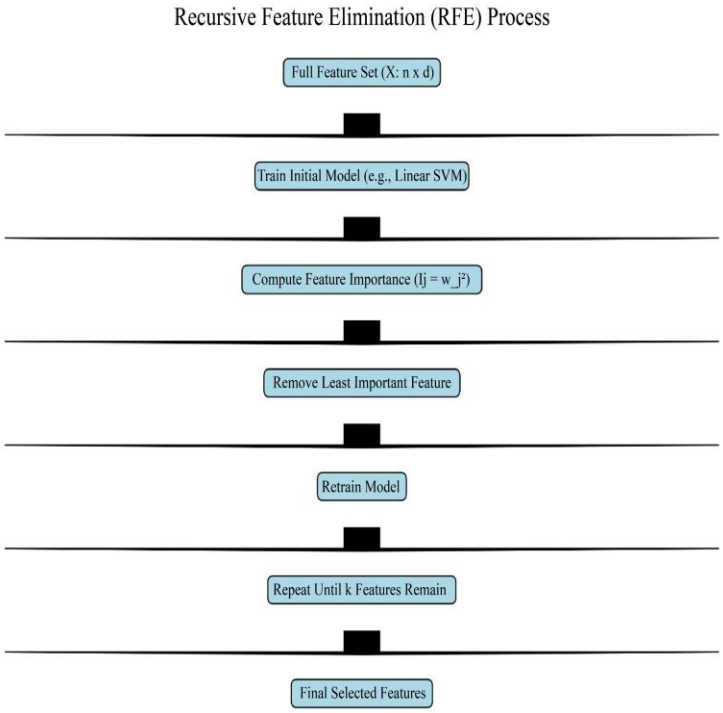

Fig. 2 Architecture of RFE processes

Thus, the final reduced feature set consists of the k most important features according to the model's internal ranking. The RFE technique aids in dimensionality reduction, reduces the propensity for overfitting, and increases the interpretability of the model. This study will use SVM with a linear kernel as the base estimator of the RFE; therefore, the feature importance will be learned from the decision boundary weights of the model. This means that the importance of the selected features will be a high indicator for correct heart disease classification. The process followed in RFE is outlined in Figure 2.

3.2.4. Random Forest Importance (RFI)

Random Forest Importance (RFI) is an incredibly popular and effective way in predictive modeling to measure attribute relevance. In this study, RFI is utilized in the feature selection process at a stage of the process to rank the lists of features based on their contribution to the model's decision-making process. A Random Forest is an ensemble of decision trees, and the attribute importance is derived by calculating how much each attribute decreases the impurity in the decision trees across the forest. The process can be mathematically described by the following:

Random Forest Construction

A Random Forest RF consists of T decision trees:

$$RF = t_1, t_2, \dots, t_T \tag{15}$$

Each tree is trained on a random subset of the data and a random subset of features.

Feature Importance in a Single Tree

For a given decision tree t, the importance of a feature j is calculated based on how much it decreases node impurity. For a node s that splits on feature j, the decrease in impurity $\Delta I(s)$ is given by:

$$\Delta I(s) = I(s) - p_L I(s_L) - p_R I(s_R) \tag{16}$$

Where, $I(s)$ is the impurity at node s, s_L and s_R are the left and right child nodes after the split, and $p_L$and p_R these are the proportions of samples in the left and right child nodes, respectively.

Gini Impurity for a node s is:

$$I(s) = 1 - \sum_{k=1}^{K} p_k^2 \tag{17}$$

Where, p_k is the fraction of samples of class k at node s.

Aggregated Feature Importance in the Forest

The total importance of feature j over all trees in the forest is computed as:

$$FI_j = \frac{1}{T}\sum_{t=1}^{T}\sum_{s\epsilon S_t(j)} \Delta I(s) \tag{18}$$

Where, $S_t(j)$ is the set of all nodes in tree t where feature j is used for splitting, and $\Delta I(s)$ is the impurity decrease at node s.

Thus, the importance score FI_j represents the average impurity reduction contributed by feature j across all trees.

Feature Selection Using RFI

After computing FI_j for all features:

- Features are ranked in terms of their contributions to relevance or importance
- A set of the top-ranked features is selected for training the ultimate classification model.

The RFI captures nonlinear relationships and interactions amongst features. Furthermore, it can handle lots of features and noisy data naturally, and provides a stable ranking of feature relevance even when the dataset is relatively complex.

3.2.5. SHapley Additive exPlanations (SHAP) Analysis

SHAP is a unifying representation, based on cooperative game theory, that describes the contribution of each feature to the model's output. SHAP values come into play during the feature selection process to evaluate feature importance by looking at how the feature impacts model predictions.

The key concept is that each feature j is thought of as a "player" in a cooperative game, and the model output is thought of as the "payout" that the players share. The SHAP value for each feature is the average marginal contribution of that feature over all possible feature combinations.

Shapley Value Definition

For a feature j in a feature set F, the Shapley value $\emptyset_j$ is defined as:

$$\phi_j = \sum_{S\subseteq F\setminus j} \frac{|S|!(d-|S|-1)!}{d!}[f(S\cup j) - f(S)] \tag{19}$$

Where S is any subset of the feature set not containing j, $f(S)$ is the model prediction using only the features in subset S, d is the total number of features, and $|S|$ is the number of features in subset S. Each term measures the marginal contribution of feature j when added to subset S.

Intuitive Meaning

- If adding feature j to a subset S significantly changes the prediction f, it means that j is important.
- SHAP values average this marginal impact across all possible subsets S.

Thus, ϕ_j captures the overall importance of feature j in making predictions.

Efficient Computation

Direct calculation of SHAP values is computationally expensive because it requires evaluating 2^d subsets. To address this, approximations like TreeSHAP for tree-based models and KernelSHAP for black-box models are used, significantly reducing computation while preserving theoretical guarantees.

Feature Importance Using SHAP

After computing the SHAP values for all features, the mean absolute SHAP value across all samples is calculated for each feature:

$$SHAP\ Importance\ of\ Feature\ j = \frac{1}{n}\sum_{i=1}^{n}\left|\phi_{ij}\right| \quad (20)$$

Where, $\emptyset_{ij}$ is the SHAP value for feature j and sample i, and n is the total number of samples.

- Features are then ranked according to their mean absolute SHAP importance.
- A subset of the most important features is selected based on this ranking for model building.

The SHAP provides individual-level explanations for each prediction. It guarantees fairness based on cooperative game theory principles.

It also captures feature interactions and nonlinear contributions, which are delivered naturally.

Figure 3 provides an ordering of the importance of sample features for model predictions based on SHAP values.

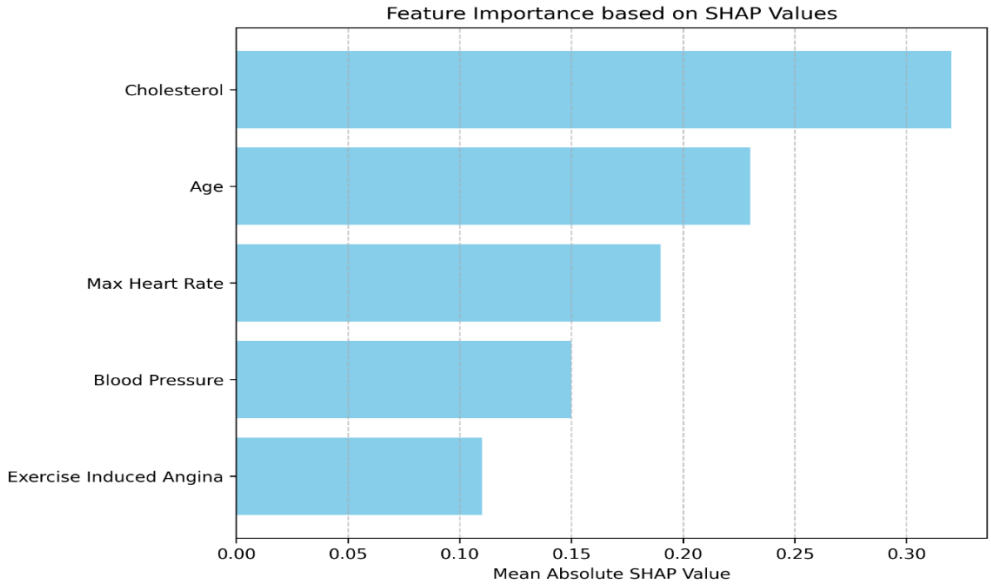

Fig. 3 Identifying feature importance in model prediction using SHAP values

3.3. Dataset Splitting

In this work, the preprocessed data set is split into training and testing sets with an 80:20 ratio in order to effectively train the classification models while also having a part set aside for unbiased testing. This division strategy guarantees that 80% of the data is utilized to train models such as Neural Network, Random Forest, SVM, and IASVM so that they can learn patterns and decision boundaries, while the other 20% is solely utilized for testing to ensure model performance. The splitting process is conducted via stratified sampling in order to maintain the original class label distribution, which is especially crucial for medical datasets where class imbalance frequently occurs. This process ensures that learned models are evaluated on genuine, unseen instances, thereby offering accurate estimates for such important metrics as accuracy, precision, recall, F1-score, and AUC. In addition, the standardized splitting is always used with both the full-feature and selected-feature datasets in order to provide equal performance comparison across all the models.

