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Heart Failure Classification Using Support Vector Machine with Firefly Optimization

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Abstract- Heart failure remains a major global cause of death, making accurate mortality prediction crucial for effective clinical decision-making. This study proposes a mortality classification model using a Support Vector Machine (SVM) optimized with the Firefly Algorithm (FA). This approach overcomes the limitations of conventional machine learning methods that rely on manual hyperparameter tuning and frequently produce suboptimal performance when applied to complex clinical datasets. The dataset contains 299 heart failure patient records with 12 clinical attributes and one target label. Preprocessing steps include winsorizing for outlier, feature standardization, and handling class imbalance using the Synthetic Minority Oversampling Technique (SMOTE). FA is applied to automatically optimize the SVM hyperparameters, specifically cost (C) and gamma (γ), to improve classification performance. The proposed FA–SVM model achieved 90.24% test accuracy and a recall score of 0.93 for deceased patients, demonstrating strong capability in detecting high-risk cases. These results indicate that combining FA with SVM improves predictive accuracy and model stability, showing promise as a clinical decision support tool for early heart failure risk detection.

Index Terms- Firefly Algorithm, Heart Failure Classification, Machine Learning, Support Vector Machine, FA-SVM

I. INTRODUCTION

Heart failure (HF) is a chronic cardiovascular condition which the inability of heart to pump blood efficiently because structural or functional abnormalities [1]. HF remains one of the leading causes of mortality and morbidity worldwide, with a prevalence of more than 26 million cases globally and an increasing incidence rate [2]. Clinical studies have shown that risk factors such as advanced age, diabetes, hypertension, and poor nutritional status significantly contribute to increased mortality risk among heart failure patients [3]. Therefore, early diagnosis and survival prediction in heart failure patients are crucial for improving prognosis and reducing mortality rates [4].

Advancements in artificial intelligence, particularly machine learning (ML), have contributed significantly to the healthcare sector, including heart disease prediction. The Naïve Bayes algorithm has achieved an accuracy of 85.25% in detecting heart disease patients [5], while the K-Nearest Neighbor (KNN) method reached a higher accuracy of 94.92% using RapidMiner at $k = 7$ [6]. Other approaches using the Support Vector Machine (SVM) with a linear kernel reported an accuracy of 86.92% in heart failure classification [7], and the combination of SVM with Forward Selection (FS) further improved the AUC score from 0.790 to 0.881 [8].

In contrast, studies utilizing ensemble-based methods such as Weighted Random Forest (WRF) reported relatively poor performance, achieving an AUC score of only 0.5825 [9]. These findings suggest that although machine learning algorithms have considerable potential in heart failure prediction, their performance is highly influenced by hyperparameter configuration which remains a critical factor affecting model accuracy and generalization capability [10].

To address these limitations, various metaheuristic optimization methods have been applied in ML modeling. One promising optimization technique is the Firefly Algorithm (FA), which is inspired by the flashing behavior of fireflies in attracting mates through light intensity. FA is recognized for strong global search capability and effectiveness in identifying optimal hyperparameter combinations [2].

Integrating FA with SVM has the potential to improve heart failure classification accuracy by producing a more stable and robust model [7].

This study aims to: (1) implement the SVM algorithm for heart failure classification; (2) optimize SVM hyperparameters using the Firefly Algorithm (FA); and (3) evaluate the performance of this model in predicting mortality risk among heart failure patients. Researchers are expected to develop clinical decision support systems that can facilitate early detection, more accurate diagnosis, and improved healthcare service quality [4].

II. RELATED WORK

The application of machine learning in heart disease and heart failure prediction has been widely explored to improve diagnostic accuracy and support clinical decision-making. Early approaches mainly relied on conventional machine learning algorithms such as Decision Tree, K-Nearest Neighbor (KNN), and Random Forest. Tree-based and ensemble methods, particularly Random Forest, generally achieved more stable and accurate performance compared to KNN which often shows performance degradation when handling high-dimensional and complex datasets [12–14]. Nevertheless, these approaches still often face limitations in modeling complex nonlinear relationships among clinical features and indicate suboptimal recall for high-risk patient classes, raising concerns about false-negative predictions in medical applications [13], [14].

With the rapid advancement of machine learning research, Support Vector Machine (SVM) has gained significant attention in healthcare data classification due capability to construct optimal hyperplanes and effectively handle high-dimensional datasets. Numerous studies have demonstrated that SVM employing nonlinear kernels, particularly the Radial Basis Function (RBF) kernel, utilizing nonlinear kernels, especially the Radial Basis Function (RBF) kernel, exhibit robust and competitive performance in capturing complex patterns within medical datasets [14–16]. However, the effectiveness of SVM is highly dependent on the selection of hyperparameters, especially cost (C) and gamma (γ). Improper hyperparameter selection may lead to overfitting or underfitting, thereby reducing model accuracy and generalization capability [15], [16].

