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High-Accuracy Heart Disease Prediction Using Bio-Inspired Optimization

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Abstract
Heart disease remains one of the leading causes of death worldwide, making accurate and early diagnosis essential in modern healthcare. This paper proposes a hybrid predictive model that combines the Moth-Flame Algorithm (MFA) for feature selection with a Radial Basis Function Support Vector Machine (RBF-SVM) classifier to improve heart disease diagnosis. MFA eliminates redundant and irrelevant features and optimizes the SVM hyperparameters, thereby enhancing model efficiency and accuracy. The proposed hybrid MFA-RBF-SVM model was evaluated on three benchmark datasets: Cleveland, Hungarian, and Statlog. Experimental results show that the model outperforms conventional classifiers such as Decision Tree, Random Forest, K-Nearest Neighbor, Artificial Neural Network, and standard SVM, achieving up to 95.2% accuracy, 0.96 recall, and a 0.93 F1-score on the Hungarian and Cleveland datasets, with low false-positive and false-negative rates. These findings demonstrate the effectiveness of combining machine learning with bio-inspired optimization for reliable, adaptable clinical prediction.

Keywords: Heart Disease Prediction; Feature Selection; Classification; Benchmark Datasets; Bio-inspired Optimization; Predictive Accuracy; Clinical Diagnosis.

1. Introduction

Heart disease is among the leading causes of mortality in most parts of the world, with proper and timely diagnosis being one of the most serious concerns in modern healthcare systems. The advancement of electronic health records and the improved quality of medical monitoring technologies in recent years have generated large quantities of structured and unstructured patient data, presenting substantial potential for the creation of smart, information-based diagnostic models (Ashwini, Chirchi, Balasubramaniam, & Shah, 2025). Machine learning techniques have proven helpful in analysing such complex datasets, and Support Vector Machines (SVM) have been useful in medical classification problems because they can handle high-dimensional, nonlinear, and non-homogeneous data patterns. Specifically, the Radial Basis Function (RBF) kernel used in conjunction with SVM is able to model nonlinear relationships among clinical variables, including age, blood pressure, cholesterol, heart rate, and other cardiovascular risk factors (Torre-Bastida, Díaz-de-Arcaya, Osaba, Muhammad, Camacho, & Del Ser, 2025). Nevertheless, the performance of the RBF-SVM model depends greatly on appropriate hyperparameters, namely the penalty parameter and the kernel width, and manual tuning is usually inefficient and yields suboptimal results.

In this study, a hybrid MFA-RBF-SVM model that combines the classification ability of the RBF-SVM model with the optimization ability of the Moth-Flame Algorithm (MFA), a bio-inspired metaheuristic algorithm that

emulates the natural navigation of moths toward light sources, is proposed to resolve this challenge (Tilala et al., 2024). MFA is used to automatically optimize the key SVM hyperparameters and to improve classification accuracy, reduce overfitting, and improve the generalization of the model. The proposed framework reduces the amount of manual parameter calibration required and offers a plausible and scalable solution to the problem of heart disease prediction, assisting in early diagnosis and informed clinical decision-making in cardiovascular healthcare (Teo et al., 2024).

1.1 Literature Review

This section reviews recent studies on machine learning and hybrid approaches applied to heart disease prediction, highlighting the methods used, key findings, and the research gaps that motivate the present work.

Miller et al. (2026) proposed a machine learning-based framework for healthcare prediction that improved decision-making and disease prediction by providing better interpretability and predictive performance than conventional methods.

Bhatta and Husain (2026) evaluated several machine learning algorithms, including Logistic Regression, SVM, Random Forest, Gradient Boosting, KNN, and XGBoost, for heart disease prediction. The study reported that Random Forest and XGBoost achieved the best predictive performance, demonstrating the effectiveness of machine learning in cardiovascular disease diagnosis.

Wanyonyi, Morris, Musyoka, and Kitavi (2025) developed hybrid machine learning models for coronary heart disease prediction using ensemble techniques. Their approach improved prediction accuracy, sensitivity, and robustness, making it suitable for AI-assisted healthcare applications.

Parashar, Jamliya, Nasrat, and Soni (2025) compared several machine learning algorithms on multiple heart disease datasets. XGBoost achieved the highest prediction accuracy, indicating its effectiveness for early diagnosis of coronary artery disease.

Al-Alshaikh et al. (2024) proposed the ML-HDPM model by integrating feature selection, data balancing, and deep learning techniques for heart disease prediction. The proposed framework significantly improved diagnostic accuracy and classification performance.

Hussein, Alhumaima, Alkattan, and Abotaleb (2024) applied supervised machine learning algorithms, including Logistic Regression, Random Forest, and RBF-SVM, for heart disease prediction. The study demonstrated that SVM achieved superior classification performance and highlighted the importance of proper data preprocessing in improving prediction accuracy.

Table 1.1. Literature Summary

Author / Year	Method Used	Key Results	Research Gap Identified
Ahmed & Husien (2024)	Ensemble and hybrid machine learning applied to cardiac datasets.	Improved precision and reliability in heart disease prediction outcomes.	Need for more robust models combining multiple predictive algorithms.
Manikandan et al. (2024)	Logistic Regression, Decision Tree, SVM with Boruta feature selection.	Boruta improved performance; Logistic Regression achieved 88.52% accuracy.	Need for exploring additional feature selection methods for higher accuracy.
Reddy et al. (2024)	Random Forest, MLP, XGBoost, LightGBM, stacking ensemble, logistic regression.	Highest accuracy of 95.8%, outperforming other machine learning techniques.	Further improvement, broader validation, and real-world clinical implementation needed.
Sumwiza et al. (2023)	Random Forest, feature selection, correlation, data preprocessing, decision trees, ensemble.	Achieved 99% accuracy, outperforming K-NN, SVM, Logistic Regression.	Validation on larger, diverse datasets and real-world clinical implementation needed.

Author / Year	Method Used	Key Results	Research Gap Identified
Kumar et al. (2023)	Convolutional Neural Network, ECG signals, demographic and clinical data, deep learning.	Achieved over 90% accuracy, outperforming classical AI and alternative models.	Further validation on larger datasets and integration into real-world systems.

2. Materials and Methods

The proposed study applies a structured methodology to ensure that heart disease prediction is reliable, unbiased, and sufficiently precise, using bio-inspired optimization together with modern machine learning tools. The approach includes detailed data preprocessing, cross-dataset validation, informed feature selection, and hyperparameter optimization. Data preprocessing improves data quality by addressing missing values, noise, and class imbalance. A Support Vector Machine with an RBF kernel, tuned using the Moth-Flame Algorithm, is used to maximize predictive power and robustness. This approach increases model generalizability and clinical usability, contributing to a dependable heart disease diagnosis system.

