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Improvement in Cardiovascular Disease Prediction and Control Based on Optimized Deep Learning

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Abstract: The analysis of medical data plays a critical role in improving diagnostic accuracy, refining research methodologies, and informing decisions regarding the allocation of medical resources, particularly for critical diseases. Artificial intelligence (AI) provides essential tools for analyzing such data to generate reliable predictions. This study proposes a predictive framework for cardiovascular disease that utilizes key risk factors through a hybrid model combining an Improved Particle Swarm Optimization Algorithm with Mutation Criteria (MPSO) and a Recurrent Neural Network-Long Short-Term Memory (RNN-LSTM) architecture. The model's performance was evaluated on two datasets: one from the University of California Irvine (UCI) Machine Learning Repository and another comprising real-world data collected from Baghdad Medical City Hospital and Ibn al-Bitar Hospital. The proposed framework achieved high predictive accuracy, with Data1 yielding an accuracy of 98.36%, precision of 98.48%, sensitivity of 98.48%, and specificity of 98.21%. Data2 demonstrated an accuracy of 98.75%, precision of 100%, sensitivity of 94.12%, and specificity of 100%. These results indicate that the model generalizes effectively across datasets and outperforms state-of-the-art methods in predicting cardiovascular disease, as evidenced by robust performance metrics.

Index Terms: Cardiovascular Disease, Prediction, Deep Learning, Recurrent Neural Network, Long Short-Term Memory, Particle Optimization Algorithm

1. Introduction

Heart disease is a dangerous and common disorder which can strike at any age, although it usually starts showing signs more frequently around 40. There are several different physiological indications that impact the development of cardiovascular disease, but age is one among them. Therefore, algorithms that can detect abnormalities among these markers that could indicate heart failure are in high demand [1]. High blood pressure, insulin resistance, and high levels of cholesterol in the blood have been identified as significant predictors for cardiovascular disease, according to a large investigation. Other important lifestyle factors that increase the likelihood of heart disease are unhealthy eating, excessive alcohol use, smoking, and overweight [2]. Evaluating the association between illness-related characteristics and underlying knowledge within the data is an important part of heart attack prediction [3]. The application of various deep learning (DL) and machine learning (ML) techniques has led to substantial advancements in the forecasting of heart diseases. Splitting huge data sets into smaller ones and drawing conclusions from connections within them is what ML is all about [4]. To measure the degree of cardiovascular disease and to forecast negative results, state-of-the-art ML approaches are used [5, 6, 7]. There must be a system that is automated to allow early detection of diseases and prevent misclassification. However, current systems have obtained accuracy levels between 65% – 85% [8].

Artificial intelligence, particularly DL methods, has emerged as an indispensable tool for the diagnosis of persistent illnesses, thanks to its remarkable ability to handle complicated tasks. Variable tuning and feature identification are popular applications of optimization techniques such as the jellyfish optimization algorithm (JOA), the lion algorithm (LA), Particle Swarm Optimization Algorithm (PSO), and the cuttlefish-swarm optimization algorithm (CSOA) [9,10, 11, 12, 13] This study employs PSO, a method of optimization that mimics the flocking actions of birds, to tune DL parameters, thereby enhancing the accuracy of the model used for detection [14]. Conventional neural networks (CNNs) are an excellent choice for detecting cardiovascular conditions, and there are other DL techniques used in healthcare settings. This is because as the network's layers get more intricate, both the framework and the characteristics can be precisely specified. Also presented in this work is the Long Short-Term Memory (LSTM) model, a time-based Recurrent Neural Network (RNN). The research suggests a CNN-LSTM combination that uses the MPSO method to find the best learning rate, which improves the accuracy of classification. The principal contributions of the investigation are as follows:

- Presenting a novel and effective methodology for predicting cardiovascular diseases through the utilization of a model-driven optimal RNN-LSTM on datasets sourced from real-time sources and online resources.
- Developing an optimal rate of learning by increasing the rate at which the RNN converges, its capacity to generalize is strengthened, and its overall performance is enhanced.
- By integrating mutation into the PSO algorithm, greater exploration of the search space can be encouraged, local minimum can be avoided, and superior solutions can be discovered more efficiently.
- Maintaining a regulated learning rate to minimize the potential for overfitting and underfitting in the LSTM model to attain optimal accuracy on the cardiovascular disease dataset.
- Improving the predictive model to incorporate five distinct classes of cardiac conditions—coronary artery disease, angina pectoris, congestive heart failure, and arrhythmias—into the classification scheme. By expanding the model's scope beyond binary classification (i.e., normal, and abnormal), a prediction is achieved that is more nuanced and clinically relevant.

The structure of the following sections guides the subsequent content. An exhaustive literature review concerning the subject matter is presented in the "Literature review" section. The "Methodology" section provides comprehensive explanations of the techniques and approaches utilized. Subsequently, the proposed task is described in detail, including its conceptual framework and essential elements. The experimental findings are thoroughly documented and evaluated in the "Simulation results and discussion" section, which also includes a discussion of how the proposed methodology compares to alternative algorithms. In the "Conclusion and future work" section, final remarks are succinctly summarized.