Many SVM-based studies still employ manual or trial-and-error approaches for hyperparameter tuning by testing multiple combinations of C and γ. Such methods are computationally inefficient and may result in inconsistent or suboptimal parameter configurations across different datasets [16], [17]. RBF kernel frequently produces superior performance in medical datasets and manual tuning procedures cannot systematically guarantee optimal classification performance [15], [16].

To overcome these limitations, various metaheuristic optimization methods including Particle Swarm Optimization (PSO) and other optimization strategies, have been incorporated into classification models. Previous research have shown that integrating optimization techniques with SVM can enhance classification performance and computational efficiency, particularly when dealing with high-dimensional and noisy datasets [18]. Among these methods, the Firefly Algorithm (FA) has attracted considerable attention due to strong global search capability and relatively rapid convergence toward optimal solutions. Previous research has explored the development of a palm vein recognition system based on the integration of Linear Discriminant Analysis and the Firefly Algorithm (LDA-FA). They used 500 palm vein images collected from 100 individuals and demonstrated that the proposed LDA-FA model achieved higher accuracy, lower false-positive and false-negative rates, and faster training time than the conventional LDA approach, indicating superior effectiveness and computational efficiency [19]. FA outperformed optimization methods such as PSO and Bayesian Optimization in terms of classification accuracy and generalization performance, particularly in small and complex datasets [20].

Despite these promising results, the application of the Firefly Algorithm for SVM hyperparameter optimization in heart failure classification remains relatively limited. Furthermore, most previous studies have not combined hyperparameter optimization with comprehensive data preprocessing techniques, such as outlier treatment and class imbalance handling, despite these issues being common in real-world clinical datasets. Researchers propose a heart failure classification framework based on a Support Vector Machine optimized using the Firefly Algorithm to enhance model accuracy, stability, and sensitivity in predicting mortality risk among heart failure patients.

III. METHODOLOGY

Cross Industry Standard Process for Data Mining (CRISP-DM) framework as methodology which consists of six main stages: Business Understanding, Data Understanding, Data Preparation, Modeling, Evaluation, and Deployment. The phases of CRISP-DM are illustrated in Figure 3.1.

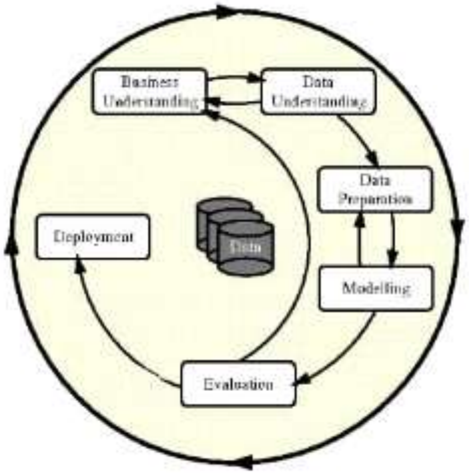

Figure 3.1 CRISP-DM Methodology [20]

A. Business Understanding

The high prevalence of heart disease has driven the development of a machine-learning-based classification system to predict the survival likelihood of heart failure patients based on multiple clinical indicators. The final output of this model is expected to support medical practitioners in identifying high-risk heart failure patients who may require more intensive monitoring and treatment.

B. Data Understanding

This study utilized the heart_failure_dataset.csv dataset obtained from a previous study [11]. The dataset consists of 299 records of heart failure patients records, including 12 predictor attributes and one target variable, for a total of 13 attributes. A detailed description of each feature is presented in Table 3.1.

Table 3.1: Dataset Features

Feature Name	Feature Description
age	Age of the patient
anaemia	Anaemia status (0 = no, 1 = yes)
creatinine_phosphokinase	Level of CPK enzyme in the blood (mcg/L)
diabetes	Diabetes (0 = no, 1 = yes)
ejection_fraction	Percentage of blood leaving the heart at each contraction (%)
high_blood_pressure	Hypertension (0 = no, 1 = yes)
platelets	Platelet count in the blood (kiloplatelets/mL)
serum_creatinine	Serum creatinine level (mg/dL)
serum_sodium	Serum sodium level (mEq/L)
sex	Sex (0 = female, 1 = male)
smoking	Smoking habit (0 = no, 1 = yes)
time	Follow-up period (days)
death_event	Death event (0 = survived, 1 = deceased)

Initial exploratory analysis indicates that the dataset contains no missing values or duplicate records. However, outliers were detected in several numerical features, including creatinine_phosphokinase, ejection_fraction, platelets, serum_creatinine, and serum_sodium, as shown in Figure 3.2. Additionally, the target class distribution is imbalanced, with a higher number of survivors compared to non-survivors.