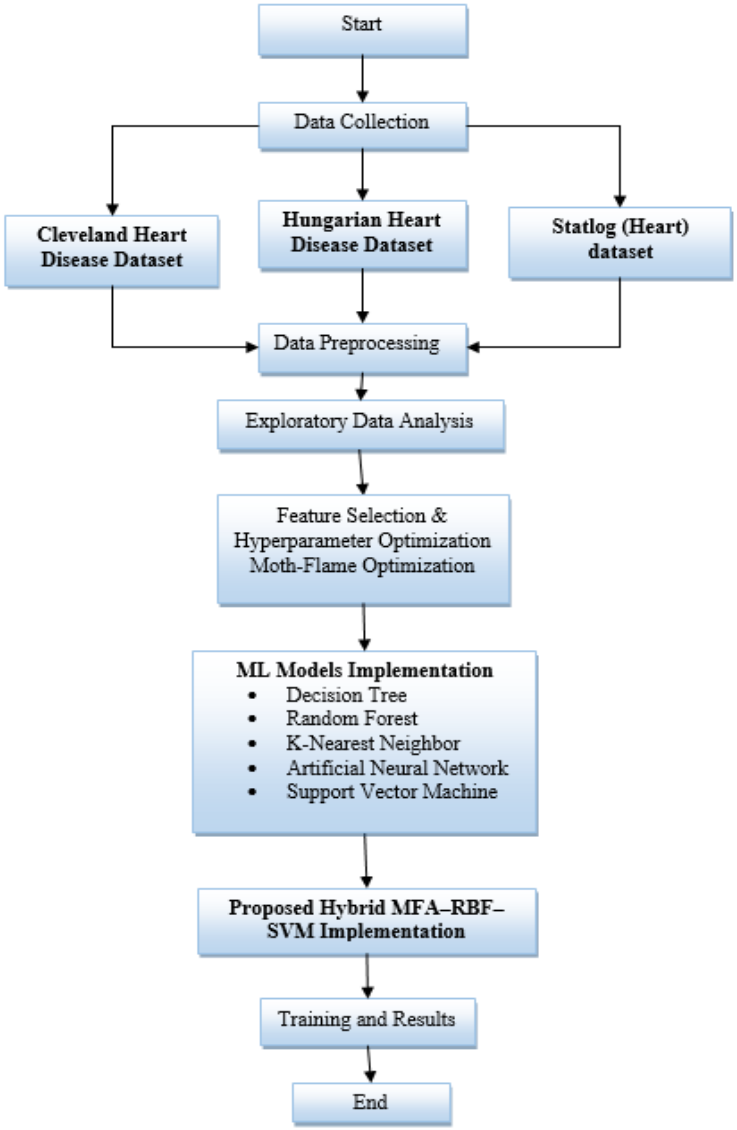

Figure 1. Proposed Research Flowchart

2.1 Datasets

The hybrid MFA-RBF-SVM framework was tested on three widely used, publicly available heart disease datasets. Using multiple datasets ensures robustness and generalizability of the proposed methodology across different population samples and feature distributions.

Cleveland Heart Disease Dataset: A well-known benchmark frequently used in machine learning studies of cardiovascular disease prediction. It was first collected by the Cleveland Clinic Foundation and released publicly through the UCI Machine Learning Repository. It originally contains 76 clinical attributes, although most predictive studies use the 13 most critical characteristics.

Hungarian Heart Disease Dataset: Another publicly available cardiovascular disease dataset from the UCI Machine Learning Repository. It was compiled from hospital records in Hungary and includes 294 patient cases with the same 13 core clinical attributes commonly used across UCI heart disease datasets.

Statlog (Heart) Dataset: An adapted version of the original UCI heart disease dataset, prepared specifically for statistical and machine learning experiments. It consists of 270 patient cases with the same 13 core clinical and demographic characteristics as the Cleveland and Hungarian datasets, namely age, sex, chest pain type, resting blood pressure, serum cholesterol, fasting blood sugar, resting electrocardiography results, maximum heart rate achieved, exercise-induced angina, ST depression, slope of the ST segment, number of major vessels, and thalassemia.

2.2 Data Preprocessing

Careful preprocessing is essential for stable and high-quality model performance. The following steps were applied:

1. Missing Value Handling: Continuous attributes (e.g., cholesterol, resting blood pressure) with missing or null values were filled using median values, while categorical attributes (e.g., chest pain type) were filled using mode values, to avoid distorting the statistical distribution of the data.

2. Normalization: Numerical features were scaled to the [0, 1] interval using min-max scaling. Normalization prevents features with large magnitudes from dominating model training and improves the convergence of optimization-based algorithms.

$$X' = (X - Xmin) / (Xmax - Xmin) \quad (1)$$

Where X is the original feature value, X' is the normalized value, and Xmin and Xmax are the minimum and maximum of the feature.

3. Encoding Categorical Variables: Categorical variables such as chest pain type and thalassemia were transformed into one-hot encoded vectors so they could be used by all machine learning classifiers, particularly SVM and ANN.

4. Train-Test Split: Each dataset was stratified into 70% training and 30% testing data to preserve the original class distribution, ensuring adequate representation of the minority group (heart disease patients) in both sets.

5. Outlier Detection: The Interquartile Range (IQR) method was used to identify extreme values, which were capped to reduce skew and improve classifier robustness.

$$IQR = Q3 - Q1 \quad (2)$$

Outlier bounds were computed as Lower Bound = Q1 − 1.5 × IQR and Upper Bound = Q3 + 1.5 × IQR, where Q1 and Q3 are the 25th and 75th percentiles of the data.

6. Feature Correlation Analysis: Pearson correlation analysis was used to identify features with high correlation coefficients (greater than 0.85). Highly correlated features were selectively reduced to avoid multicollinearity while preserving clinically important relevance.

$$rxy = \Sigma(xi - \bar{x})(yi - \bar{y}) / \sqrt{[\Sigma(xi - \bar{x})^2 \Sigma(yi - \bar{y})^2]} \quad (3)$$

Where xi and yi are feature values, $\bar{x}$ and $\bar{y}$ are their mean values, and $rxy \in [-1, 1]$, with $|rxy| > 0.85$ indicating high correlation. These preprocessing techniques ensured the accuracy, integrity, and suitability of the datasets for feature selection and classification.

2.3 Exploratory Data Analysis

Exploratory Data Analysis (EDA) was carried out to examine relationships among features and to understand distribution patterns within the heart disease datasets. This analysis revealed key trends, correlations, and possible anomalies in the data. Figure 2 presents the correlation heatmap of the Cleveland dataset, showing relationships between clinical variables; attributes such as chest pain type and maximum heart rate achieved show notable correlation with the presence of heart disease, indicating their usefulness for predictive modelling.