2. Literature Review

Numerous scholarly investigations have utilized ML, DL, and neural network (NN) models to classify and forecast cardiac ailments. Additionally, swarm algorithms have been suggested and shown to be exceptionally effective, specifically in terms of improving the model's overall performance and efficacy. Numerous scholarly articles have been devoted to the classification of cardiovascular disease.

Rabbi et al. [15] address the class disparity through two balancing methods: oversampling and the artificial minority over-sampling technique. These methods contribute to a more accurate dataset, resulting in enhanced prediction accuracy. This study presents a novel combination method that integrates random forest (RF), support vector machine (SVM), K-nearest neighbors (KNN), logistic regression (LR), decision tree (DT), and Gaussian naive Bayes (GNB) to enhance the accuracy of cardiovascular disease forecasting. Integrate with advanced collaborative learning methods, including Stacking, Bagging, Boosting, and Voting, to facilitate early and accurate prediction of cardiovascular disease. The performance assessment is performed on three datasets: Framingham Heart Disease, Cleveland Heart Disease, and the indices of Heart Disease Dataset (2020), thereby ensuring a rigorous verification of proposed methods. The findings indicate that the voting ensemble machine learning algorithm (VEMLA) attained an accuracy of 92% on the Cleveland Heart Disease dataset, whereas the bagging ensemble machine learning algorithm (BEMLA) reached an accuracy of 97% on both other datasets. While, Mohapatra et al. [16] devised novel methodologies for automating the identification of anomalies in human cardiac situations, thereby enabling medical professionals to achieve expedited analyses by minimizing diagnostic time and improving outcomes. Electronic Health Records (EHRs) are frequently employed to identify valuable data trends that enhance the predictive capabilities of machine learning (ML) algorithms. Machine Learning plays a crucial role in addressing challenges such as forecasts across multiple disciplines, including healthcare. Given the plethora of accessible healthcare data, it is imperative to utilize this information for the advancement of humanity. This study proposes a predictive model for heart disease forecasting via a two-level stacking of many classifiers. Diverse heterogeneity learners are amalgamated to yield a robust model output. The model achieved 92% accuracy in prediction, with a score for precision of 92.6%, sensitivity of 92.6%, and specificity of 91%.

Bhavekar and Goswami [17] proposed a hybrid deep neural network approach for the classification of cardiac diseases. The classification of synthetic data utilizing a combination of RNN and LSTM has been conducted through various a cross-valid methods. The system's efficiency can be evaluated through various machine learning methods and soft computing approaches. In the classification process, RNN utilizes three distinct functions for activation. Data balancing was achieved through the application of specific preparation techniques for sorting and classification. The extraction of features has been conducted utilizing relational, bigram, and density-based methodologies. A range of machine learning and deep learning techniques was utilized to evaluate the system's efficiency during the trial. The outcomes section presents the accuracy of the categorization performed by every method. Consequently, it can be concluded that deep hybrid learning demonstrates greater accuracy compared to traditional deep learning (DL) or standalone ML techniques.

Safa et al. [18] introduce a Deep Spectral Time-varying Feature Analytical Model that employs a SoftMax RNN within a network of wireless sensors to enhance the accuracy of heart disease forecasting. Internet of Things devices with sensors first gather data from patient observations to verify the transfer of data during route transmission. The gathered data is structured as features within the overall dataset. The components are first processed into an ineffective dataset to calculate the Cardiovascular Protection Influence Rate based on a time-varying selection of features system. The predicted weights are integrated as spectral attributes within the classifiers. The Soft-Max Activity Function establishes a rational function based on the Cardiac Feelings Rate. The trained, logical neurons are organized RNN that utilizes the feed-forward attributes through a classifier and assesses the Rate of Conditions Affection by the category type. The model suggested demonstrates high predictive accuracy regarding classification, precision, and recall to facilitate early intervention for heart disease risk assessment.

Dileep et al. [19] employed DL strategies in comparison with traditional approaches. To enhance the precision of traditional approaches, cluster-based bi-directional long-short term memory (C-BiLSTM) was developed and introduced. The UCI and real-time heart disease datasets are utilized for experiment outcomes, serving as inputs to the K-Means clustering technique for data duplication and elimination, followed by heart disease prediction employing the C-BiLSTM approach. Traditional classification approaches, including Regression Tree (RT), SVM, KNN, LR, Ensemble, and Gated Recurrent Unit, are evaluated versus C-BiLSTM, with overall efficacy illustrated through accuracy, recall, and F1-score metrics. The findings indicate that the C-BiLSTM achieves the highest accuracy, with 94.78% on the data set from UCI and 92.84% on the real dataset, surpassing six traditional techniques in predicting cardiovascular disease. Narayanan et al. [20] introduce supervised ML-based classifiers that effectively identify important characteristics through mL strategies aimed at predicting cardiovascular disease. This work introduces a technique for over-sampling aimed at addressing the challenges posed by imbalanced data sets. Various methods for classification are utilized, each incorporating distinct features within the forecasting model. The efficacy of metrics for performance is assessed in relation to the UCI heart data set through the application of ML techniques, specifically utilizing SMOTE technology oversampling. The Random Forest method accomplished an optimal accuracy of 96.6%, along with 90% sensitivity and 100% precision and specificity.