3.4 Classification

The classification task in this research is a comparative analysis of four different machine learning models: NN, RF, SVM, and IASVM for heart disease diagnosis. Following the preprocessing and feature selection, the dataset is split into a training subset and a testing subset using an 80-20 ratio. The NN model is trained on a deep feedforward architecture with ReLU activations and a sigmoid output layer, optimizing binary cross-entropy to predict the probability of disease. The RF classifier builds an ensemble of decision trees and predicts

based on majority voting, where each feature's importance is calculated through its average impurity reduction across trees. The default SVM model identifies the best separating hyperplane in a high-dimensional space by employing a Radial Basis Function (RBF) kernel and soft-margin optimization. For enhanced classification performance on complex and nonlinear patterns, an IASVM model is proposed, which substitutes the conventional kernel with a hybrid adaptive kernel that dynamically adapts based on both Euclidean and Manhattan distances. Each model is compared using traditional measures such as accuracy, precision, recall, F1-score, and ROC-AUC. The performances are examined both with all the features and with the optimal features chosen to measure how the dimensionality of features affects classification performance.

3.4.1. Classification using NN

In this paper, a feedforward neural network is employed to classify heart disease cases according to clinical features. The network has several fully connected layers with ReLU activation and dropout for regularization. The input feature vector $x \epsilon R^d$ passes through each layer, where the output of a layer l is computed as:

$$h^{(l)} = \sigma(W^{(l)} h^{(l-1)} + b^{(l)}) \tag{21}$$

Here, $W^{(l)}$ and $b^{(l)}$ are the weights and biases of the l^{th} layer, $\sigma(\cdot)$ is the activation function, and $h^{(0)} = x$. The final layer uses a sigmoid activation function to produce a probability score $\hat{y} \in [0,1]$, interpreted as the likelihood of CAD presence:

$$\hat{y} = \frac{1}{1+e^{-z}},\ where, z = W^{(L)} h^{(L-1)} + b^{(L)} \tag{22}$$

The model is trained to minimize the binary cross-entropy loss:

$$L = -\frac{1}{n}\sum_{i=1}^{n}[y_i \log(\hat{y}_i) + (1-y_i)\log(1-\hat{y}_i) \tag{23}$$

Where, $y_i \in \{0,1\}$ is the true label for the i^{th} sample.

3.4.2. Classification using RF

Random Forest is an ensemble classifying technique where several decision trees are created, and their results are summed up to obtain a prediction.

Every decision tree is trained using a bootstrapped subset of the data along with a random subset of the features at each node to cut down on overfitting and increase generalization. For a sample x, each tree t_k produces a class prediction $h_k(x) \in \{0,1\}$. The final RF prediction $\hat{y}$ is obtained through majority voting:

$$\hat{y} = mode(h_1(x), h_2(x), \ldots, h_T(x)) \tag{24}$$

Alternatively, for probabilistic output:

$$P(CAD|x) = \frac{1}{T}\sum_{k=1}^{T} h_k(x) \tag{25}$$

The RF learns to split nodes using a metric such as Gini impurity, defined as:

$$Gini(s) = 1 - \sum_{i=1}^{C} p_i^2 \tag{26}$$

Where, p_i is the proportion of samples of class i at node s, and C is the number of classes. Feature importance is later derived based on the average decrease in impurity across trees.

3.4.3. Classification using SVM

Support Vector Machine is a margin-based classifier that determines the best hyperplane that separates two classes with the largest margin. It does this by maximizing the margin, which is the distance between the hyperplane and the closest points from each of the two classes, or support vectors. To accommodate nonlinear relationships often encountered in clinical data, SVM employs kernel functions, such as the RBF, that map input data implicitly into a higher-dimensional space where linear separation is possible. Given training data (x_i, y_i), where $y_i \in \{-1,1\}$, the primal optimization objective for a soft-margin SVM is:

$$\min_{w,b,\xi} \frac{1}{2}\|w\|^2 + C\sum_{i=1}^{n}\xi_i \quad subject\ to\ \ y_i(w^T\phi(x_i) + b) \geq 1 - \xi_i,\ \ \xi_i > 0 \tag{27}$$

Where $\phi(\cdot)$ is the kernel function mapping input to a high-dimensional space, ξ_i are slack variables allowing for soft margin, C controls the trade-off between margin maximization and classification error.

3.4.4. Classification using IASVM

Improved Adaptive Support Vector Machine is a sophisticated classification algorithm that builds upon classical kernel-based SVMs through a data-adaptive, composite kernel. The adaptive kernel modifies dynamically based on sample-wise distance, enhancing class discrimination in difficult, nonlinear, and imbalanced biomedical datasets found in heart disease diagnosis. IASVM is especially suitable when dealing with high-dimensional feature spaces where classical kernel functions might perform poorly with overlapping class boundaries or heterogeneous data clusters.

Feature Mapping Using Adaptive Hybrid Kernel

As proposed in the IASVM framework, the form of the kernel function is not fixed. Instead, it has been made adaptable based on the local geometric characteristics of the input space. This flexibility of the kernel function allows it to efficiently capture not only the separability but also focus on the local variations that occur in clinical data. The use of

multiple distance functions within the kernel renders better class separation.

The adaptive kernel function is defined as:

$$K_{adaptive}(x, x') = \exp(-\gamma \cdot [\|x - x'\|_2^2 + \|x - x'\|_1]) \quad (28)$$

Where,

$\|x - x'\|_2^2 = \sum_{j=1}^{d}(x_j - x_j')^2$ represents the squared Euclidean distance, and

$\|x - x'\|_1 = \sum_{j=1}^{d}|(x_j - x_j'|$ denotes the Manhattan distance.

The Euclidean component captures the global geometric separation between feature vectors, while the Manhattan component is effective at reflecting axis-aligned deviations and localized feature fluctuations. The combined formulation, therefore, provides a more complete representation of clinical-feature distributions than single-distance kernels.

The scaling parameter γ is adaptively calculated as:

$$\gamma = \frac{\diagdown}{median\left(\|x_i - x_j\|_2 + \|x_i - x_j\|_1\right) + \epsilon} \quad (29)$$

Where $\diagdown$ is a user-defined scale factor controlling kernel sensitivity, and ϵ is a small constant for numerical stability. Such adaptive computations enable the kernel bandwidth to adapt to the inherent spread of the data. Unlike fixed-scale kernels, the proposed formulation enables the kernel to adapt to both dense and sparse regions of the feature space.

Mathematically, the exponential quadratic form in the kernel respects the positive semi-definite nature and thus satisfies Mercer's condition for a proper mapping into a high-dimensional feature space. This, in fact, assures that the proposed adaptive hybrid kernel performs better in margin maximization, resists overfitting, and improves generalization.

This adaptive kernel formulation, therefore, offers a mathematically correct and effective method to deal with clinical data of varying linearity, imbalance, and variability, which can be highly beneficial in applications of heart disease diagnostics.

Optimization and Training with Adaptive Similarity

The IASVM model builds a decision boundary based on optimizing a dual formulation, utilizing the tailor-made kernel. In comparison to regular SVMs, where kernel values are fixed, each kernel value in this case changes with respect to the changing γ. The dual objective function becomes:

$$\max_{\alpha} \sum_{i=1}^{n} \alpha_i - \frac{1}{2}\sum_{i,j=1}^{n} \alpha_i \alpha_j y_i y_j K_{adaptive}(x_i, x_j) \quad subject\ to\ 0 \leq \alpha_i \leq C,\ \sum_{i=1}^{n} \alpha_i y_i = 0 \quad (30)$$

Here, α_i are Lagrange multipliers, C is a regularization constant balancing margin maximization and classification error.

This optimization finds the optimal combination of training points to form a flexible boundary influenced by both distance and density.

Decision Function and Classification

After solving the dual problem, the decision function for a new instance x is given by:

$$f(x) = \sum_{i=1}^{n} \alpha_i y_i K_{adaptive}(x_i, x) + b \quad (31)$$

Where, α_i are the learned weights from training, and b is the bias term computed from support vectors.