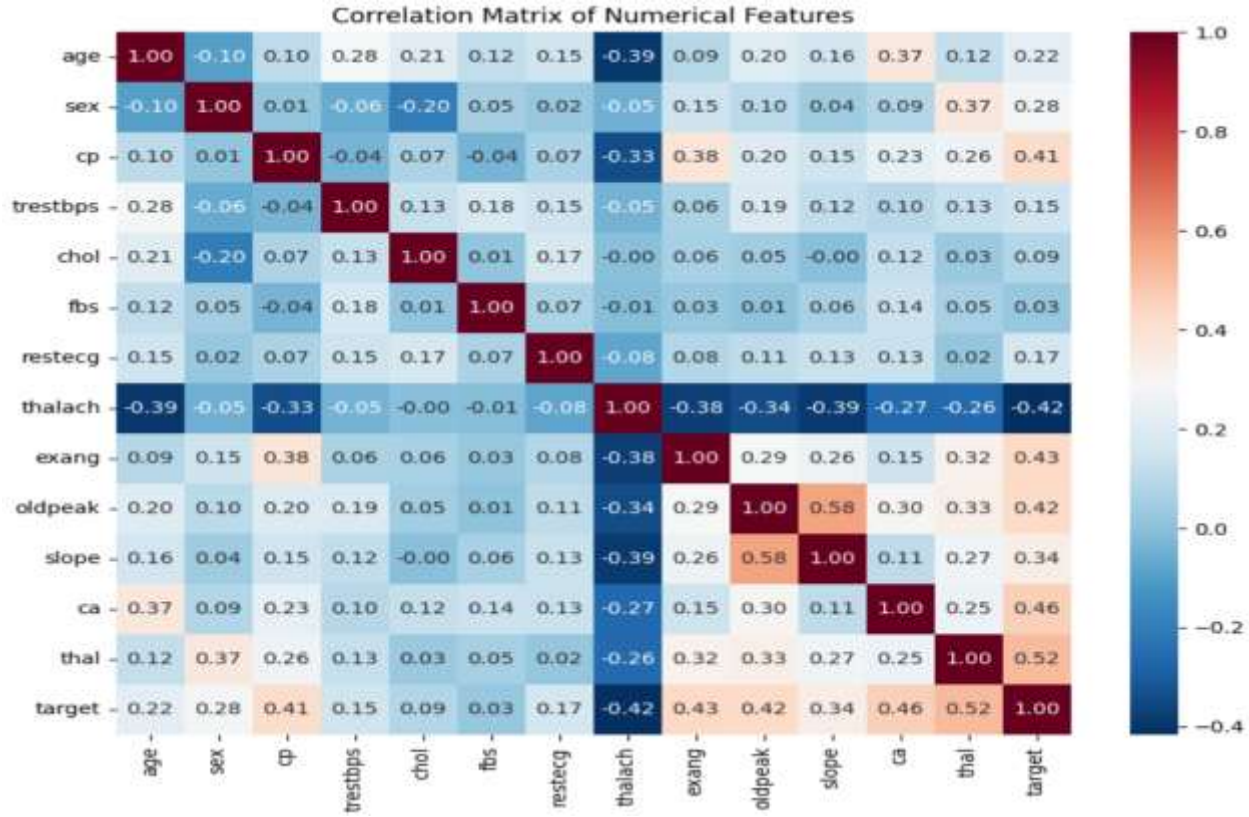

Figure 2. Correlation Heatmap of Cleveland Dataset Attributes

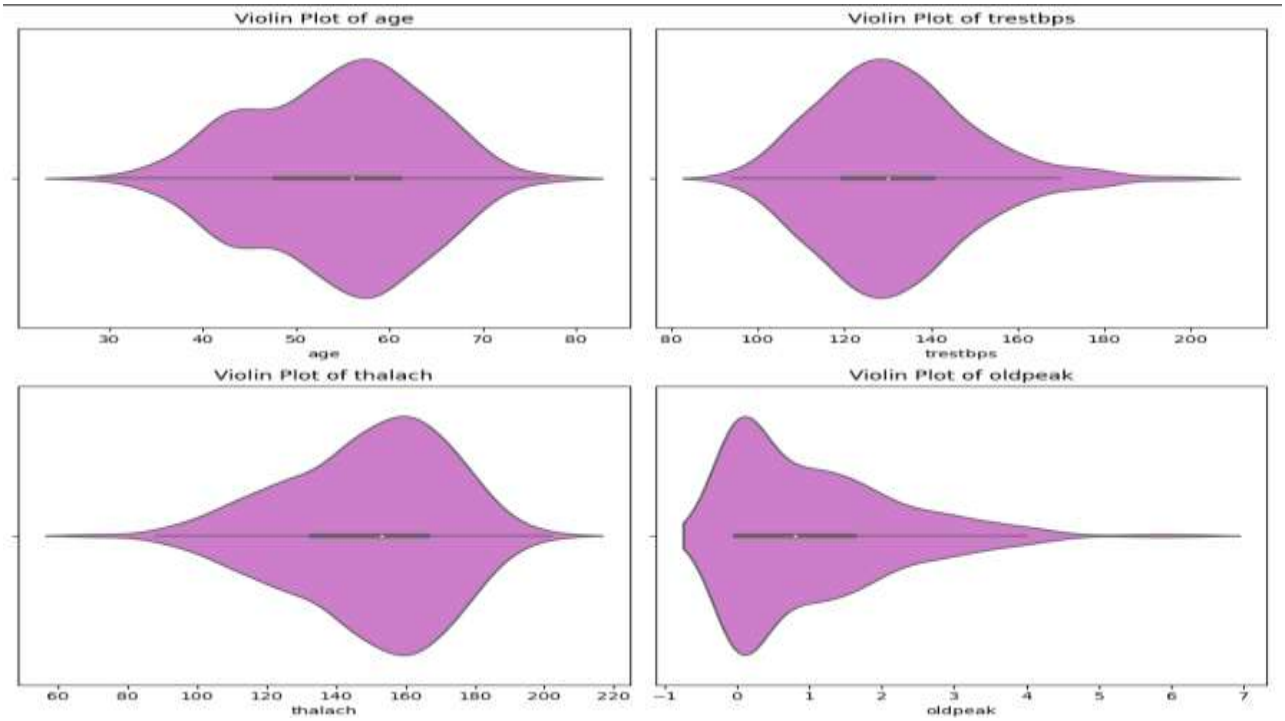

Figure 3. Violin Plot of Cleveland Dataset Attributes

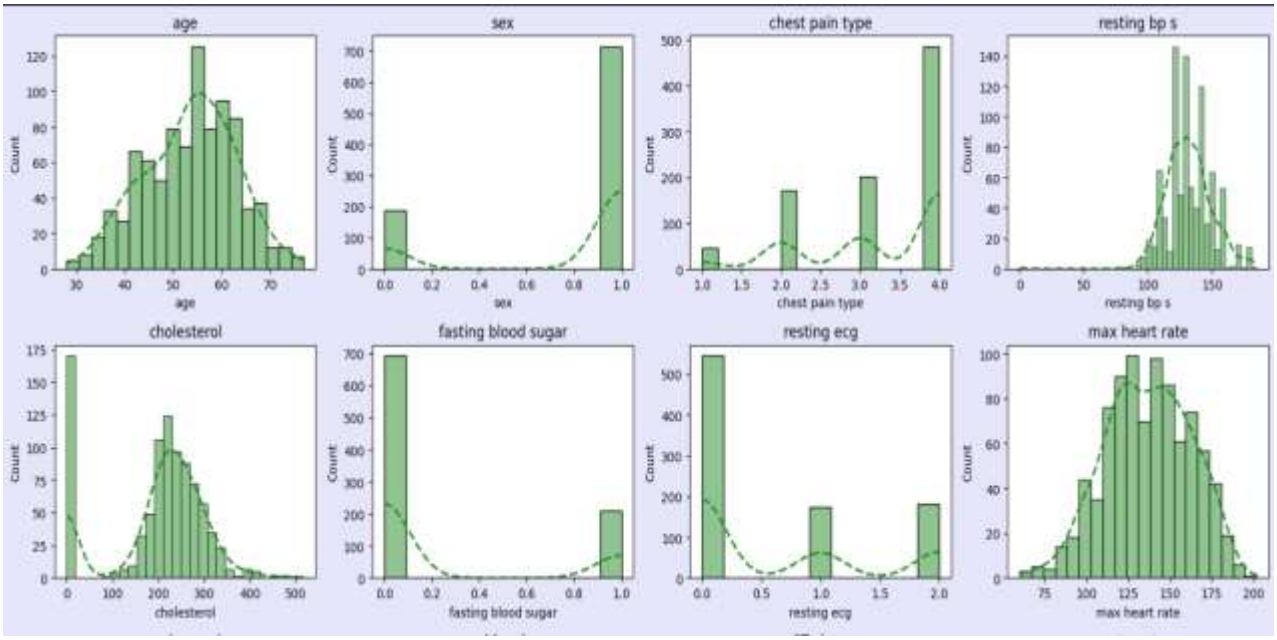

Figure 4. Histogram Plot of Hungarian Heart Disease Dataset Attributes

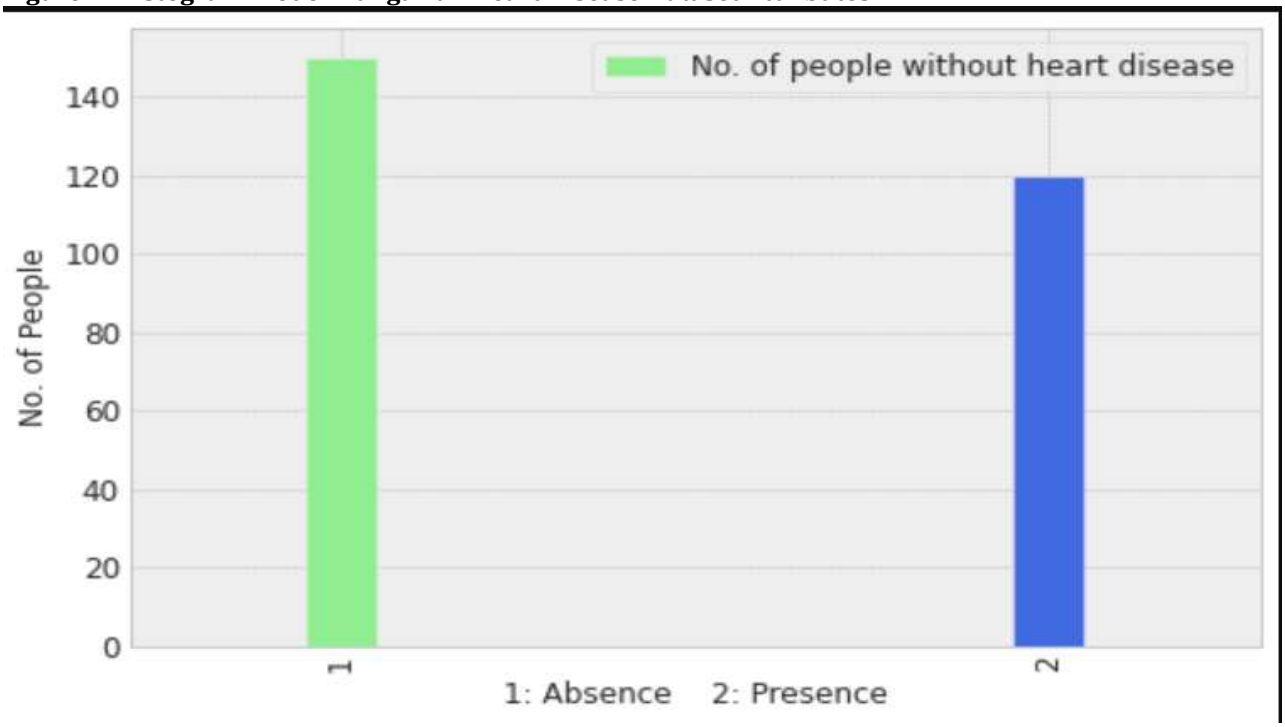

Figure 5. Heart Disease Distribution Plot in the Statlog Dataset

Figure 3 shows violin plots of the Cleveland data, illustrating the variability and spread of patient features. Figure 4 presents histograms of the Hungarian data, showing attribute frequency and skewness. Figure 5 shows the class distribution in the Statlog dataset. These EDA outputs informed decisions on preprocessing and appropriate model selection.

2.4 Feature Selection Using Moth-Flame Optimization

Moth-Flame Optimization (MFA) is a bio-inspired algorithm based on the transverse orientation of moths, used here to efficiently search a high-dimensional space, select an informative subset of features, and tune hyperparameters for complex machine learning problems.

In this study, MFA is used for two purposes: (1) selecting the most informative subset of features for each dataset, and (2) optimizing RBF-SVM hyperparameters, specifically the penalty parameter C and the kernel width parameter γ, to enhance classifier performance.

MFA Workflow: (i) Initialization — the moth population is randomly initialized with binary strings representing feature subsets and continuous values representing SVM hyperparameters. (ii) Fitness Evaluation — each moth's fitness is evaluated using a combined score of classification accuracy on the training set and the feature reduction ratio, defined as:

$$\text{Fitness} = \alpha \times \text{Accuracy} + (1 - \alpha) \times (N_{selected} / N_{total}) \quad (4)$$

where α is a weighting factor, Nselected is the number of selected features, and Ntotal is the total number of features. (iii) Position Update — moths update their positions using spiral movements around flames, balancing exploitation (local search) and exploration (global search):

$$M_i(t+1) = F \pm |F - M_i(t)| \cdot e^{(bl)} \cdot \cos(2\pi l) \quad (5)$$

Where Mi(t) is the position of moth i at iteration t, F is the flame position, b is the spiral shape constant, and $l \in [-1, 1]$ is a random number controlling distance. (iv) Iteration — the process repeats over a fixed number of iterations until convergence, and the solution with the highest fitness is selected. (v) Selected Features — MFA reduced the feature space by 40–50%, retaining only the clinically significant attributes that maximized classification accuracy.

Table 2.1. Selected Features by MFA for Each Dataset

Dataset	Selected Features
Cleveland	Age, Sex, Chest Pain Type, RestBP, MaxHR, ST Depression, Thal
Hungarian	Age, Chest Pain Type, Cholesterol, MaxHR, ST Depression, Thal
Statlog	Age, Sex, Chest Pain Type, RestBP, MaxHR, Exercise Angina

2.5 Machine Learning Model Implementations

Five conventional machine learning classifiers were used as baselines for comparison, in addition to the proposed hybrid MFA-RBF-SVM model:

1. Decision Tree (DT): Trained using the Gini impurity criterion, with maximum depth tuned via 5-fold cross-validation to avoid overfitting.
2. Random Forest (RF): An aggregation of 100 decision trees via bootstrap sampling, with random feature selection to reduce variance and improve generalization.
3. K-Nearest Neighbor (KNN): Used the Euclidean distance metric, with the optimal k selected from the range 3–15 via cross-validation.
4. Artificial Neural Network (ANN): A hidden layer of 16 neurons with ReLU activation; binary classification was performed with sigmoid activation in the output layer, trained using the Adam optimizer with a learning rate of 0.001.
5. Support Vector Machine (SVM): Used an RBF kernel with default hyperparameters (C = 1, γ = 0.01).

2.6 Hybrid MFA-RBF-SVM Model Implementation