To decrease data dimension and complexities, the research highlights the use of significant observable features. Heart disease prediction is an important part of healthcare, and Al-Taie et al. [7] investigate using data analysis techniques for this purpose when This research makes use of the Waikato environment for knowledge analysis (Weka 3.8.3) with methods such as Bayes Net, Random Forest, sequential minimum optimization (SMO), and multilayer perceptron (MLP). The research shows that Bayes Net is more effective and has made a big impact on heart disease forecasting, with a demonstrated accuracy of 94.5%. This study makes use of the identical data set collected from Ibn al-Bitar and Baghdad Medical City hospitals. Applying identically collected data from Ibn al-Bitar and Baghdad Medical City hospitals, Saleh et al. [6] use four techniques for data mining and the Weka 3.8.3 program to aid Iraqi cardiologists and doctors in analyzing cardiac disorders. The J48 technique has a 94.5% accuracy rate, which is higher than any prior method. The study highlights the potential of data mining to improve cardiovascular disease diagnosis using several categorization algorithms. Authors Sudha and Kumar [21] suggested a methodology that integrates convolutional neural networks with LSTM network to attain superior accuracy compared to conventional ML approaches. The hybrid CNN and LSTM approach was utilized on the cardiovascular disease data to categorize it as either normal or abnormal. The combined system had an accuracy of 89% and had been verified using the cross-validation k-fold method. To evaluate the efficacy of the suggested method, it is contrasted with many ML methods, including Naïve Bayes, SVM, and Decision Tree. The outcomes indicate that the suggested technique outperforms the current ML models.

Numerous optimization techniques exist within the realm of swarm intelligence algorithms. PSO, introduced in 1995, is a prominent example due to its simplicity and effectiveness. It has been successfully applied in various domains, such as adjusting SVM parameters [6], optimizing the weights of back-propagation neural networks [22], and selecting optimal feature subsets. Despite its advantages, PSO's stochastic nature means it cannot guarantee the discovery of the global optimum for every problem. Consequently, numerous variants have been developed to enhance their performance. For instance, Bataineh et al. [23] build and assess multiple intelligent systems utilizing ML algorithms to forecast an individual's likelihood of developing heart disease, employing the publicly accessible Cleveland Heart Disease dataset. This work presents an alternate training strategy for MLP that employs PSO algorithm for the identification of heart disease. This study employs the MLP-PSO hybrid algorithm alongside ten distinct ML methods to detect cardiac disease. Diverse classification measures are employed to assess the efficacy of the algorithms. The MLP-PSO method surpasses all other algorithms, with an accuracy of 84.61%.

Similarly, Feshki et al. [24] employed feature ranking on disease-related characteristics from the Cleveland Clinic database, utilizing PSO and Neural Network Feed Forward Back-Propagation, resulting in the reduction of 13 effective factors to 8 optimum features concerning cost and accuracy. The evaluation of specific characteristics of categorized methods indicated that PSO approach, in conjunction with Feed Forward Back-Propagation Neural Networks, achieved the highest accuracy rate of 91.94% for these features. These studies highlight PSO's potential but also underscore the need for improvements to address its limitations, particularly in balancing exploration and exploitation to achieve higher accuracy. Your research addresses the following problem statements:

- The accurate and objective assessment of heart disease prediction using computer-aided techniques remains an ongoing research challenge.
- This challenge is underscored by the current state-of-the-art research, where the same collected dataset has been utilized in diverse ML and ANN methods. However, these approaches have not exhibited highly performant metrics, with accuracy rates failing to surpass 95% and 97% for real-time datasets and UCI online datasets, respectively.
- The dataset utilized comprises real-world data, emphasizing the need for further generalization. To enhance the applicability of the models, it is imperative to extend the analysis to public datasets, such as the UCI heart disease data.
- Current research primarily focuses on the binary classification of heart disease cases, leaving a gap in literature that doesn't include the four popular types.
- Numerous current models depend on static learning rates during training, which may impede optimal convergence and elevate computational expenses due to ineffective training cycles.

3. Methodology

This section presents a detailed summary of the research methodologies employed, specifics of the datasets, and the hybrid optimal RNN-LSTM techniques utilized in the experiment.