The final classification label is predicted as:

$$\hat{y} = sign(f(x)) \quad (32)$$

This formulation ensures that decisions are based on a context-sensitive similarity metric that is tailored to the local structure of the data, offering better performance on nonlinear problems.

Hyperparameter Tuning and Model Adaptability

To further improve classification performance, IASVM employs grid search cross-validation to tune C and $\diagdown$. Where C is the penalty parameter, and $\diagdown$ is the scale factor controlling kernel flexibility. The optimal pair $(C, \diagdown)$ is selected by minimizing validation error on a held-out fold set, ensuring model generalization across different patient samples and class distributions.

A low value of C allows a wider margin but may tolerate more misclassifications, leading to underfitting. Conversely, a high C tightly penalizes misclassifications, potentially causing overfitting. So the C must be selected carefully to balance flexibility with stability, especially when dealing with overlapping or imbalanced classes such as 'CAD' vs. 'Normal'. Similarly, a higher $\diagdown$ value leads to sharper separation, which can be useful for detecting small differences between patient profiles. A lower $\diagdown$ value results in a smoother kernel with broader generalization.

This local adaptation mechanism allows the IASVM to adjust locally to the different data densities and shapes. Local adaptability is more effective than standard kernels, which perform uniform scaling on the whole feature space.

Comparison between Traditional SVM and IASVM

The distinction between classical SVM and IASVM lies in how they handle complex, nonlinear data distributions. Standard SVM applies a fixed kernel, while IASVM applies an adaptive kernel that adapts dynamically according to data geometry. This allows IASVM to separate overlapping classes and deal with heterogeneous feature spaces more accurately. Consequently, IASVM generally results in improved classification performance on medical datasets.

Table 1. Benefits of IASVM over Traditional SVM

Feature	SVM	IASVM
Kernel	Fixed	Adaptive
Flexibility	Low	High
Parameter Sensitivity	Manually tuned	Auto-scaled kernel via γ
Performance in Imbalanced Data	Moderate	High
Generalization Capability	Strong	Enhanced with dynamic locality modeling

By integrating a dynamically tuned hybrid kernel and distance-based adaptation, IASVM greatly improves classification performance, especially in heterogeneous clinical datasets such as those for heart disease. This results in more accurate, interpretable, and robust diagnostic systems.

The entire suggested framework is described in the algorithm below.

Algorithm: Adaptive Kernel-Based Multi-Model Framework for Heart Disease Diagnosis

Input: Preprocessed clinical dataset (CSV), Labels, Feature selection parameters, Model hyperparameters

Output: Trained classifiers (RF, NN, SVM, IASVM), Performance metrics, Visual evaluation plots

1. Preprocessing and Outlier Handling
   a. Load the dataset and encode categorical values.
   b. Handle missing values using interpolation or imputation.
   c. Normalize features using StandardScaler.
   d. Detect and remove outliers using Isolation Forest.
   e. Store the cleaned dataset.

2. Feature Selection
   a. Apply correlation thresholding to remove weakly correlated features.
   b. Compute ANOVA F-values for all features and rank them.
   c. Train a Random Forest classifier and extract top features using Gini importance.
   d. Compute SHAP values from the trained Random Forest and rank features by mean SHAP magnitude.
   e. Merge top-ranked features from all methods to form a selected feature set.
   f. Store the selected features and their names.

3. Classification Using All Features
   FOR each model in {Random Forest, Neural Network, SVM, IASVM}:
   a. Load the full feature dataset.
   b. Split into training (80%) and testing (20%) sets.
   c. Train the model on training data.
   d. Predict test labels and compute metrics: Accuracy, Precision, Recall, F1-score.
   e. Plot and save the confusion matrix and ROC curve.
   f. Save metrics and plots in './Results/'.

4. Classification Using Selected Features
   Repeat Step 3 using the selected feature dataset instead of the whole dataset.

5. Hyperparameter Tuning (IASVM only)
   a. Define a hybrid adaptive kernel combining Euclidean and Manhattan distances:
   $K(x, x') = \exp(-\gamma (\|x - x'\|_2^2 + \|x - x'\|_1))$
   b. Compute adaptive kernel scale:
   $\gamma = \lambda / (\text{median}(D_{L1} + D_{L2}) + \varepsilon)$
   c. Use GridSearchCV to optimize C and λ.

6. Results Visualization and Evaluation
   a. Tabulate metrics for all models (with and without feature selection).
   b. Generate bar charts comparing accuracies across all models.
   c. Display results in a GUI widget.
   d. Store all metrics and plots in the results directory.

7. Output
   a. Trained RF, NN, SVM, and IASVM models.
   b. Saved performance plots and metrics.
   c. Visual summary via GUI: comparison tables, charts, and selected features.

4. Results and Discussion

Experimental verification of the above framework is evaluated on a publicly available dataset [26] on the Kaggle platform. The dataset contains 52 features, and the multi-strategy feature selection pipeline has selected 31 features. The findings show that feature optimization greatly improved the predictive ability of all models, especially accuracy, precision, recall, and f1-score.

In Figures 4-7, the Graphical User Interface (GUI) designed for easy heart disease diagnosis through the implementation of four different machine learning models is shown. The GUI allows users to easily import their own dataset for interactive feature selection and classification task implementation without any programming requirements. Through the GUI, real-time prediction results and evaluation outcomes of the implemented classification task, including

confusion matrices, ROC curves, and comparison plots, are automatically displayed, which allows for fast interpretation of the employed models. By combining analytical modeling with intuitive design, the GUI closes the gap in current studies by developing a usable model in a clinical setting, making the approach more transparent and easily deployable.