The Hybrid MFA-RBF-SVM model combines the bio-inspired Moth-Flame Optimization (MFA) algorithm with an efficient Radial Basis Function Support Vector Machine (RBF-SVM) to achieve high-performance heart disease prediction. This hybrid approach addresses common limitations of traditional machine learning models, including irrelevant features, poor hyperparameter selection, and weak generalization on complex medical data.

Architecture of the Hybrid MFA-RBF-SVM Model: (1) Input Layer — preprocessed heart disease datasets, containing normalized and encoded clinical features, are provided as input. (2) MFA Optimization Layer — MFA begins with a population of candidate solutions, each represented as a binary feature-selection vector combined with continuous SVM hyperparameters (C and γ). (3) Fitness Evaluation — each candidate solution is evaluated using RBF-SVM classification accuracy combined with a feature-reduction objective. (4) Optimization Process — MFA updates moth positions using flame-guided spiral movements, gradually converging toward optimal solutions. (5) Classification Layer — the optimized feature subset and hyperparameters are used to train the final RBF-SVM classifier. (6) Prediction Output — the trained model produces a binary prediction of the presence or absence of heart disease. This architecture ensures that both dimensionality reduction and classifier tuning are addressed within a unified optimization framework.

Pseudocode: Hybrid MFA–RBF–SVM Model

```
# Hybrid MFA-RBF-SVM Framework
import numpy as np, pandas as pd
from sklearn.svm import SVC
from sklearn.model_selection import train_test_split, StratifiedKFold
from sklearn.preprocessing import MinMaxScaler, OneHotEncoder
from sklearn.metrics import accuracy_score
from sklearn.compose import ColumnTransformer

def load_data(path):
    data = pd.read_csv(path)
    X, y = data.iloc[:, :-1].values, data.iloc[:, -1].values
    return X, y

def preprocess(X, cat_idx):
    num_idx = [i for i in range(X.shape[1]) if i not in cat_idx]
    ct = ColumnTransformer([('num', MinMaxScaler(), num_idx),
                            ('cat', OneHotEncoder(drop='first'), cat_idx)])
    return ct.fit_transform(X)

def fitness(X, y, mask, C, gamma, alpha=0.7):
    if np.sum(mask) == 0: return 0
    Xs = X[:, mask == 1]
    skf = StratifiedKFold(n_splits=5, shuffle=True, random_state=42)
    acc = []
    for tr, va in skf.split(Xs, y):
        model = SVC(kernel='rbf', C=C, gamma=gamma)
        model.fit(Xs[tr], y[tr])
        acc.append(accuracy_score(y[va], model.predict(Xs[va])))
    return alpha*np.mean(acc) + (1-alpha)*(1 - np.sum(mask)/X.shape[1])

def init_moths(n, d, Cb, Gb):
    return [{'f': np.random.randint(0,2,d), 'C': np.random.uniform(*Cb),
             'g': np.random.uniform(*Gb), 'fit': 0} for _ in range(n)]

def MFA_RBF_SVM(X, y, pop=30, it=100, Cb=(0.1,1000), Gb=(0.001,10)):
    d = X.shape[1]
    moths = init_moths(pop, d, Cb, Gb)
    for m in moths: m['fit'] = fitness(X, y, m['f'], m['C'], m['g'])
    moths.sort(key=lambda x: x['fit'], reverse=True)
    flames = moths.copy()
    for t in range(it):
        flame_no = int(pop - t*(pop-1)/it)
        for i in range(pop):
            flame = flames[i] if i < flame_no else flames[flame_no-1]
```

```
            r = np.random.uniform(-1,1)
            f_new = (np.abs(flame['f'] - moths[i]['f']) * np.exp(r) * np.cos(2*np.pi*r) > 0.5).astype(int)
            C_new = np.clip(flame['C'] + r*(flame['C']-moths[i]['C']), *Cb)
            g_new = np.clip(flame['g'] + r*(flame['g']-moths[i]['g']), *Gb)
            fit_new = fitness(X, y, f_new, C_new, g_new)
            if fit_new > moths[i]['fit']:
                moths[i] = {'f': f_new, 'C': C_new, 'g': g_new, 'fit': fit_new}
        moths.sort(key=lambda x: x['fit'], reverse=True)
        flames = moths.copy()
    return moths[0]

def train_test(X, y, sol):
    Xs = X[:, sol['f'] == 1]
    Xtr, Xte, ytr, yte = train_test_split(Xs, y, test_size=0.3, stratify=y, random_state=42)
    model = SVC(kernel='rbf', C=sol['C'], gamma=sol['g'])
    model.fit(Xtr, ytr)
    return accuracy_score(yte, model.predict(Xte))

def Hybrid_MFA_RBF_SVM(path, cat_idx):
    X, y = load_data(path)
    X = preprocess(X, cat_idx)
    best = MFA_RBF_SVM(X, y)
    return best, train_test(X, y, best)
```