C. Data Preparation

The first step was handling outliers detected in several numerical features using the winsorizing method, ensuring that extreme values do not dominate the overall data distribution. Then, all numerical features were standardized using z-score standardization to place them on a uniform scale with a mean of zero and a standard deviation of one.

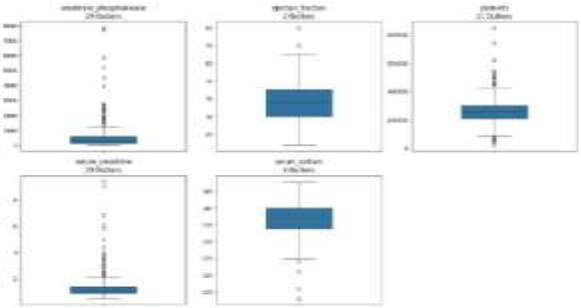

Figure 3.2 Outliers in The Dataset

The target class distribution before balancing is shown in Table 3.2, where the survivor class consist of 203 samples, while the non-survivor class contains only 96 samples. This imbalance may lead to bias during model training. To mitigate this issue, the Synthetic Minority Oversampling Technique (SMOTE) was applied, resulting in a balanced balanced class distribution with 203 samples for both survivor and non-survivor classes in Table 3.3.

Table 3.2: Class Distribution of DEATH_EVENT Before SMOTE

Class	Number of Samples
Survived	203
Died	96

Table 3.3: Class Distribution of DEATH_EVENT After SMOTE

Class	Number of Samples
Survived	203
Died	203

Following the balancing process, the dataset was split into training and testing sets using an 80:20 ratio with stratified sampling to preserve the class distribution. Consequently, 325 training samples were allocated for model training, while 81 samples were reserved for model evaluation.

D. Modeling

The modeling focuses on the implementation of the Support Vector Machine (SVM) algorithm with a Radial Basis Function (RBF) kernel integrated with the Firefly Algorithm (FA) as a metaheuristic optimization technique. The FA–SVM approach was selected to gain robust classification performance in complex medical prediction tasks, particularly for predicting survival outcomes among heart failure patients. SVM is well known for its capability to construct optimal hyperplanes that enable nonlinear class separation through kernel functions, whereas FA is employed to optimize the hyperparameters C and γ to ensure optimal model performance [1], [2].

1. Firefly Algorithm (FA) for Hyperparameter Optimization

The Firefly Algorithm (FA) is a swarm intelligence-based metaheuristic optimization technique inspired by the flashing behavior of fireflies used for mate attraction. FA is based on three primary principles: (i) all fireflies are considered unisex and can attract one another, (ii) the attractiveness between fireflies is proportional to their light intensity and decreases as the distance increases, and (iii) the light intensity of each firefly is determined by the objective function value at its current position.

Each firefly represents a candidate solution defined by a pair of SVM hyperparameters (C, γ). The light intensity is computed based on the average classification accuracy obtained from 10-fold cross-validation on the training data. Since FA is formulated as a minimization problem, the objective function is defined as the negative value of the validation accuracy.

The optimization process starts with the random initialization of 30 fireflies within the predefined search space, where $C \in [1.0, 3.0]$ and $\gamma \in [0.1, 1.0]$. The fitness value of each firefly is subsequently evaluated, followed by iterative position updates using an exponential attractiveness function that presented in Equation 3.1.

$\beta = \beta_0 e^{-\gamma r^2}$ (eq 3.1)

It combined with a stochastic movement component controlled by the parameter α. To gradually reduce random exploration and strengthen exploitation during later iterations, the value of α is adaptively decreased according to $\alpha \leftarrow 0.97\alpha$. This optimization procedure is iteratively executed until the maximum number of evaluations set to 50 evaluations. Finally, the optimal hyperparameter pair (C, γ) corresponding to the highest validation accuracy is selected as the final solution.