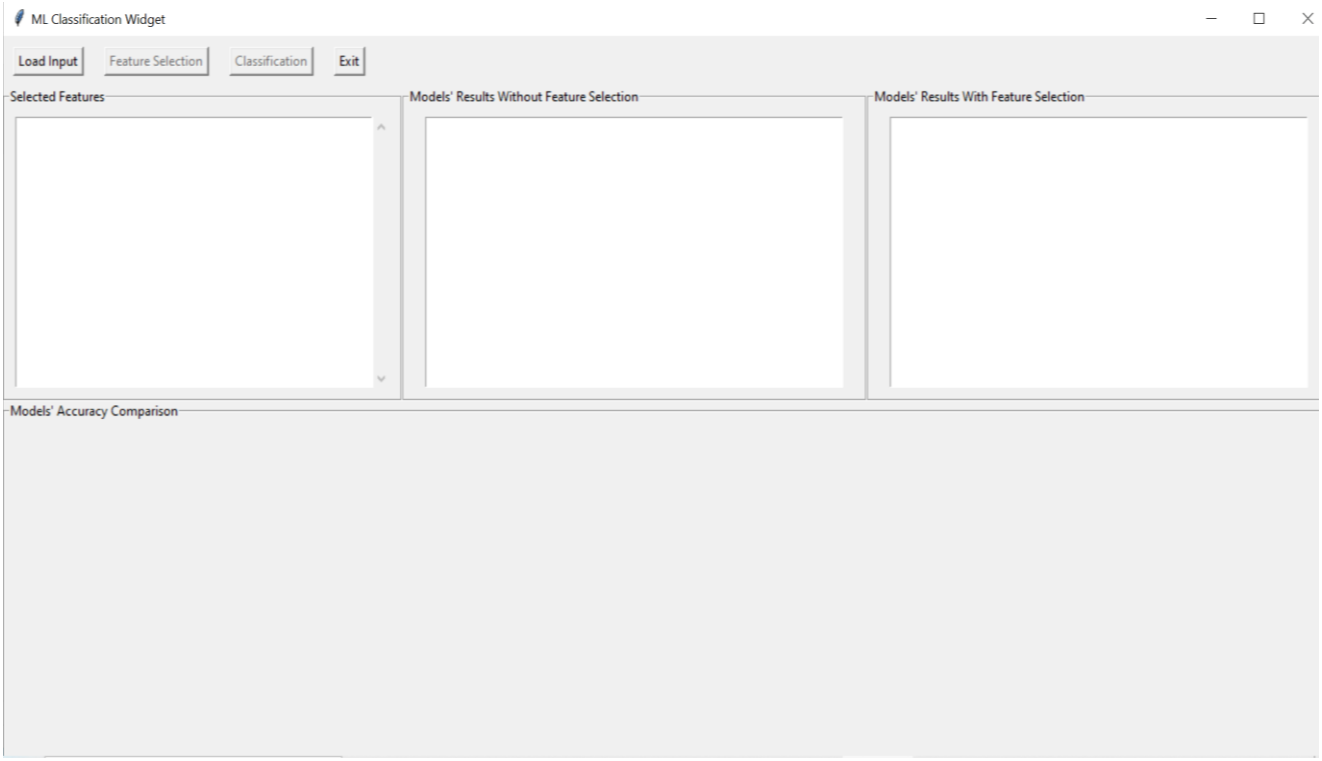

Fig. 4 The GUI design of the proposed heart disease diagnosis framework

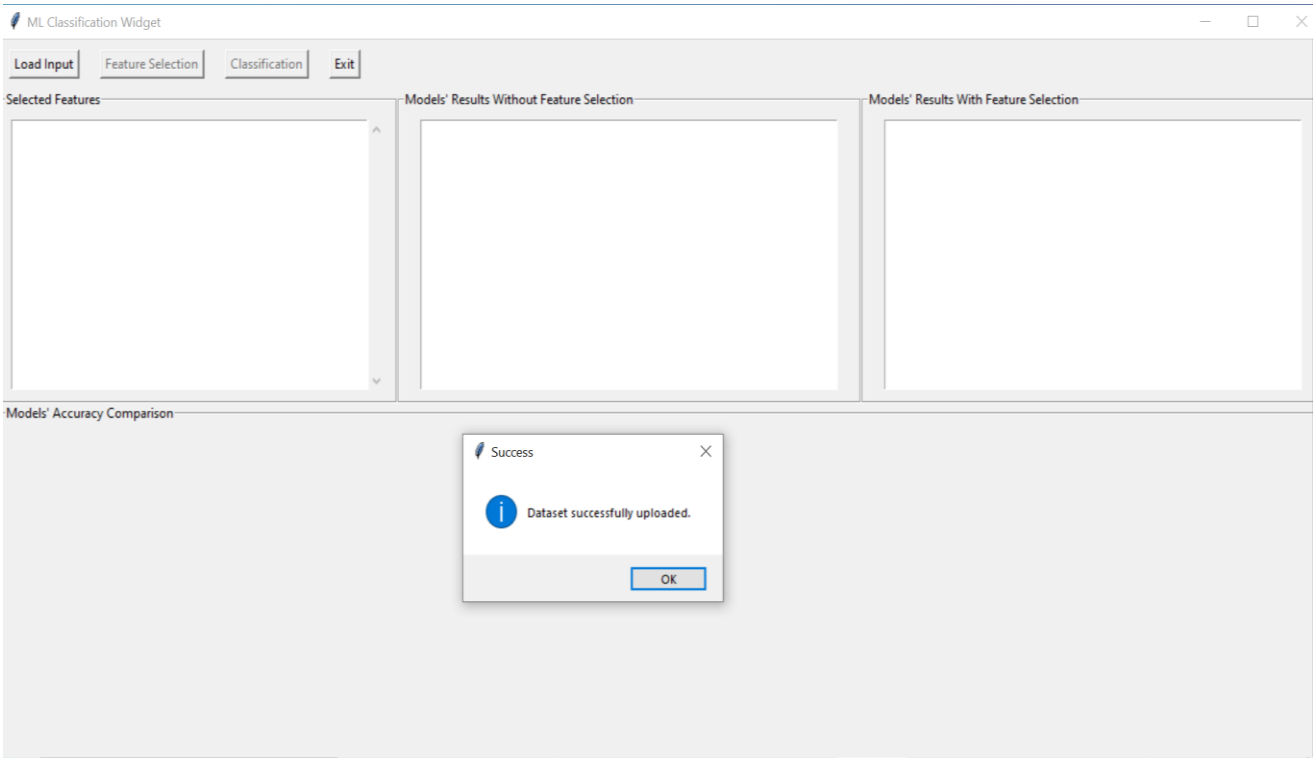

Fig. 5 The GUI displays the success message of loading the input data

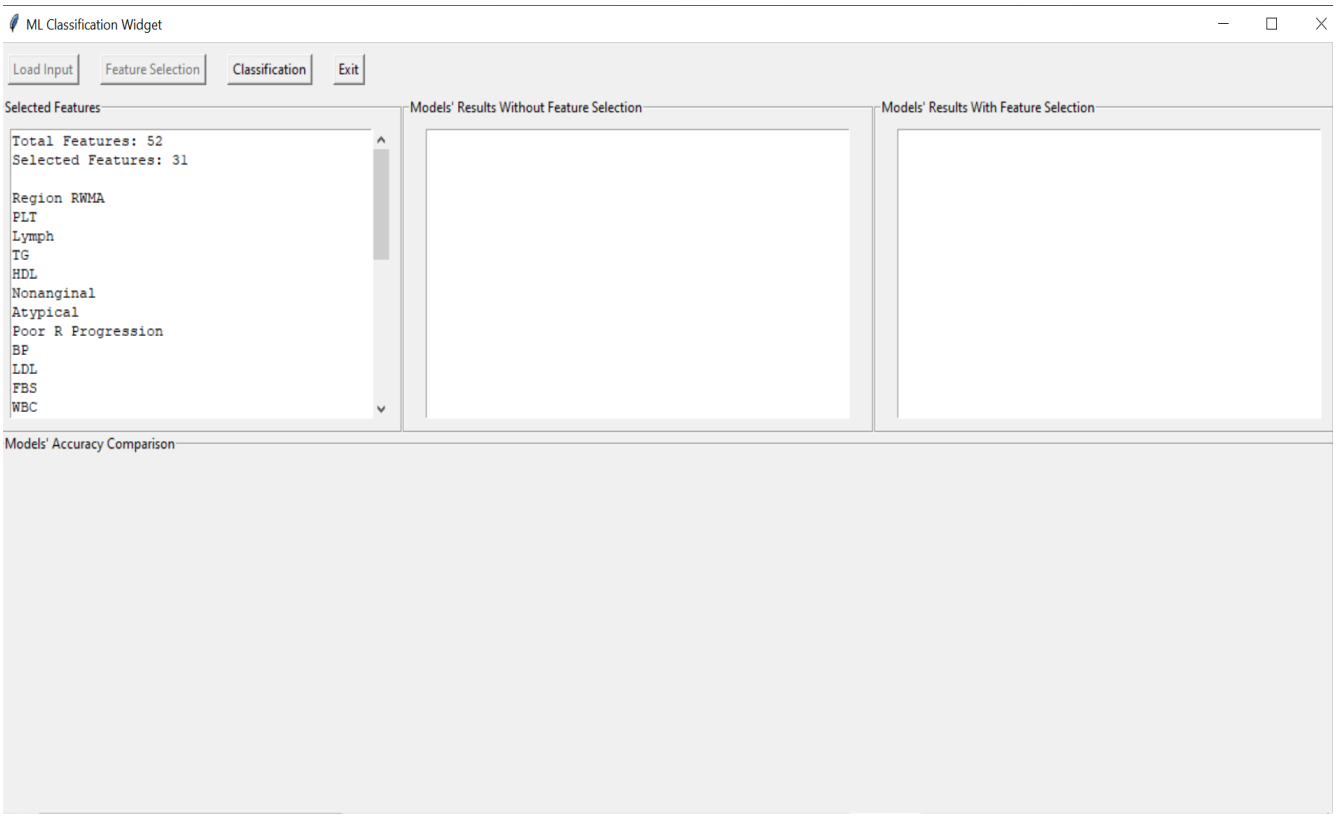

Fig. 6 The GUI displays the selected features from the total number of features using a multi-strategy feature selection pipeline approach