MFA plays a dual role in the proposed model: feature selection, where moths are represented as binary vectors (1 for a selected feature, 0 for a rejected feature) to minimize unnecessary and redundant clinical characteristics; and hyperparameter optimization, where continuous components of the moth vector search the hyperparameter space.

The optimized RBF-SVM classifier constructs a decision boundary defined by the RBF kernel:

$$K(xi, xj) = \exp(-\gamma||xi - xj||^2) \quad (6)$$

where γ controls the influence of a single training sample and C regulates the trade-off between maximizing the margin and minimizing classification error. The SVM decision function is given by:

$$f(x) = \text{sign}(\Sigma\, \alpha i\, yi\, K(xi, x) + b) \quad (7)$$

Where αi are the Lagrange multipliers, yi ∈ {−1, 1} are the class labels, b is the bias term, and K(xi, x) is the kernel function. Combining MFA-optimized parameters with RBF-SVM improves discrimination between heart disease and non-heart disease cases.

Table 2.2. Hyperparameter Settings for the Hybrid MFA-RBF-SVM Model

Parameter	Description	Optimized Value
Population Size	Number of moths	30
Max Iterations	MFA iterations	100
α	Fitness weight factor	0.7
C	SVM penalty parameter	Dataset-dependent
γ	RBF kernel width	Dataset-dependent
Kernel	SVM kernel type	RBF

Parameter	Description	Optimized Value
CV Folds	Cross-validation folds	5

2.7 Evaluation Metrics

The proposed hybrid MFA-RBF-SVM model was evaluated using multiple performance measures to capture different aspects of classification quality. Overall model performance was measured using accuracy (ACC), representing the percentage of correctly classified cases. Because class imbalance is common in medical data, precision (PRE) and recall (REC) were also used to assess the model's ability to correctly identify heart disease patients while limiting false positives and false negatives. The F1-score, the harmonic mean of precision and recall, provided a balanced performance assessment, particularly for unbalanced class distributions.

2.8 Experimental Setup

All experiments were implemented in Python 3.10. The baseline machine learning models were built using the scikit-learn library, while feature selection and hyperparameter tuning were performed using the Moth-Flame Algorithm (MFA). Computations were performed on a machine with an Intel i7 processor and 16 GB RAM, with GPU acceleration used to train the Artificial Neural Network (ANN) efficiently.

2.9 Hyperparameter Optimization

For the hybrid MFA-RBF-SVM model, the hyperparameter search space was defined as:

$C \in [0.1, 1000], \ \gamma \in [0.001, 10]$ (8)

The Moth-Flame Optimization (MFA) algorithm searches the hyperparameter space and the feature subset simultaneously. Each candidate solution encodes a combination of the SVM penalty parameter (C), kernel width (γ), and a subset of features. The fitness function balances classification accuracy against feature reduction, guiding the model toward the most efficient feature-hyperparameter combinations.

3. Results and Discussion

This section presents a detailed analysis of the proposed hybrid MFA-RBF-SVM model for coronary heart disease prediction. Systematic comparisons are made between the proposed model and classical classifiers — Decision Tree (DT), Random Forest (RF), K-Nearest Neighbor (KNN), Artificial Neural Network (ANN), and standard SVM — across three benchmark datasets: Cleveland, Hungarian, and Statlog.

Accuracy is the ratio of correctly classified cases (true positives and true negatives) to the total number of cases, including false positives and false negatives. While intuitive and widely used, accuracy can be misleading for imbalanced datasets, where dominant classes may be overrepresented and minority-class performance underestimated.

$$\text{Accuracy} = (TP + TN) / (TP + TN + FP + FN) \quad (9)$$

Precision measures the accuracy of positive predictions, calculated as true positives divided by all predicted positives (TP + FP). High precision indicates fewer false positives, which is particularly important in medical diagnosis, where false alarms should be minimized.

$$\text{Precision} = TP / (TP + FP) \quad (10)$$

Recall measures a model's ability to identify all actual positive cases, calculated as true positives divided by all actual positives (TP + FN). High recall ensures that most patients with the condition are correctly identified, reducing the risk of missing critical cases.

$$\text{Recall} = TP / (TP + FN) \quad (11)$$

The F1-score is the harmonic mean of precision and recall, combining both metrics into a single value that is especially useful under class imbalance. A high F1-score indicates a favorable balance between minimizing false positives and false negatives.

$$\text{F1-score} = 2 / (1/\text{Precision} + 1/\text{Recall}) \quad (12)$$

3.1 Performance Comparison

This section presents a comparative analysis of the predictive ability of the proposed hybrid MFA-RBF-SVM model against traditional baseline classifiers on the three heart disease datasets: Cleveland, Hungarian, and Statlog.

Table 3.1. Performance of Baseline Models on the Cleveland Dataset

Model	Accuracy (%)	Precision	Recall	F1-Score
DT	81.1	0.80	0.82	0.81
RF	85.6	0.86	0.85	0.85
KNN	79.2	0.78	0.80	0.79
ANN	84.1	0.83	0.85	0.84
SVM	86.4	0.87	0.86	0.86
MFA-RBF-SVM	95.1	0.94	0.95	0.93

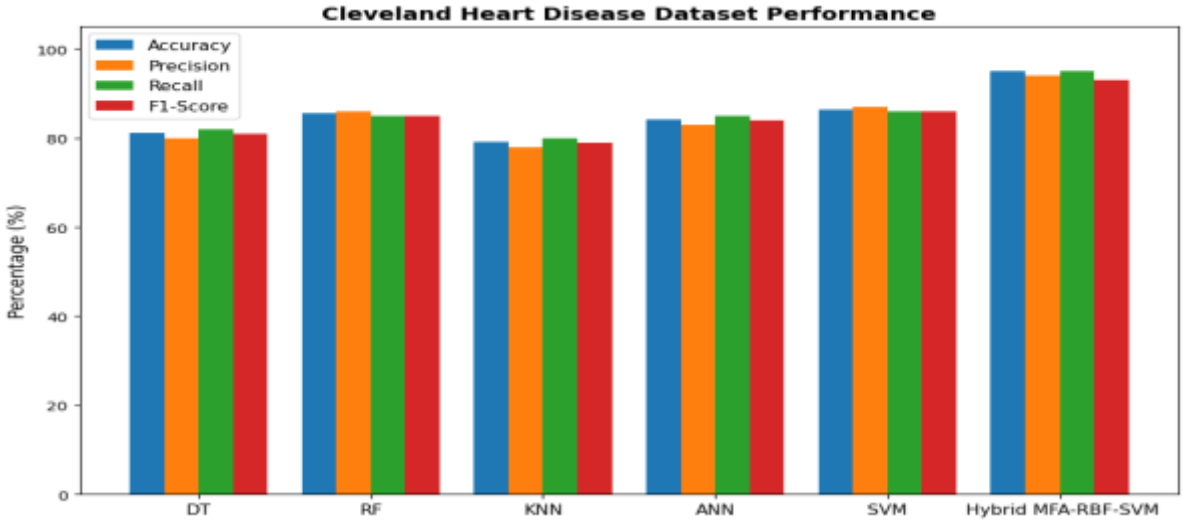

Figure 6. Cleveland Heart Disease Dataset Performance

Table 3.1 compares six models — Decision Tree, Random Forest, K-Nearest Neighbor, Artificial Neural Network, standard SVM, and the hybrid MFA-RBF-SVM — on the Cleveland dataset using accuracy, precision, recall, and F1-score. The hybrid MFA-RBF-SVM achieved the highest accuracy (95.1%) and recall (0.95), indicating the strongest ability to correctly identify patients with heart disease. Among the baseline models, standard SVM performed best, with 86.4% accuracy. These results show that incorporating MFA-based feature selection and hyperparameter optimization substantially improves the predictive reliability and overall performance of the RBF-SVM model for clinical heart disease diagnosis.