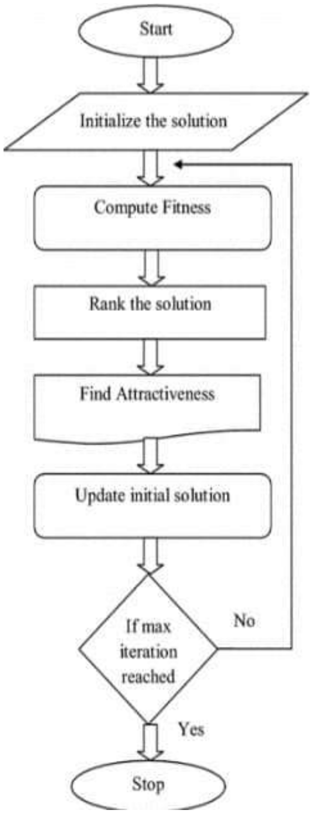

Figure 3.3 Firefly Algorithm Flowchart [22]

2. FA–SVM Model Construction

After obtaining the optimal hyperparameters, an SVM model with an RBF kernel was constructed using the optimized values of C and γ. The modeling architecture can be summarized as follows:

- Input Layer: The model includes 12 clinical features, namely age, anaemia, creatinine phosphokinase, diabetes, ejection fraction, high blood pressure, platelets, sex, serum creatinine, serum sodium, smoking, and time with DEATH_EVENT as the binary target variable (0 = survived, 1 = died).
- Preprocessing: Standard Scaler normalization was applied standardize feature distributions with a mean of 0 and a standard deviation of 1. Class imbalance was addressed using the Synthetic Minority Oversampling Technique (SMOTE) to equalize the distribution between the "survived" and "died" classes, while outliers were handled through winsorizing.
- Training: The SVM model was trained using the preprocessed training set with the hyperparameter configuration (C = 2.7312, γ = 0.1464). The RBF kernel was selected because to its ability to capture nonlinear decision boundaries which is advantageous for modeling complex medical data.
- Model Persistence: The trained model and the scaling object were serialized using pickle and stored as fa_svm_model.pkl and scaler.pkl, respectively. This ensures that the inference pipeline can be consistently reproduced during evaluation and deployment.
- Output Layer: The output layer generates a binary prediction representing either survival (0) or death (1).

E. Evaluation

The evaluation stage aims to objectively assess the performance of the FA–SVM model using an unseen test data. Evaluation metrics include Accuracy, Precision, Recall, and F1-Score. In addition, the Confusion Matrix was employed to visualize the distribution of correct and incorrect predictions for both the positive (died) and negative (survived) classes. This comprehensive evaluation ensures that the proposed model does not overfit and is capable of generalizing effectively to new patient data.

F. Deployment

The trained model was implemented in a production environment through a web-based interface developed using Streamlit framework. The serialized SVM model and scaler were integrated into the application, enabling users to input clinical parameters manually and obtain real-time mortality risk predictions. This implementation allows the system to function as a practical clinical decision-support tool.

IV. RESULTS AND DISCUSSIONS

Following the experimental workflow based on the CRISP-DM methodology, the optimization and performance evaluation of the model yielded the following results.

A. Firefly Algorithm Optimization Results

The Firefly Algorithm was employed to identify the optimal hyperparameter combination (C, γ) for

maximizing model accuracy. The search space was defined as:
$C \in [1.0, 3.0]$
$\gamma \in [0.1, 1.0]$

A total of 50 evaluations were performed. The algorithm successfully converged and identified the optimal parameters:
Cost (C): 2.7312
Gamma (γ): 0.1464

This configuration achieved a best-performing validation accuracy of 86.77% using 10-fold cross-validation, demonstrating that the Firefly Algorithm effectively navigated the search space to obtain a robust SVM configuration.

B. Firefly Algorithm Optimization Results

By using the optimized hyperparameters, the final model was retrained on the complete training dataset after normalization and SMOTE processing and subsequently evaluated on the test set comprising 20% of the original dataset. In Table 4.1, the test results show strong performance with a test accuracy of 90.24%.

Table 4.1: Classification Report of the FA-SVM Model

Class	Precision	Recall	F1-Score
Survived	0.92	0.88	0.9
Died	0.88	0.93	0.908888

V. CONCLUSION

This study successfully developed a mortality risk classification model for heart failure patients by integrating a Support Vector Machine with the Firefly Algorithm (FA) for hyperparameter optimization. The FA effectively identified the optimal hyperparameter configuration (C = 2.7312, γ = 0.1464). Combined with preprocessing steps such as winsorizing and SMOTE, the final model achieved a test accuracy of 90.24%. Furthermore, the model exhibits high sensitivity with a recall value of 0.93 in detecting high-risk patients, making its potential as an early screening tool in clinical practice. The successful deployment of the model through a web-based system also demonstrates its practical applicability in supporting data-driven clinical decision-making.

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