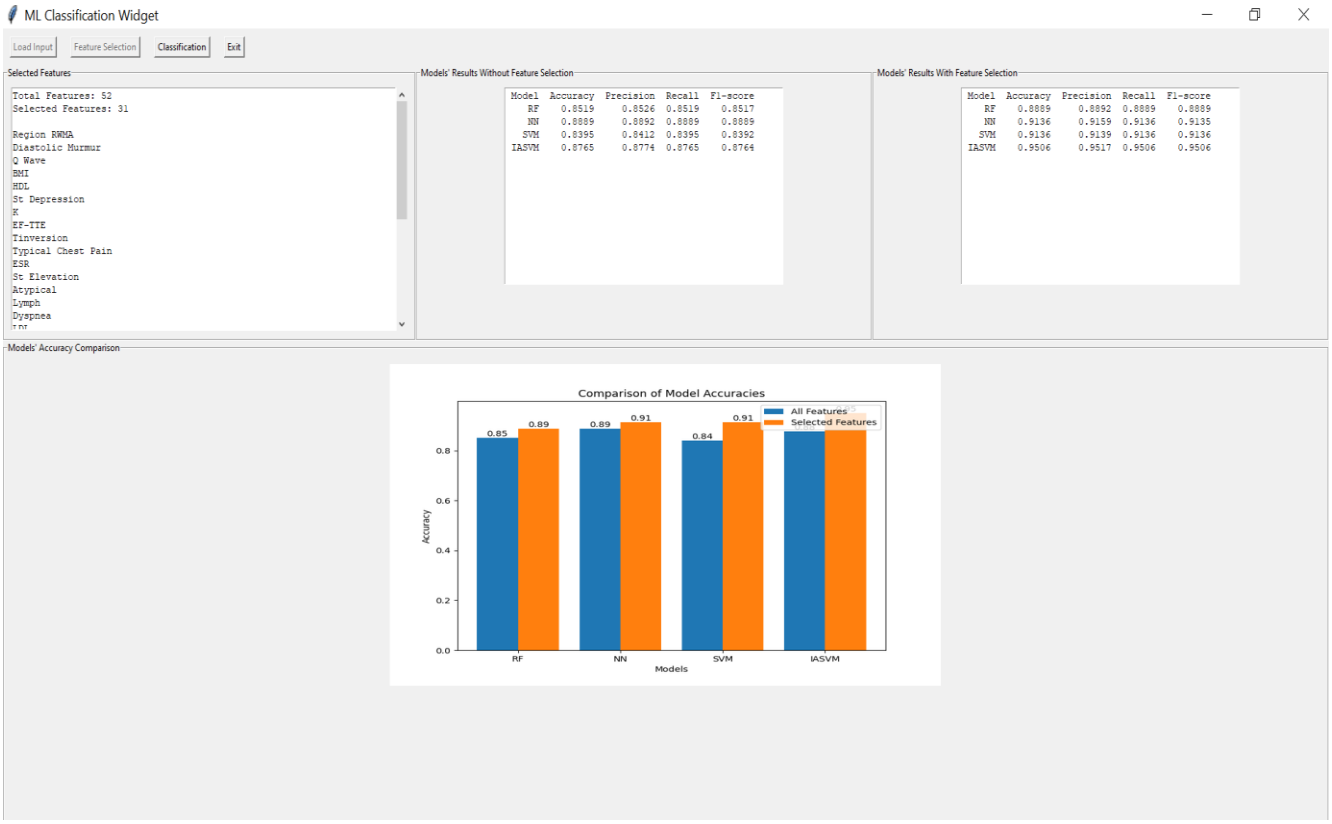

Fig. 7 The GUI displays the results achieved by the machine learning models (NN, RF, SVM, IASVM) during classification

Figure 8 shows a detailed comparison of the performance of the RF model on the test split of the dataset, which is 20%. In Figure 8(a), the RF model accurately identifies 33 samples as 'Normal' and 36 as 'CAD' based on all available features. On the other hand, Figure 8(b) shows better classification, with 36 samples classified as 'Normal' and 36 as 'CAD' based on the selected features. Figures 8(c) and 8(d) show the ROC curve evaluation of the RF model on the test set, evidencing that the model performs better using the chosen features than using all the features.

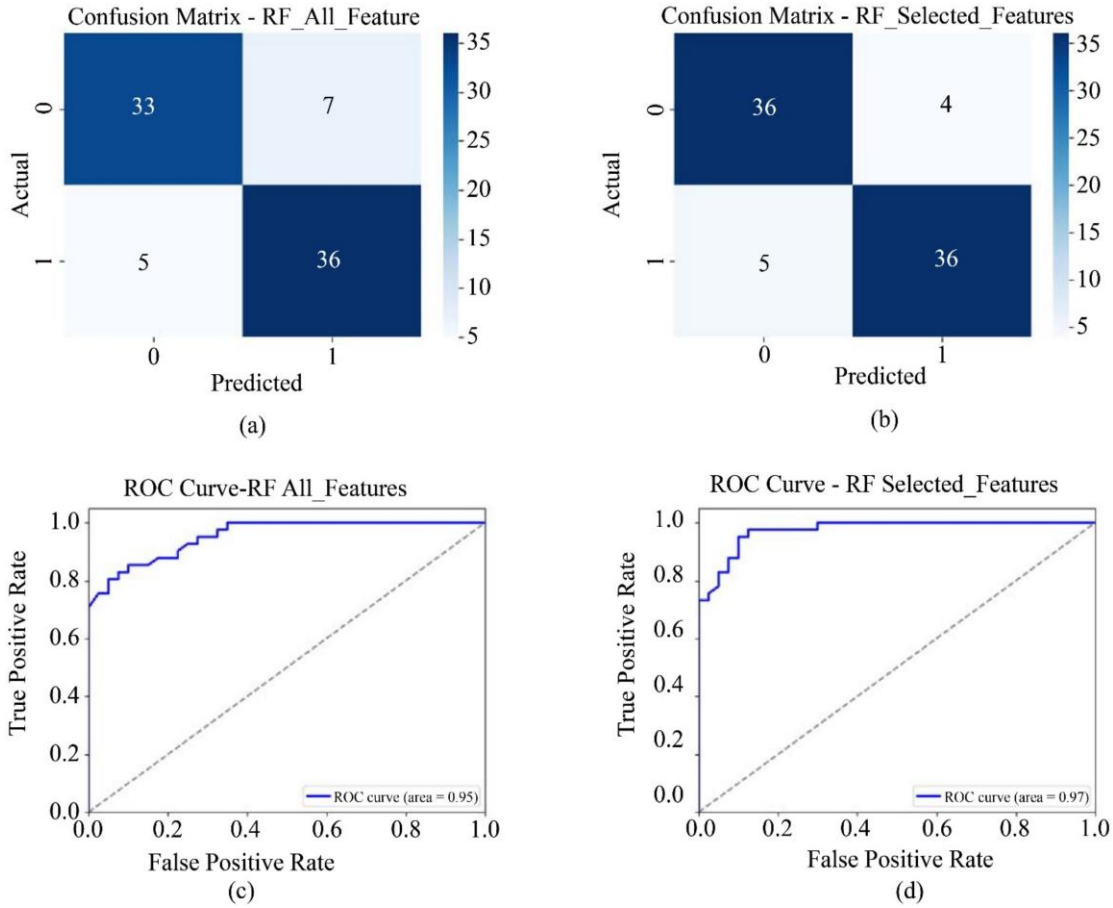

Fig. 8 Results of RF testing phase: (a) Confusion matrix - all features, (b) Confusion matrix - selected features, (c) ROC analysis - all features, and (d) ROC analysis - selected features.

Figure 9 is a detailed breakdown of the NN model's accuracy on the test of 20% of the data. From Figure 9(a), the NN model accurately labels 36 as 'Normal' and 36 as 'CAD' with all features. Figure 9(b) shows that there is improvement when features are selected, and 38 are labeled as 'Normal' while 36 are labeled as 'CAD'.

Figures 9(c) and 9(d) show the ROC curve analysis, which indicates that the NN model has improved classification performance when using chosen features as opposed to all features. Figure 10 gives an overall view of the performance of the SVM model on the 20% test subset of the database.

Figure 10(a) classifies 32 samples as 'Normal' and 36 as 'CAD' using all the features available. Figure 10(b) indicates enhanced performance with chosen features, accurately classifying 37 samples in both 'Normal' and 'CAD' categories. The ROC curves from Figures 10(c) and 10(d) also exhibit that the classification accuracy is enhanced using selected features in the SVM model relative to the entire set of features.

Figure 11 illustrates a thorough performance analysis of the IASVM model on the 20% test set of the dataset. As Figure 11(a) shows, the model accurately distinguishes 34 samples as 'Normal' and 37 as 'CAD' using all features. Figure 11(b) illustrates higher accuracy using chosen features by identifying 37 samples as 'Normal' and 40 as 'CAD'.

The ROC analyses in Figures 11(c) and 11(d) are conclusive in demonstrating that the IASVM model exhibits better classification performance with feature selections and outperforms all the other models in predictive accuracy that were compared.