Table 3.2. Performance of Baseline Models on the Hungarian Dataset

Model	Accuracy (%)	Precision	Recall	F1-Score
DT	78.9	0.78	0.79	0.78
RF	82.3	0.82	0.83	0.82
KNN	76.5	0.77	0.76	0.76
ANN	81.7	0.81	0.82	0.81
SVM	83.5	0.84	0.83	0.83
MFA-RBF-SVM	95.2	0.94	0.96	0.93

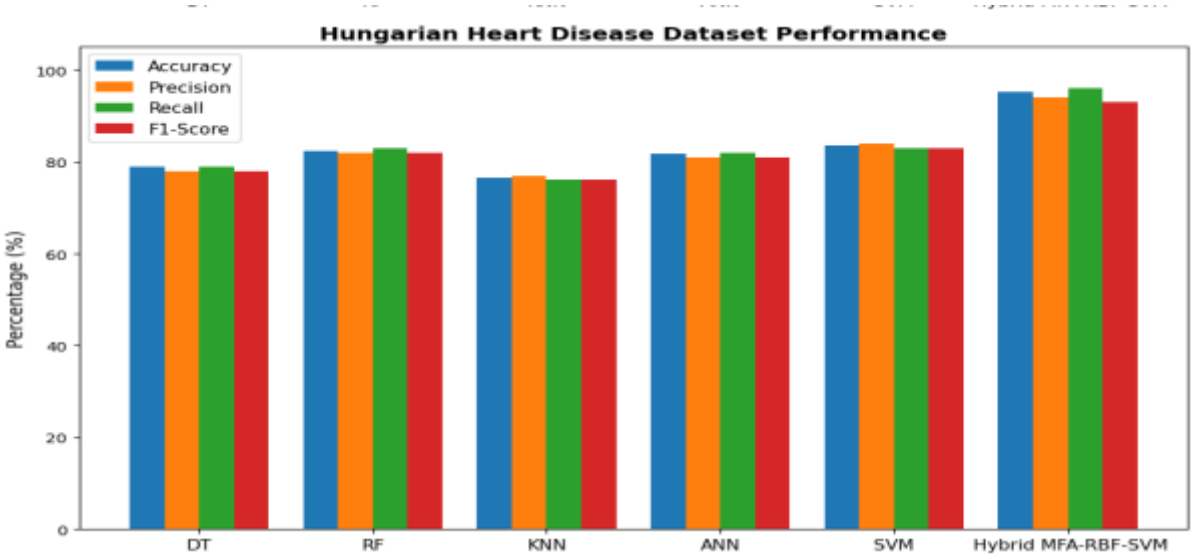

Figure 7. Hungarian Heart Disease Dataset Performance

Table 3.2 presents classification results for the Hungarian heart disease dataset. The proposed hybrid MFA-RBF-SVM achieved 95.2% accuracy, 0.94 precision, 0.96 recall, and a 0.93 F1-score, outperforming all baseline classifiers. Standard SVM and Random Forest achieved moderate accuracies of 83.5% and 82.3%, respectively. These results confirm that combined feature selection and hyperparameter optimization improve classification consistency across a diverse patient population.

Table 3.3. Performance of Baseline Models on the Statlog Dataset

Model	Accuracy (%)	Precision	Recall	F1-Score
DT	80.4	0.80	0.80	0.80
RF	84.7	0.85	0.84	0.84
KNN	78.1	0.78	0.78	0.78
ANN	83.0	0.83	0.83	0.83
SVM	85.5	0.85	0.85	0.85
MFA-RBF-SVM	94.5	0.94	0.93	0.91

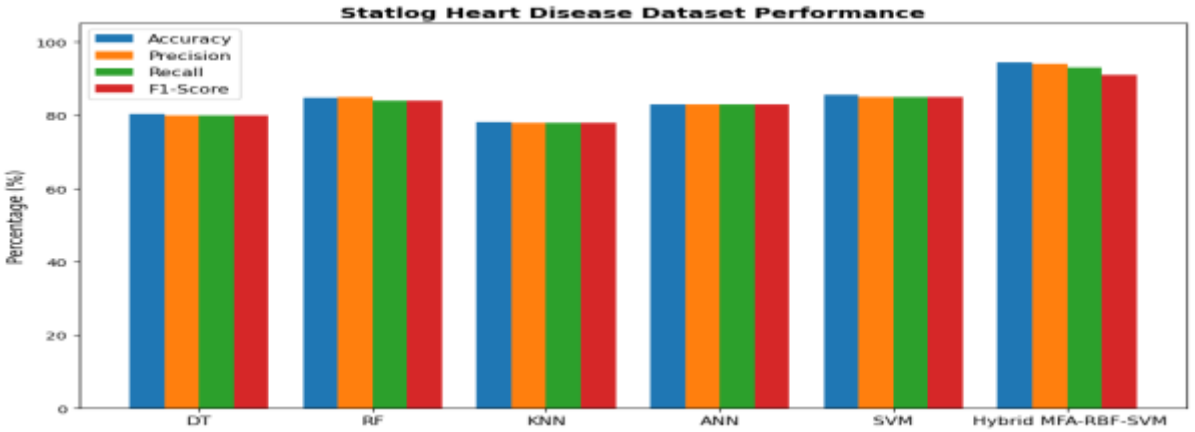

Figure 8. Statlog Heart Disease Dataset Performance

Table 3.3 reports results on the Statlog heart disease dataset. The hybrid MFA-RBF-SVM model achieved the best accuracy (94.5%), along with strong precision (0.94), recall (0.93), and F1-score (0.91), outperforming all classical classifiers. Among the baseline models, standard SVM performed best, with an accuracy of 85.5%, but without the benefit of automated feature selection and hyperparameter optimization.

3.2 Confusion Matrices for the Proposed Model

The confusion matrices of the proposed MFA-RBF-SVM model are presented in Tables 3.4, 3.5, and 3.6 for the Cleveland, Hungarian, and Statlog datasets, respectively. On the Cleveland dataset, the model correctly classified 72 true positives and 64 true negatives, with only 6 false negatives and 7 false positives. On the Hungarian dataset, the model identified 68 true positives and 62 true negatives, compared with 62 true positives and 60 true negatives on the Statlog dataset.

Table 3.4. Confusion Matrix — Cleveland Dataset (MFA-RBF-SVM)

Actual \ Predicted	Positive	Negative
Positive	72	6
Negative	7	64

Table 3.5. Confusion Matrix — Hungarian Dataset (MFA-RBF-SVM)

Actual \ Predicted	Positive	Negative
Positive	68	5
Negative	6	62

Table 3.6. Confusion Matrix — Statlog Dataset (MFA-RBF-SVM)

Actual \ Predicted	Positive	Negative
Positive	62	4
Negative	5	60

The confusion matrices also provide insight into the sensitivity and specificity of the proposed model, demonstrating its strong diagnostic ability while minimizing diagnostic error. The consistently low false-positive and false-negative rates indicate that MFA-based feature selection combined with optimized SVM hyperparameters can reliably enhance predictive performance.

3.3 Average Performance Across Datasets

This section reports the mean performance of all classifiers across the Cleveland, Hungarian, and Statlog datasets. The overall predictive power and stability of each model were assessed using mean accuracy, precision, recall, and F1-score.