3.1 Dataset details

This research utilizes two datasets for heart disease prediction. Preprocessing was conducted on the collected data by increasing the sample size. Subsequently, the Z-score is utilized to standardize all attributes to the corresponding coefficient.

3.1.1 First dataset: UCI Heart Disease Dataset

The dataset was acquired from the University of California, Irvine Machine Learning Repository [19]. Through rigorous experimentation, 14 out of the 76 features yielding the most significant results were identified. The Cleveland dataset includes 14 prominent features and 303 samples, comprising 8 categorical attributes and 6 numerical attributes. The selected patients range in age from 29 to 77 years. Key features include:

- Sex: Female patients are assigned a value of 0, and male patients are assigned a value of 1.
- Chest Pain Type: Three categories of chest pain are included, with Type 1 angina being the most common.
- Resting Blood Pressure (trestbps): Measured in mm Hg.
- Cholesterol (Chol): Serum cholesterol levels in mg/dL.
- Fasting Blood Sugar (Fbs): A value of 1 is assigned if fasting blood sugar is above 120 mg/dL; otherwise, 0.
- Resting Electrocardiogram (Restecg): Results of the resting ECG.
- Maximum Heart Rate (Thalach): The highest heart rate achieved during exercise.
- Exercise-Induced Angina (Exang): A binary variable where 0 denotes no angina and 1 denotes angina.

- ST Depression (Oldpeak): Induced by exercise relative to rest.
- Slope of Peak Exercise ST Segment: Indicates the slope during peak exercise.
- Number of Major Vessels: Visualized through fluoroscopy.
- Exercise Duration: Captured during the stress test.
- Target Variable: Classifies patients as having heart disease (1) or not (0).

3.1.2 Second dataset: ibn al-Bitar hospital and Baghdad medical city dataset (real data)

This dataset comprises 200 instances collected from real-world medical settings. It includes four categories of cardiac diseases (coronary heart disease, angina pectoris, congestive heart failure, arrhythmias) and a normal category. The multiclass classification approach employed in this study corresponds with the increasing focus on precision medicine, wherein treatments are customized for individual patients according to their distinct diagnostic profiles. The proposed MPSO-RNN-LSTM model, by utilizing this approach, offers a more thorough and clinically pertinent instrument for the diagnosis and management of cardiovascular disease [6]. The dataset distribution is as follows:

- Coronary Heart Disease: 41 instances
- Angina Pectoris: 26 instances
- Congestive Heart Failure: 16 instances
- Arrhythmias: 17 instances
- Normal: 100 instances

Key features include:

- Age: Ranging from 0 to 76 years.
- Blood Pressure (BP): Normal (0) or abnormal (1).
- Heart Rate (HR): Standardized to match the scale of other features.
- Chest Pain Type: Categorized as typical angina (1), atypical angina (2), asymptomatic angina (4), or angina-free (3).
- Cholesterol (Chol): Serum cholesterol levels.
- Fasting Blood Sugar (Fbs): Binary classification based on a threshold of 120 mg/dL.
- Electrocardiographic Results (Restecg): Normal (0) or abnormal (1).
- Exercise-Induced Angina (Exang): Binary classification.
- Family History (FH): Binary classification.
- Smoking Status: Binary classification.
- Echo Findings for Hypokinesia: Binary classification.
- Previous Angina Attack: Binary classification.

3.1.3 Feature selection rationale for real dataset

The selection of the 13 features in Dataset 2 was based on a combination of medical relevance, statistical significance, and their proven effectiveness in prior heart disease prediction studies. Fig. 1 illustrates the feature representation of the second dataset, highlighting the distribution of key attributes such as age, blood pressure, and heart rate, which were standardized to ensure consistency with other features. Below is the rationale for including or excluding specific features:

- Age: Age is a well-established risk factor for cardiovascular diseases, as the likelihood of heart disease increases with age. It was included due to its strong correlation with heart disease prevalence.
- Sex: Gender differences play a significant role in heart disease risk and manifestation. Men and women may exhibit different symptoms or risk profiles. This feature was included in accounting for gender-based variations.
- Chest Pain Type: Chest pain is one of the most common symptoms of heart disease. The four categories (typical angina, atypical angina, asymptomatic angina, and angina-free) were included to capture the nuanced differences in symptom presentation.
- Blood Pressure (BP): High blood pressure is a major risk factor for heart disease. It was included because of its direct impact on cardiovascular health.
- Cholesterol (Chol): Elevated cholesterol levels are strongly associated with the development of coronary artery disease. This feature was included to account for lipid profile abnormalities.