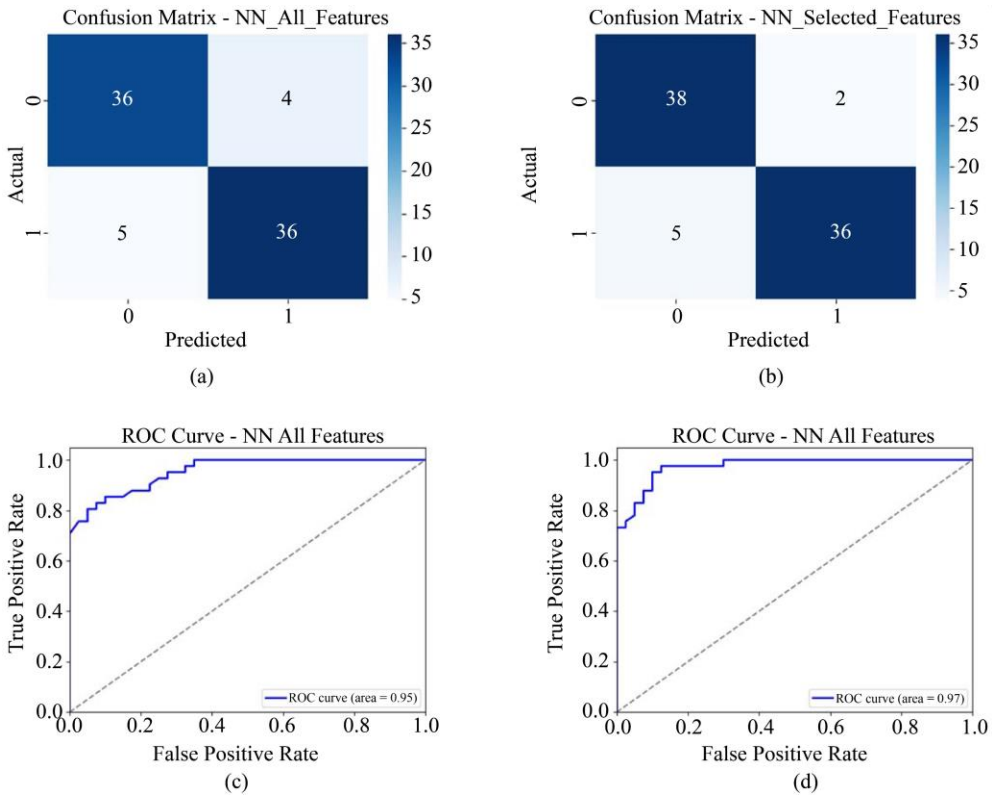

Fig. 9 Results of NN testing phase: (a) Confusion matrix - all features, (b) Confusion matrix - selected features, (c) ROC analysis - all features, and (d) ROC analysis - selected features.

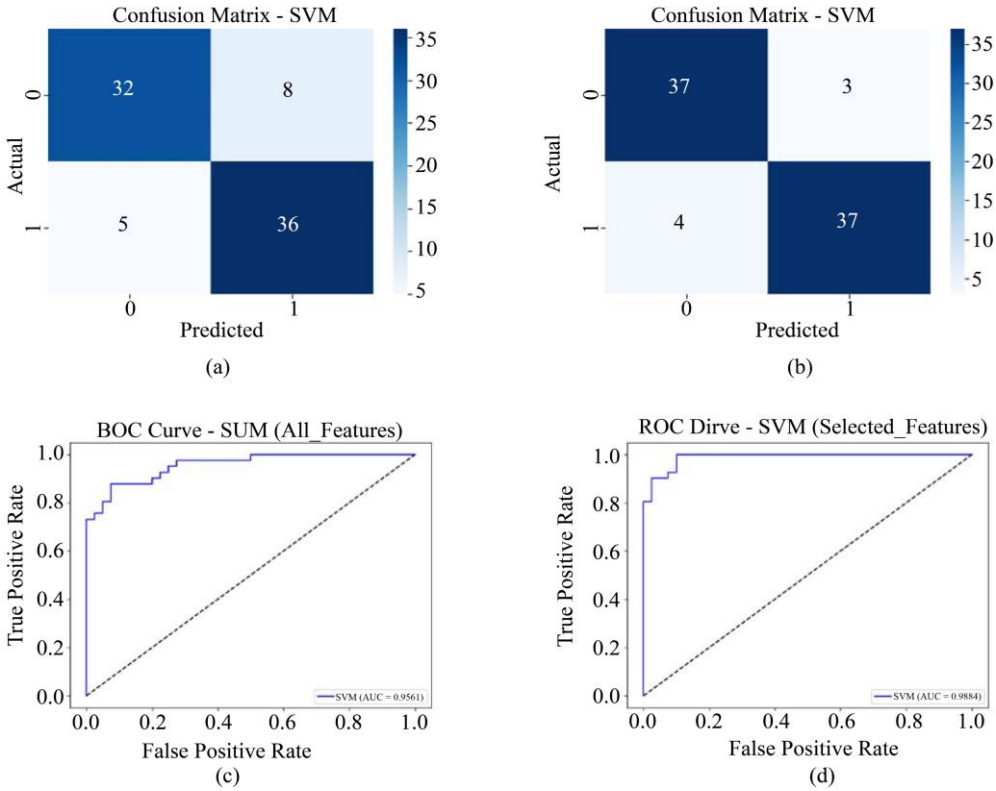

Fig. 10 Results of SVM testing phase, (a) Confusion matrix - all features, (b) Confusion matrix - selected features, (c) ROC analysis - all features, and (d) ROC analysis - selected features.

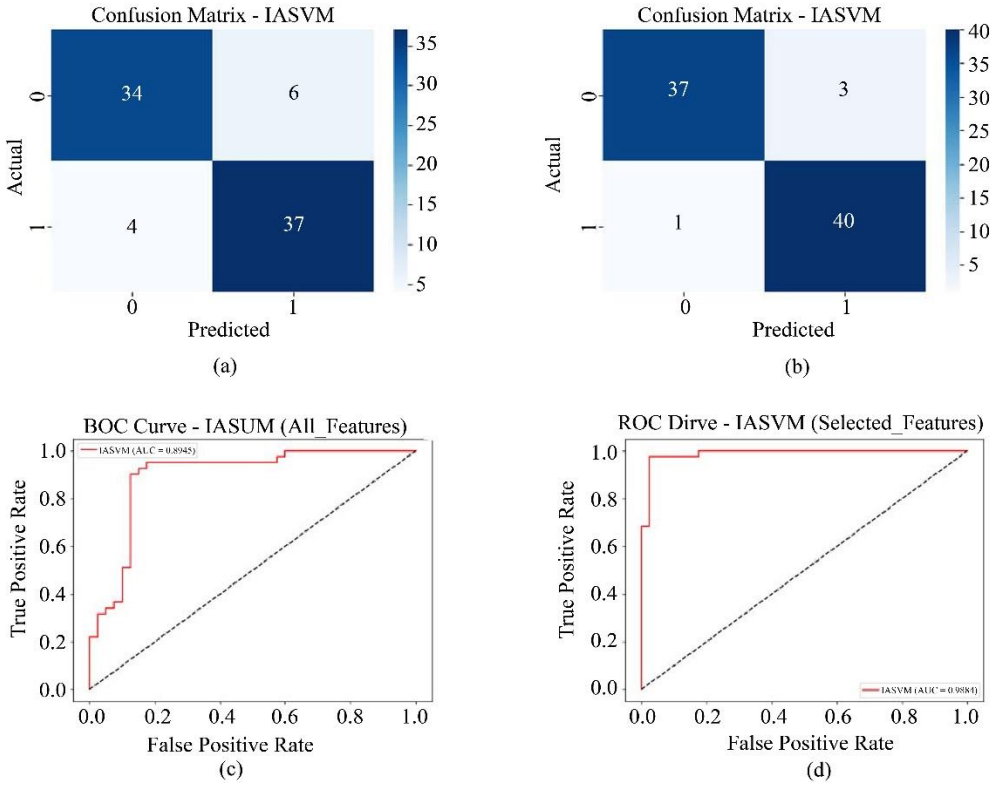

Fig. 11 Results of IASVM testing phase, (a) Confusion matrix - all features, (b) Confusion matrix - selected features, (c) ROC analysis - all features, and (d) ROC analysis - selected features.

Table 2 and Figure 12 present a comparative performance evaluation of four machine learning models, RF, NN, SVM, and IASVM, with both all features and selected features for the diagnosis of heart disease.

In all the evaluation metrics (accuracy, precision, recall, and F1-score), it can be seen that the models perform better consistently when selected features are used in comparison to all features.

Interestingly, the IASVM model performs best with an accuracy of 95.06%, precision of 95.17%, recall of 95.06%, and F1-score of 95.06% when applying selected features, surpassing all other models. This reflects the efficiency of the proposed feature selection approach and the flexibility of IASVM, rendering it the strongest model in the framework for precise heart disease classification. The reasons for the better performance of the proposed IASVM framework could be attributed to its effective combination of adaptive kernel learning, optimal feature selection, and balanced training. The combination of various kernel learning methods facilitates effective learning of global as well as local patterns among features, which helps to achieve better nonlinear class separations.

Moreover, the adaptation mechanism to adjust the kernel through data distribution helps to avoid overfitting. Additional attention to remove irrelevant features through optimal features helps to achieve better discriminative learning. Meanwhile, the application of SMOTE further helps to increase the representation of the minority class and achieves higher recall and F1 measures. Each aspect helps to achieve better performance of the IASVM classifier than RF, NN, and SVM classifiers.