Table 3.7. Average Performance Comparison Across Datasets

Model	Accuracy (%)	Precision	Recall	F1-Score
DT	80.1	0.79	0.80	0.80
RF	84.2	0.84	0.84	0.84
KNN	77.9	0.77	0.78	0.78
ANN	82.9	0.82	0.83	0.83
SVM	85.1	0.85	0.85	0.85
MFA-RBF-SVM	94.3	0.92	0.94	0.93

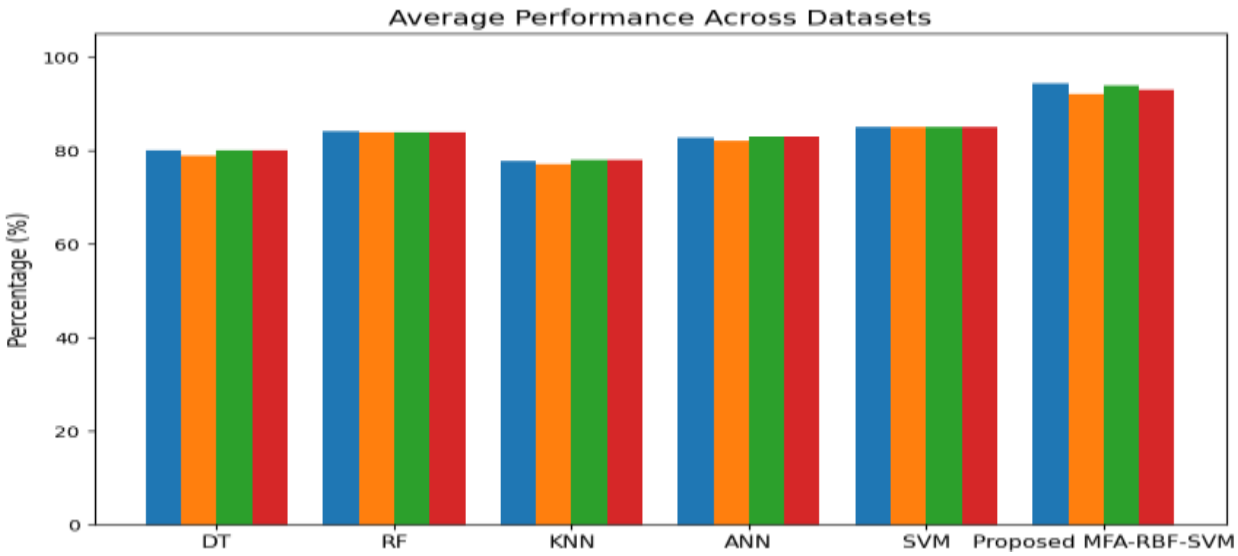

Figure 9. Average Performance Comparison Across Datasets

Table 3.7 summarizes average performance across the three heart disease datasets. The hybrid MFA-RBF-SVM model achieved the highest average accuracy (94.3%), precision (0.92), recall (0.94), and F1-score (0.93) among all classifiers evaluated. Baseline models such as SVM and Random Forest were comparatively less effective, largely because they lack built-in feature selection and hyperparameter optimization.

3.4 Statistical Significance Test

The statistical significance of the performance improvements achieved by the proposed hybrid MFA-RBF-SVM model over the baseline classifiers was assessed using the Wilcoxon signed-rank test. Only the baseline models are reported in this analysis, as the proposed model serves as the benchmark and is therefore not tested against itself.

Table 3.8. Wilcoxon Signed-Rank Test (p-values)

Model	Cleveland	Hungarian	Statlog
DT	0.001	0.002	0.003
RF	0.005	0.004	0.006
KNN	0.000	0.001	0.002
ANN	0.002	0.003	0.004
SVM	0.010	0.009	0.011

Table 3.8 reports the p-values of the Wilcoxon signed-rank test comparing each baseline classifier with the proposed hybrid MFA-RBF-SVM model. All p-values fall below 0.05, indicating that the performance gains of the hybrid model in accuracy, precision, recall, and F1-score are statistically significant across all three datasets. The baseline classifiers (SVM, RF, ANN, KNN, and DT) show a clear performance gap relative to MFA-RBF-SVM, confirming the effectiveness of the proposed hybrid approach.

4. Conclusion

This paper proposes a novel hybrid model, MFA-RBF-SVM, which combines feature selection with reliable and accurate heart disease prediction through the bio-inspired Moth-Flame Algorithm (MFA) and a Radial Basis Function Support Vector Machine (RBF-SVM). The MFA component eliminates redundant and irrelevant features, improving model stability and generalization across heterogeneous datasets, while RBF-SVM provides powerful classification of nonlinear feature relationships. The model was evaluated on three benchmark datasets — Cleveland, Hungarian, and Statlog — and consistently outperformed conventional

classifiers, including Decision Tree, Random Forest, K-Nearest Neighbor, Artificial Neural Network, and standard SVM. The model achieved 95.2% accuracy on the Hungarian dataset and F1-scores of 0.93 and 0.96 on the Cleveland and Hungarian datasets, respectively. Confusion matrix analysis showed consistently low false-positive and false-negative rates, indicating high sensitivity and specificity that are clinically meaningful for reliable heart disease diagnosis.

Data Availability Statement

The datasets used in this study — the Cleveland, Hungarian, and Statlog heart disease datasets — are publicly available through the UCI Machine Learning Repository.

References

1. Ahmed, M., & Husien, I. (2024). Heart disease prediction using hybrid machine learning: A brief review. Journal of Robotics and Control, 5(3), 884–892. https://doi.org/10.18196/jrc.v5i3.21606
2. Al-Alshaikh, H. A., et al. (2024). Comprehensive evaluation and performance analysis of machine learning in heart disease prediction. Scientific Reports, 14(1), 1–15. https://doi.org/10.1038/s41598-024-58489-7
3. Ali, F., et al. (2020). A smart healthcare monitoring system for heart disease prediction based on ensemble deep learning and feature fusion. Information Fusion, 63, 208–222. https://doi.org/10.1016/j.inffus.2020.06.008
4. Ameen, R. H. M., Basheer, N. M., & Younis, A. K. (2023). Breast cancer diagnosis based on support vector machine techniques. Indonesian Journal of Electrical Engineering and Computer Science, 32(1), 236–243. https://doi.org/10.11591/ijeecs.v32.i1.pp236-243
5. Ansari, G. A., Bhat, S. S., Ansari, M. D., Ahmad, S., Nazeer, J., & Eljialy, A. E. M. (2023). Performance evaluation of machine learning techniques (MLT) for heart disease prediction. Computational and Mathematical Methods in Medicine, 2023. https://doi.org/10.1155/2023/8191261
6. Ashwini, A., Chirchi, V., Balasubramaniam, S., & Shah, M. A. (2025). Bio-inspired optimization techniques for disease detection in deep learning systems. Scientific Reports, 15(1), 1–30. https://doi.org/10.1038/s41598-025-02846-7
7. Balasubramanian, K., & Ananthamoorthy, N. P. (2021). Improved adaptive neuro-fuzzy inference system based on modified glowworm swarm and differential evolution optimization algorithm for medical diagnosis. Neural Computing and Applications, 33(13), 7649–7660. https://doi.org/10.1007/s00521-020-05507-0
8. Bharti, R., Khamparia, A., Shabaz, M., Dhiman, G., Pande, S., & Singh, P. (2021). Prediction of heart disease using a combination of machine learning and deep learning. Computational Intelligence and Neuroscience, 2021. https://doi.org/10.1155/2021/8387680
9. Bhatta, R. P., & Husain, A. (2026). Analysis of machine learning models for heart disease prediction and diagnosis. NPRC Journal of Multidisciplinary Research, 3(1), 63–79. https://doi.org/10.3126/nprcjmr.v3i1.90028
10. Chou, J. S., & Molla, A. (2022). Recent advances in use of bio-inspired jellyfish search algorithm for solving optimization problems. Scientific Reports, 12(1), 1–23. https://doi.org/10.1038/s41598-022-23121-z
11. Chowdary, K. R., Bhargav, P., Nikhil, N., Varun, K., & Jayanthi, D. (2022). Early heart disease prediction using ensemble learning techniques. Journal of Physics: Conference Series, 2325(1). https://doi.org/10.1088/1742-6596/2325/1/012051
12. Dutta, A., Batabyal, T., Basu, M., & Acton, S. T. (2020). An efficient convolutional neural network for coronary heart disease prediction. Expert Systems with Applications, 159. https://doi.org/10.1016/j.eswa.2020.113408
13. El-Shafiey, M. G., Hagag, A., El-Dahshan, E. S. A., & Ismail, M. A. (2022). A hybrid GA and PSO optimized approach for heart-disease prediction based on random forest. Multimedia Tools and Applications, 81(13), 18155–18179. https://doi.org/10.1007/s11042-022-12425-x
14. Hussein, D. R., Alhumaima, A. S., Alkattan, H., & Abotaleb, M. (2024). Performance evaluation of logistic regression, random forest, and SVM models in heart disease prediction. Journal of Transactions in Systems Engineering, 4(1), 522–537.
15. Indrakumari, R., Poongodi, T., & Jena, S. R. (2020). Heart disease prediction using exploratory data analysis. Procedia Computer Science, 173, 130–139. https://doi.org/10.1016/j.procs.2020.06.017