- Fasting Blood Sugar (Fbs): High fasting blood sugar levels are indicative of diabetes, which is a significant risk factor for heart disease. This feature was included to capture the impact of metabolic conditions.
- Resting Electrocardiogram (Restecg): ECG results provide critical insights into heart function and abnormalities. This feature was included due to its diagnostic importance.
- Maximum Heart Rate (Thalach): Heart rate during exercise is a key indicator of cardiovascular fitness and stress on the heart. It was included to assess exercise-induced cardiac responses.
- Exercise-Induced Angina (Exang): The presence or absence of angina during exercise is a strong indicator of coronary artery disease. This feature was included to capture exercise-related symptoms.
- ST Depression (Oldpeak): ST segment depression during exercise is a marker of myocardial ischemia. It was included due to its diagnostic significance in detecting heart disease.
- Slope of Peak Exercise ST Segment: This feature provides additional information about the heart's response to stress and was included to enhance the model's ability to detect abnormalities.
- Number of Major Vessels: The number of major vessels affected by blockages is a direct indicator of coronary artery disease severity. This feature was included to quantify the extent of vascular involvement.
- Family History (FH): A family history of heart disease is a significant risk factor. This feature was included on account of genetic predispositions.

3.2 Deep Learning Architecture

Artificial neural networks (ANN) are a crucial component of the DL paradigm, a subset of ML techniques. DL networks, also known as deep networks, are characterized by their multi-layer architecture. Networks such as CNN, RNN, DNN, and Deep Belief Networks (DBN) are instances of DL systems. The structure of RNN as well as LSTM will be discussed in more detail in the following paragraphs.

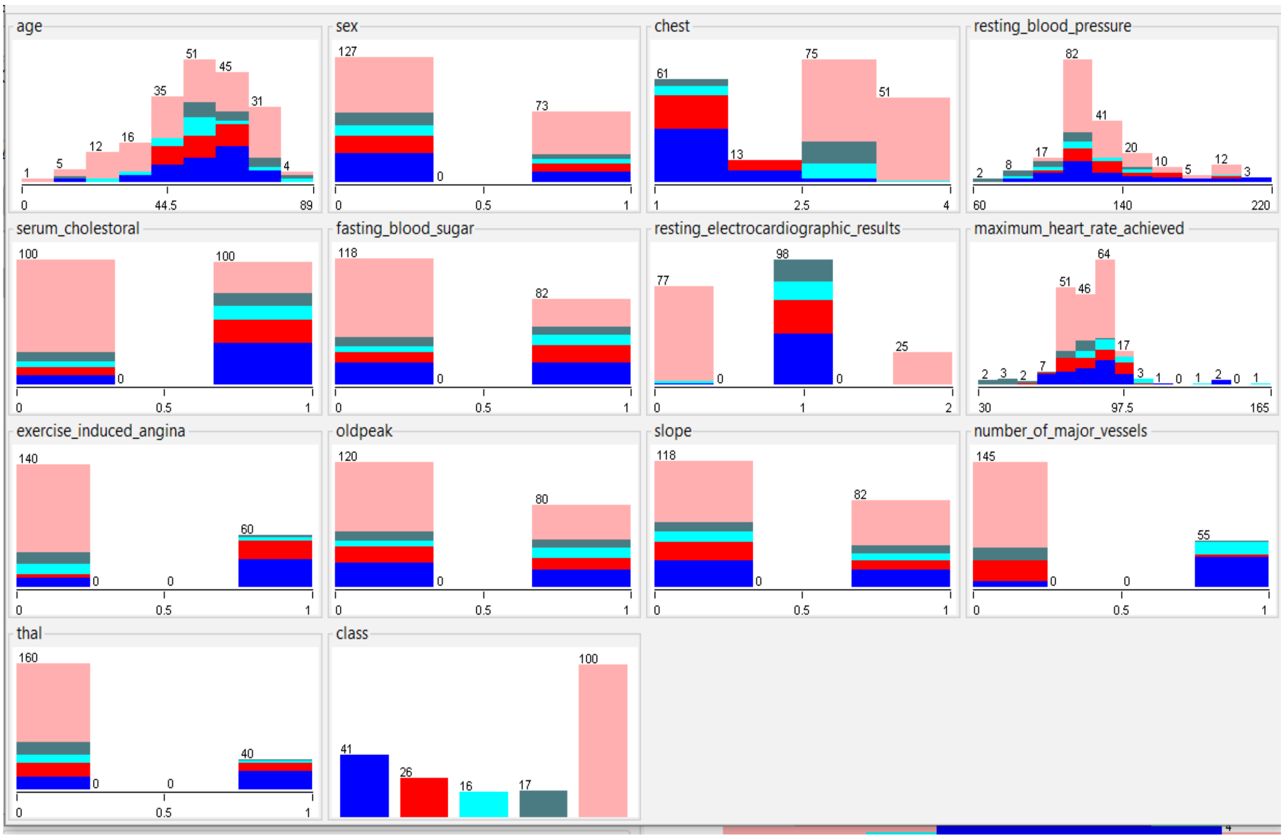

Fig. 1. Feature Representation of Medical Dataset2 for Cardiovascular Analysis.