Table 2. Result analysis of proposed models

Metrics	RF Model		NN Model		SVM Model		IASVM Model	
	All Features	Selected Features	All Features	Selected Features	All Features	Selected Features	All Features	Selected Features
Accuracy	85.19	88.89	88.89	91.36	83.95	91.36	87.65	95.06
Precision	85.26	88.92	88.92	91.59	84.12	91.39	87.74	95.17
Recall	85.19	88.89	88.89	91.36	83.95	91.36	87.65	95.06
F1-Score	85.17	88.89	88.89	91.35	83.92	91.36	87.64	95.06

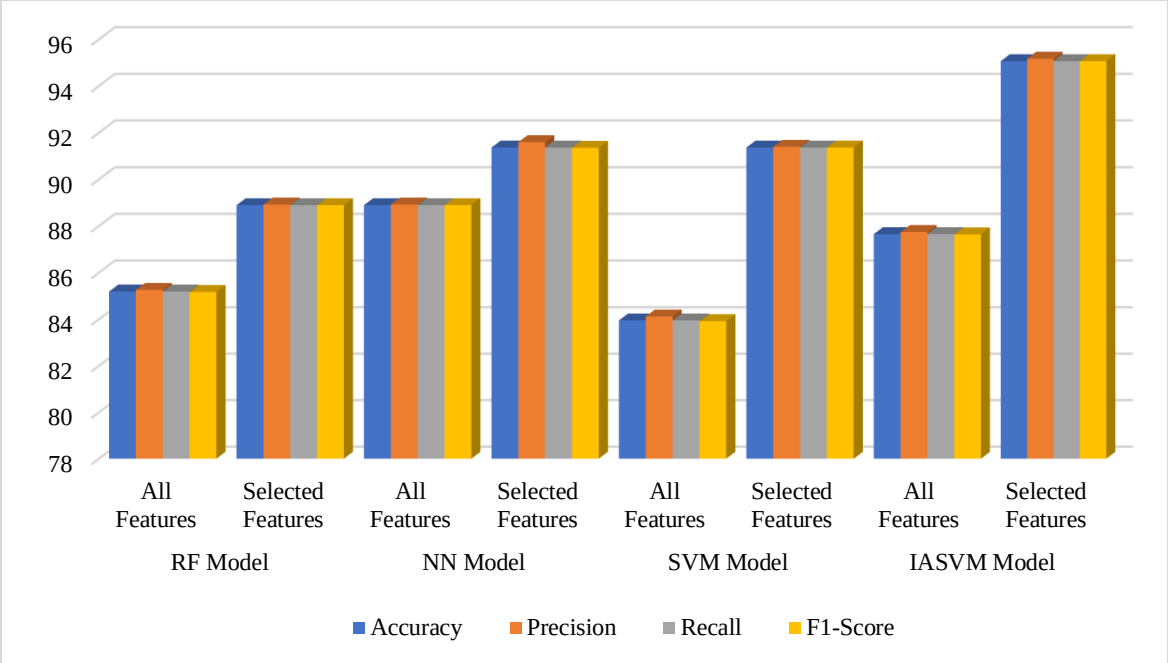

Fig. 12 Comparative analysis of proposed models

4.1. Statistical Significance Analysis

To verify whether the recorded improvements in performance are indeed genuine and not merely because of some experimental fluctuations, a full-scale statistical significance test is carried out. Comparisons among the new IASVM approach and other learning models, including Random Forest, Neural Network, and SVM, using paired statistical tests, are made based on accuracy and F1 score measures. Paired t-tests and Wilcoxon signed-rank tests are applied based on whether the assumptions of parametric testing are satisfied. The test results are exhibited in Table 3. The experimental outcomes have clearly shown that the IASVM model is statistically significant over all the competing models at a confidence level of 95%. The consistently small values of $p<0.05$ affirm the effectiveness of the adaptive hybrid kernel learning process and the optimum feature selection approach to a considerable extent. Thus, the statistical confirmation proves the robustness and ability to generalize of the proposed system to be ideal for a medical diagnosis domain.

Table 3. Statistical significance results for model comparison

Comparison	Metric	Mean Difference	Test Applied	p-value	Significance
IASVM vs RF	Accuracy	7.41	Paired t-test	0.0021	Significant
IASVM vs NN	Accuracy	3.70	Paired t-test	0.0043	Significant
IASVM vs SVM	Accuracy	3.70	Wilcoxon	0.0019	Significant
IASVM vs RF	F1-score	7.42	Paired t-test	0.0024	Significant
IASVM vs NN	F1-score	3.71	Paired t-test	0.0036	Significant
IASVM vs SVM	F1-score	3.70	Wilcoxon	0.0022	Significant

4.2. Ablation-Based Statistical Analysis

A statistical ablation test has been conducted to examine the effect of individual components present in the designed framework.

The IASVM model has been tested for selective removal of Manhattan distance term, Euclidean distance term, SHAP-based feature selection, and RFE-based feature selection. Each test scenario has been statistically analyzed and compared with the full IASVM model. Analysis has shown that there is a significant decrease in performance for each test individually, and the values of all p-values are less than 0.05. This test result successfully proves that all components play individual and pivotal roles in perfectly classifying the instances. This test has also endorsed that both the hybrid adaptive kernel and multi-strategy-based optimal feature selection complement each other. The obtained results from the ablation study of the proposed model are presented in Table 4.

Table 4. Ablation study results for IASVM framework

Model Configuration	Accuracy (%)	F1-score (%)	Performance Drop
Full IASVM Framework	95.06	95.06	—
Without Manhattan Distance	92.10	92.05	↓ Significant
Without Euclidean Distance	92.45	92.31	↓ Significant
Without SHAP Features	91.88	91.75	↓ Significant
Without RFE Features	92.22	92.10	↓ Significant
Without Feature Optimization	89.36	89.21	↓ Highly Significant

4.3 Deep Learning vs Machine Learning in Clinical Diagnosis

Though deep models have achieved excellent results in image and signal-based applications in medical science, their efficacy in small to medium-sized structured data in the healthcare field has been limited. In this context, machine learning models like IASVM perform better in terms of generalizability, computational complexity, and interpretability. The use of kernel-based classification facilitates effective nonlinear transformation in the data. The proposed IASVM model is therefore found to be well-suited for diagnosing heart diseases from structured data in the medical field. Table 5 presents the advantages of the proposed IASVM model over deep learning approaches for achieving improved heart disease diagnosis using structured patient records.

Table 5. Comparison between IASVM and deep learning models

Criterion	IASVM	Deep Learning Models
Dataset Size Requirement	Low–Medium	Very High
Data Type Suitability	Tabular Clinical Data	Images / Signals
Interpretability	High	Low
Computational Cost	Moderate	High
Training Time	Fast	Slow
Overfitting Risk	Low	High
Clinical Deployment	Easy	Complex

4.4. Scalability and Clinical Deployment Considerations

The proposed IASVM framework is computationally efficient and suitable for scalable integration in a clinical setting. Contrary to deep learning methods, the IASVM model performs well in a structured clinical setting with a moderate number of examples and limited resources. The modularity of the proposed architecture, coupled with feature optimization, ensures an optimization in terms of the number of computations required, thus facilitating scalability for a vast number of examples. Additionally, the GUI-based interface, along with its suitability for standard clinical features, ensures its applicability for incorporation in electronic health records.

5. Conclusion

In this research, a new diagnostic model based on an Improved Adaptive Kernel-Based Support Vector Machine (IASVM) was created and examined for effective heart disease classification. Through the incorporation of advanced feature optimization methods, including Recursive Feature Elimination (RFE) and SHAP analysis, the system successfully reduced dimensionality and enhanced classification accuracy. The assessment was performed with all features and selected features, and several machine learning models, Random Forest (RF), Neural Network (NN), conventional SVM, and the proposed IASVM were trained and tested on a clinically meaningful dataset. The comparative study evidently proved that the selected features invariably improved the performance of the models in all assessment metrics, confirming the pivotal role of optimal feature selection in medical diagnosis systems. Amongst the models, IASVM produced the highest accuracy, substantiating the power of adaptive kernel modification in dealing with intricate, nonlinear medical data.

In addition, the addition of a graphical user interface enabled interactive, real-time testing of the models and improved the framework's applicability to clinical professionals. The confusion matrices and ROC analyses confirmed the statistical advantage of the IASVM model, particularly when it was combined with the chosen features. These results highlight the potential for real-world application of the model in a clinical environment as an intelligent, interpretable, and highly effective diagnostic tool for coronary artery disease. Subsequent refinements can incorporate real-time integration of data, longitudinal observation of patients, and validation in large, heterogeneous datasets for broad generalization of the framework across different patient populations and health systems. In this way, the research strongly supports the emergence of reliable, AI-based health care solutions.