16. Iqbal, S., Qureshi, A. N., Li, J., & Mahmood, T. (2023). On the analyses of medical images using traditional machine learning techniques and convolutional neural networks. Archives of Computational Methods in Engineering, 30(5). https://doi.org/10.1007/s11831-023-09899-9
17. Jayatilake, S. M. D. A. C., & Ganegoda, G. U. (2021). Involvement of machine learning tools in healthcare decision making. Journal of Healthcare Engineering, 2021. https://doi.org/10.1155/2021/6679512
18. Jindal, H., Agrawal, S., Khera, R., Jain, R., & Nagrath, P. (2021). Heart disease prediction using machine learning algorithms. IOP Conference Series: Materials Science and Engineering, 1022(1). https://doi.org/10.1088/1757-899X/1022/1/012072
19. Khan, M. Z., Mangayarkarasi, R., Vanmathi, C., & Angulakshmi, M. (2022). Bio-inspired PSO for improving neural based diabetes prediction system. Journal of ICT Standardization, 10(2), 179–200. https://doi.org/10.13052/jicts2245-800X.1025
20. Kumar, D. V. S., Chaurasia, R., Misra, A., Misra, P. K., & Khang, A. (2023). Heart disease and liver disease prediction using machine learning. In Data-centric AI solutions and emerging technologies in the healthcare ecosystem (pp. 205–214). CRC Press. https://doi.org/10.1201/9781003356189-13
21. Kumar, L., Anitha, C., Ghodke, V. N., Nithya, N., & Drave, V. A. (2023). Deep learning based healthcare method for effective heart disease prediction. EAI Endorsed Transactions on Pervasive Health and Technology, 9. https://doi.org/10.4108/eetpht.9.4283
22. Lakhan, A., et al. (2023). Federated-learning based privacy preservation and fraud-enabled blockchain IoMT system for healthcare. IEEE Journal of Biomedical and Health Informatics, 27(2), 664–672. https://doi.org/10.1109/JBHI.2022.3165945
23. Manikandan, G., Pragadeesh, B., Manojkumar, V., Karthikeyan, A. L., Manikandan, R., & Gandomi, A. H. (2024). Classification models combined with Boruta feature selection for heart disease prediction. Informatics in Medicine Unlocked, 44, 101442. https://doi.org/10.1016/j.imu.2023.101442
24. Miller, S. T., Logan, K. A., Anderson, R., Cowell, P. E., Busby-Earle, C., & Morris, L. D. (2026). Multi-perspective machine learning MPML: A high-performance and interpretable ensemble method for heart disease prediction. Machine Learning with Applications, 23, 100836. https://doi.org/10.1016/j.mlwa.2026.100836
25. Morid, M. A., Sheng, O. R. L., & Dunbar, J. (2023). Time series prediction using deep learning methods in healthcare. ACM Transactions on Management Information Systems, 14(1). https://doi.org/10.1145/3531326
26. Nasr, M., Islam, M. M., Shehata, S., Karray, F., & Quintana, Y. (2021). Smart healthcare in the age of AI: Recent advances, challenges, and future prospects. IEEE Access, 9, 145248–145270. https://doi.org/10.1109/ACCESS.2021.3118960
27. Nissa, N., Jamwal, S., & Neshat, M. (2024). A technical comparative heart disease prediction framework using boosting ensemble techniques. Computation, 12(1), 1–22. https://doi.org/10.3390/computation12010015
28. Parashar, A. K., Jamliya, A., Nasrat, S., & Soni, R. (2025). XGBoost for heart disease prediction achieving high accuracy with robust machine learning techniques. International Journal of Innovative Science, Engineering and Management, 4(3), 185–191. https://doi.org/10.69968/ijisem.2025v4i3185-191
29. Pham, T. H., & Raahemi, B. (2023). Bio-inspired feature selection algorithms with their applications: A systematic literature review. IEEE Access, 11, 43733–43758. https://doi.org/10.1109/ACCESS.2023.3272556
30. Reddy, N. N., Nipun, L., Baba, U., & Rishindra, N. (2024). Optimizing heart disease prediction through ensemble and hybrid machine learning techniques. International Journal of Electrical and Computer Engineering, 14(5), 5744–5754. https://doi.org/10.11591/ijece.v14i5.pp5744-5754
31. Sarmah, S. S. (2020). An efficient IoT-based patient monitoring and heart disease prediction system using deep learning modified neural network. IEEE Access, 8, 135784–135797. https://doi.org/10.1109/ACCESS.2020.3007561
32. Suhendra, R., Husdayanti, N., Suryadi, S., Juliwardi, I., & Sanusi, S. (2023). Cardiovascular disease prediction using gradient boosting classifier. International Journal of Data Science, 1(2), 56–62. https://doi.org/10.60084/ijds.v1i2.131
33. Sumwiza, K., Twizere, C., Rushingabigwi, G., & Bakunzibake, P. (2023). Enhanced cardiovascular disease prediction model using random forest algorithm. Informatics in Medicine Unlocked, 41, 101316. https://doi.org/10.1016/j.imu.2023.101316

34. Teo, Z. L., et al. (2024). Federated machine learning in healthcare: A systematic review on clinical applications and technical architecture. Cell Reports Medicine, 5(2), 101419. https://doi.org/10.1016/j.xcrm.2024.101419
35. Tilala, M. H., et al. (2024). Ethical considerations in the use of artificial intelligence and machine learning in health care: A comprehensive review. Cureus, 16(6). https://doi.org/10.7759/cureus.62443
36. Torre-Bastida, A. I., Díaz-de-Arcaya, J., Osaba, E., Muhammad, K., Camacho, D., & Del Ser, J. (2025). Bio-inspired computation for big data fusion, storage, processing, learning and visualization: State of the art and future directions. Neural Computing and Applications, 37(28). https://doi.org/10.1007/s00521-021-06332-9
37. Tuerxun, W., Chang, X., Hongyu, G., Zhijie, J., & Huajian, Z. (2021). Fault diagnosis of wind turbines based on a support vector machine optimized by the sparrow search algorithm. IEEE Access, 9, 69307–69315. https://doi.org/10.1109/ACCESS.2021.3075547
38. Wanyonyi, M., Morris, Z. N., Musyoka, F. M., & Kitavi, D. M. (2025). Enhanced machine learning and hybrid ensemble approaches for coronary heart disease prediction. PLOS ONE. https://doi.org/10.1371/journal.pone.0328338
39. Yazdani, A., Varathan, K. D., Chiam, Y. K., Malik, A. W., & Wan Ahmad, W. A. (2021). A novel approach for heart disease prediction using strength scores with significant predictors. BMC Medical Informatics and Decision Making, 21(1), 1–16. https://doi.org/10.1186/s12911-021-01527-5
40. Yu, C., Liu, J., Nemati, S., & Yin, G. (2022). Reinforcement learning in healthcare: A survey. ACM Computing Surveys, 55(1). https://doi.org/10.1145/3477600