3.2.1 Recurrent neural network

Recurrent neural networks are an ANN design that attempts to reproduce the network architecture of real cells. Signal transmission to adjacent cells or nodes is possible through NN links, just as it is through junctions in a real brain [25]. The artificial cell shares the processed signal with different nodes or cells in the network. Assigning scores to cells and links is a common way to modify the process of learning. By adjusting these amounts, one can change the amount of signal as it moves from the inputting layers to the resultant layers. An ANN comprises intermediate hidden layers positioned between the input and output layers. A RNN must include a minimum of three hidden layers, consisting of input units, output units, and hidden units. The hidden units conduct computations through weight adjustments to generate outputs [26, 27]. The RNN model exhibits a unidirectional flow of information from input units to hidden units, along with a directional loop that assesses errors in subsequent hidden layers compared to the previous ones. It then modifies the weights between the hidden layers accordingly [28]. Fig. 2 illustrates a basic RNN structure with two hidden layers.

An RNN is an extension of conventional feed-forward neural networks (FFNNs). Unlike FFNNs, which transmit information in a unidirectional manner from input nodes through hidden nodes to output nodes without any cycles or loops, RNNs introduce cycles in the network. Hidden layers are optional in FFNNs. The input vector sequence is denoted by $\mathcal{X}$, the hidden matrix sequence by H, and the output matrix sequence by $\mathcal{Y}$. The input matrix sequence is expressed as $=(\mathcal{X}_1, \mathcal{X}_2, \ldots\ldots, \mathcal{X}_k)$. A conventional RNN computes the hidden matrix sequence $\mathrm{H} = (\mathrm{H}_{m1}, \mathrm{H}_{m2}, \ldots\ldots, \mathrm{H}_{km})$ and the output matrix sequence $\mathcal{Y} = (\mathcal{Y}_1, \mathcal{Y}_2, \ldots\ldots, \mathcal{Y}_k)$ for each time step t from 1 to k in the following [28] :

$$\mathrm{H}_k = \sigma(W_{\mathcal{X}\mathrm{H}}\mathcal{X}_t + W_{\mathrm{HH}}\mathrm{H}_{t-1} + B_{\mathrm{H}}) \tag{1}$$

$$\mathcal{Y}_s = W_{\mathrm{H}\mathcal{Y}}\mathrm{H}_t + B_{\mathcal{Y}} \tag{2}$$

where B is a bias term, W is a weight matrix, and σ function is a activation function. Equation (1) represents the output of the hidden layer at time intervals t as H_t and the previous hidden layer's output as H_{t-1}. RNN utilizes gradient-based techniques for learning time sequences, such as back-propagation through time (BPTT) or immediate time recurrent learning (RTRL) [28]. During BPTT, the network is expanded into FFNN. Each sequence is processed to create the FFNN by training the model with the training data and saving the output error gradient for each step. BPTT utilizes the conventional backpropagation technique to train each FFNN and updates the weights by summing the variances

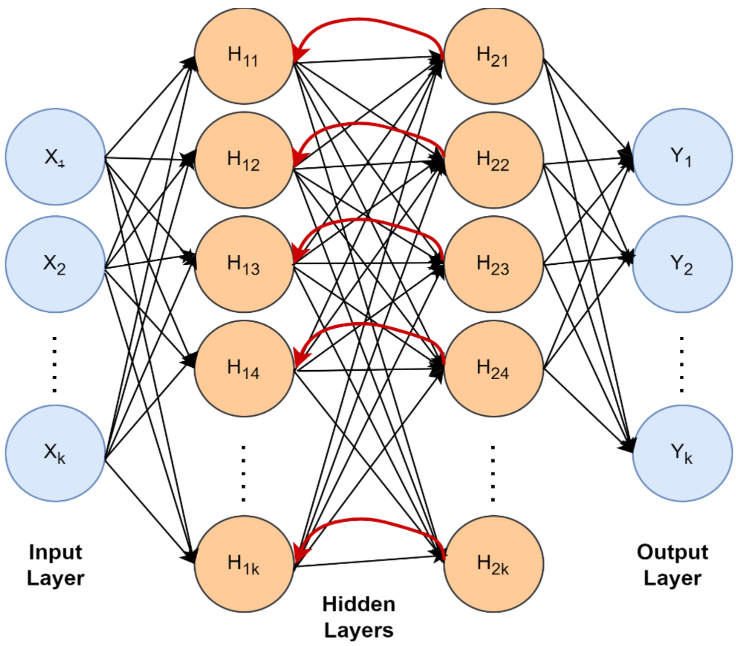

Fig. 2. Recurrent Neural Network Architecture with Hidden States and Input-Output Pathways.

obtained for weights in all layers of the network. Patterns with over 5 to10 time increments are difficult for conventional RNN to predict. The vanishing gradient issue can occur in RNN when weight updates are performed using gradient-based learning techniques. Weights are adjusted in each training iteration based on an updated proportion of the partial derivative of the error function. At times, the gradient may be small. The error signals can either escalate significantly or disappear, preventing the weight from altering its value. The disappearing error messages could lead to fluctuations in weight. Learning is hindered by a diminishing mistake, resulting in either a prolonged duration or complete failure [29]. RNN are suitable for supervised classification learning, but they pose challenges in training due to issues with vanishing and exploding gradients. These problems arise from inadequately assigned weights, which can be set to extremely high or low values. To mitigate these challenges, an LSTM model using forget gates is frequently combined with an RNN. RNNs excel in addressing challenges related to time series sequence prediction. Researchers have demonstrated in [21, 29] that certain LSTM-RNN implementations exhibit significant effectiveness in intrusion detection.