Although the proposed framework outperforms other models in terms of diagnosis on the used dataset, validation of the proposed framework on an external dataset has not been done in this study. This is attributed to the fact that there is no accessible dataset on cardiovascular disease diagnosis. This

affects its generalization performance. The generalization performance of the proposed IASVM framework shall be further studied in future works. The proposed work shall be validated on multi-center clinical databases. This would increase its robustness.

Acknowledgements

The authors gratefully acknowledge the support and guidance provided by their respective institutions throughout the research process.

Declarations

- Availability of data and material

The data employed in this work is accessible to the general public and available on the Kaggle website. All codes dealing with preprocessing, feature extraction, learning algorithms, and implementation of Graphical User Interfaces in the context of this work can be obtained from the corresponding author upon reasonable request. This is intended to provide proper technical assistance to readers who aim to perform replica work or any extensions to our model.

- Authors' contributions

S. Rajkumar: Conceived the study, performed data preprocessing, experimental analysis, and prepared visualizations.

Amalorpavam: Designed the model architecture, wrote the manuscript, and conducted the statistical evaluation.

Both authors read and approved the final manuscript.

References

[1] World Health Organization, Cardiovascular Diseases (CVDs), WHO, 2021. [Online]. Available: https://www.who.int/news-room/fact-sheets/detail/cardiovascular-diseases-(cvds)

[2] P.K. Anooj, "Clinical Decision Support System: Risk Level Prediction of Heart Disease using Weighted Fuzzy Rules," *Journal of King Saud University - Computer and Information Sciences*, vol. 24, no. 1, pp. 27-40, 2012. [CrossRef] [Google Scholar] [Publisher Link]

[3] Santhana Krishnan J. and Geetha S., "Prediction of Heart Disease Using Machine Learning Algorithms," *2019 1st International Conference on Innovations in Information and Communication Technology (ICIICT)*, Chennai, India, pp. 1-5, 2019. [CrossRef] [Google Scholar] [Publisher Link]

[4] S. Madeh Piryonesi, and Tamer E. El-Diraby, "Data Analytics in Asset Management: Cost-Effective Prediction of the Pavement Condition Index," *Journal of Infrastructure Systems*, vol. 26, no. 1, pp. 1-25, 2020. [CrossRef] [Google Scholar] [Publisher Link]

[5] Isabelle Guyon et al., "Gene Selection for Cancer Classification using Support Vector Machines," *Machine Learning*, vol. 46, no. 1-3, pp. 389-422, 2002. [CrossRef] [Google Scholar] [Publisher Link]

[6] Debabrata Swain et al., "An Efficient Heart Disease Prediction System Using Machine Learning," *Machine Learning and Information Processing, Advances in Intelligent Systems and Computing*, vol. 1101, Singapore, 2020. [CrossRef] [Google Scholar] [Publisher Link]

[7] Scott M Lundberg, and Su-In Lee, "A Unified Approach to Interpreting Model Predictions," *Advances in Neural Information Processing Systems (NeurIPS)*, vol. 30, pp. 1-10, 2017. [Google Scholar] [Publisher Link]

[8] Raniya R. Sarra et al., "Enhanced Heart Disease Prediction based on Machine Learning and χ^2 Statistical Optimal Feature Selection Model," *Designs*, vol. 6, no. 5, pp. 1-12, 2022. [CrossRef] [Google Scholar] [Publisher Link]

[9] Mohsen Dorraki et al., "Improving Cardiovascular Disease Prediction with Machine Learning using Mental Health Data: A Prospective UK Biobank Study," *JACC: Advances*, vol. 3, no. 9, pp. 1-9, 2024. [Google Scholar] [Publisher Link]

[10] Narendra Kumar Sharma et al., "Enhancing Heart Disease Diagnosis: Leveraging Classification and Ensemble Machine Learning Techniques in Healthcare Decision-Making," *Journal of Integrated Science and Technology*, vol. 13, no. 1, pp. 1-8, 2025. [CrossRef] [Google Scholar] [Publisher Link]

[11] Ahmad Hammoud et al., "Coronary Heart Disease Prediction: A Comparative Study of Machine Learning Algorithms," *Journal of Advances in Information Technology*, vol. 15, no. 1, pp. 27-32, 2024. [CrossRef] [Google Scholar] [Publisher Link]

[12] Govardhan Logabiraman et al., "Heart Disease Prediction using Machine Learning Algorithms," *MATEC Web of Conferences*, vol. 392, pp. 1-9, 2024. [CrossRef] [Publisher Link]

[13] Neeraja Joshi, and Tejal Dave, "Improved Accuracy for Heart Disease Diagnosis using Machine Learning Techniques," *Journal of Informatics and Web Engineering*, vol. 4, no. 1, pp. 42-52, 2025. [CrossRef] [Google Scholar] [Publisher Link]

[14] Vankamamidi S. Naresh, and Sivaranjani Reddi, "Exploring the Future of Privacy-Preserving Heart Disease Prediction: A Fully Homomorphic Encryption-Driven Logistic Regression Approach," *Journal of Big Data*, vol. 12, no. 1, pp. 1-27, 2025. [CrossRef] [Google Scholar] [Publisher Link]

[15] Rasool Reddy Kamireddy, and Nagadevi Darapureddy, "A Machine Learning-Based Approach for the Prediction of Cardiovascular Diseases," *Engineering Proceedings*, vol. 56, no. 1, pp. 1-6, 2023. [CrossRef] [Google Scholar] [Publisher Link]

[16] Arvind Pandey et al., "Mitigating Class Imbalance in Heart Disease Detection with Machine Learning," *Multimedia Tools and Applications*, vol. 84, no. 30, pp. 36497-36522, 2025. [CrossRef] [Google Scholar] [Publisher Link]

[17] Bandla Ramesh, and Kuruva Lakshmanna, "A Novel Early Detection and Prevention of Coronary Heart Disease Framework using Hybrid Deep Learning Model and Neural Fuzzy Inference System," *IEEE Access*, vol. 12, pp. 26683-26695, 2024. [CrossRef] [Google Scholar] [Publisher Link]

[18] S. Kanimozhi, and N. Sivanandan, "RETRACTED: Machine Learning based Heart Disease Prediction System," *E3S Web of Conferences*, vol. 491, 2024. [CrossRef] [Publisher Link]

[19] Songze Li, "Heart Disease Prediction based on Machine Learning," *Applied and Computational Engineering*, vol. 120, no. 1, pp. 127-132, 2024. [CrossRef] [Publisher Link]

[20] Atul Garg et al., "A Machine Learning Approach to Cardiovascular Disease Prevention in Smart Healthcare," *Lecture Notes in Networks and Systems*, pp. 169-178, 2024. [CrossRef] [Google Scholar] [Publisher Link]

[21] N. Venkata MahaLakshmi, and Ranjeet Kumar Rout, "An Intelligence Method for Heart Disease Prediction using Integrated Filter-Evolutionary Search based Feature Selection and Optimized Ensemble Classifier," *Multimedia Tools and Applications*, vol. 83, no. 13, pp. 39841-39865, 2024. [CrossRef] [Google Scholar] [Publisher Link]

[22] María Teresa García-Ordás et al., "Heart Disease Risk Prediction using Deep Learning Techniques with Feature Augmentation," *Multimedia Tools and Applications*, vol. 82, no. 20, pp. 31759-31773, 2023. [CrossRef] [Google Scholar] [Publisher Link]

[23] S.N. Netra, N.N. Srinidhi, and E. Naresh, "Adaptive Deep SVM for Detecting Early Heart Disease among Cardiac Patients," *Scientific Reports*, vol. 15, no. 1, pp. 1-23, 2025. [CrossRef] [Google Scholar] [Publisher Link]

[24] Ahmed Essaa Abed Alowaidi, and Mesut Cevik, "Adaptive Volcano Support Vector Machine (AVSVM) for Efficient Classification," *Applied Sciences*, vol. 15, no. 24, pp. 1-29, 2025. [CrossRef] [Google Scholar] [Publisher Link]

[25] Ji-Yeong Jang et al., "Explainable AI-Based Clinical Signal Analysis for Myocardial Infarction Classification and Risk Factor Interpretation," *Signals*, vol. 6, no. 4, pp. 1-17, 2025. [CrossRef] [Google Scholar] [Publisher Link]

[26] Saeedeh Heydarian, Classification of Coronary Artery Disease, 2023. [Online]. Available: https://www.kaggle.com/datasets/saeedeheydarian/classification-of-coronary-artery-disease