3.2.2 Long Short-Term Memory

Long Short-Term Memory is a type of RNN designed for analyzing sequence data and time series issues. The proposal was made in 1997 and acquired rapid acceptance following the resolution of the vanishing gradient issue by RNN [30]. LSTM was developed to overcome the challenge that conventional RNN face in handling long-term dependencies. During the processing of long sequences by a standard RNN, the gradient either vanishes or explodes, which hinders the ability to capture long-distance relationships. LSTM solves this problem by incorporating a gating mechanism [31]. Fig. 3 illustrates a system consisting of a memory unit, a forgetting gate (f_t), an input gate (I_t), and an output gate (O_t), current input (X_t), output of last LSTM unit (H_{t-1}), new update memory (C_t), current output (Y_t), sigmoid layer ($\boldsymbol{\sigma}$), tanh layer (Tanh), bias (b), and memory from last LSTM unit (C_{t-1}). The input gate regulates the amount of new information added to the unit state, the forgetting gate manages whether it will be forgotten at each instant, and the output gate decides whether information will be output at each moment [32].

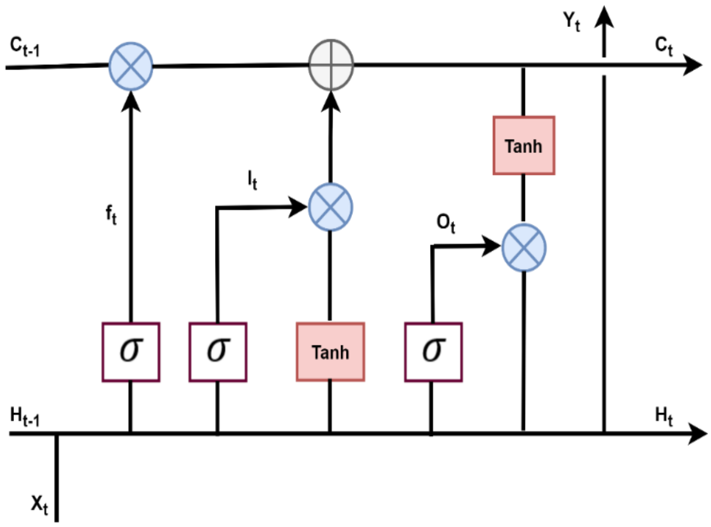

Fig. 3. Structural Diagram of the Long Short-Term Memory Network Architecture.

3.2.3 Mutation particle swarm optimization

Particle swarm optimization is an evolutionary technique that harnesses a group of potential solutions to find the optimal solution for a given problem. Proposed in 1995 by Russell Eberhart, an electrical engineer, and James Kennedy, a sociopsychologist [14], PSO utilizes basic agents known as particles. Each particle represents a potential solution, characterized by both a position (solution vector) and a velocity. Additionally, each particle maintains a memory that allows it to recall its optimal performances in terms of both position and significance, as well as the best performance achieved by neighboring particles, known as its group informant or neighborhood. The PSO is primarily governed by two fundamental updating equations for the position of a particle j. The first equation updates the velocity ($\mathcal{V}$) and is expressed as follows:

$$\mathcal{V}_j(L+1) = \mathcal{W} \times \mathcal{V}_j(L) + \mathcal{C}_1\emptyset_1\left(P_{jbest}(L) - P_j(L)\right) + \mathcal{C}_2\emptyset_2\left(\mathfrak{S}_{best}(L) - P_j(L)\right) \tag{3}$$

The second equation involves updating the particle's position after mutation and is expressed as follows:

$$P_j(L+1) = (\in\ P_j(L)\ M_{rate}) + \mathcal{V}_j(L+1) \tag{4}$$

The variable '$\mathcal{W}$' denotes the inertia weight factor, which linearly varies from 0 to 1.' $\mathcal{C}_1$'and '$\mathcal{C}_2$' represent factors associated with cognitive and social acceleration, respectively. '$\emptyset_1$' and '$\emptyset_2$' represent random integers uniformly distributed within the range of 0 to 1. In Equation (3), the subsequent velocity $\mathcal{V}_j(L+1)$ of particle j is determined, and in Equation (4), the subsequent position $P_j(L+1)$ is updated after mutation applied, '$\in$' is random vector in the range 0 to 1. Mutation introduces a random factor to the particle placements, encouraging more exploration within the search space by mutation rate denoted by 'M_{rate}'. Essentially, particle position P_j represents a potential solution to an optimization issue. The objective function (accuracy function) is evaluated at each iteration using the position vector $P_j(L)$. The position vector representing the highest fitness level is referred to as P_{best}, whereas the best solution among all particles in the population is termed $\mathfrak{S}_{best}$. The success of finding the global optimum in the MPSO method relies heavily on the initial values of control parameters like $\mathcal{W}$, $\mathcal{C}_1$, $\mathcal{C}_2$, $\emptyset_1$, $\emptyset_2$, $\in$, M_{rate} , swarm size (N), and the maximum iteration number.

The MPSO algorithm involves several critical parameters that significantly influence its performance. The mutation rate (M_{rate}) determines the probability of introducing random changes to the particles' positions, balancing exploration and exploitation. A value of M_{rate}= 0.1 was selected based on preliminary experiments, as it provided a good trade-off between escaping local optima and maintaining convergence. The population size was set to 20 to ensure sufficient diversity without excessive computational cost. The inertia weight ($\mathcal{W}$ =0.9) and acceleration coefficients ($\mathcal{C}_1$=1.5, $\mathcal{C}_2$=1.5) were chosen to balance individual and social learning, ensuring effective exploration and exploitation.

3.2.4 Optimum deep neural network techniques used

This study presents Optimum RNN-LSTM, an innovative optimal DL technique for heart disease prediction. The objective of this methodology is to efficiently tackle the intrinsic difficulties linked to the modelling of sequential data through the integration of LSTM components into RNNs, as shown in Fig. 4. The main goal of the combination is to enhance consecutive modelling of data using an improved PSO method. Unfortunately, the issue of disappearing gradients makes it difficult for conventional RNNs to properly capture dependencies over time. As a result, their capacity to handle long processes is diminished. The LSTM network, on the other hand, uses a novel design for architecture that includes storage cells and gated processes. The use of this design of architecture allows for chosen data storage, retrieval, and updates, guaranteeing that the setting is preserved for a longer duration of time. This property of models based on LSTM makes them very good at time-series forecasting and NLP, two jobs that demand understanding of chronological interdependencies.

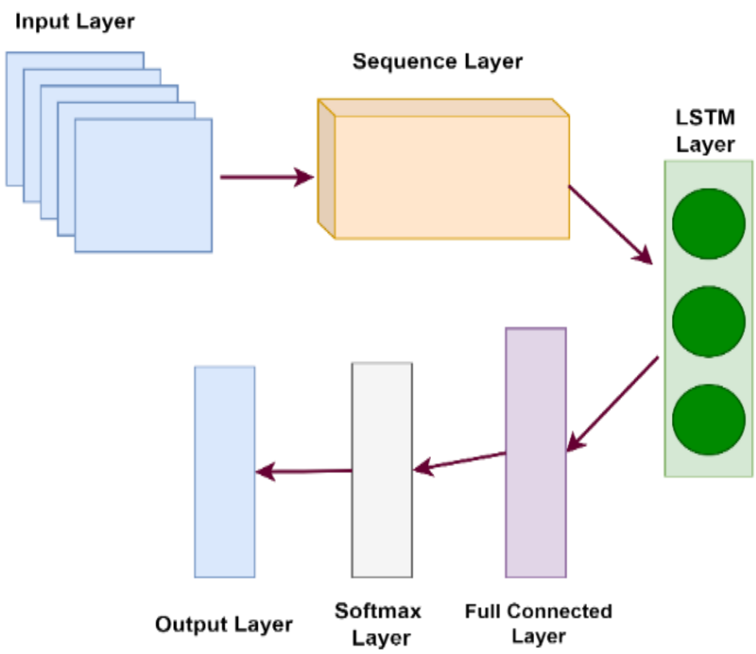

Fig. 4. Structural Diagram of the RNN with Long Short-Term Memory Architecture.

Furthermore, LSTM gated techniques help alleviate the decreasing gradient issue, which in turn encourages more reliable and efficient learning. The modular design of LSTMs also makes them easy to include into other RNN topologies. Because of this adaptability, modelling builders can modify networks to meet the needs of different data flow employment. Fig. 5 is an extensive graphical representation of the framework for discussion. Then, the Optimum RNN-LSTM network was trained using an Improved PSO technique to tune the parameters that constitute the hyperparameters. To maximize the RNN algorithm's efficiency, the technique adjusted the learning rate considering the range of parameters and mutation ratio. Because of this adjustment, the RNN converges faster, generalizes better, and performs better generally. By keeping the learning rate equilibrium, which avoids overfitting and underfitting in the model using LSTM, we aim to obtain the optimum precision on the cardiovascular disease data. An interesting approach is to modify the learning rate of models generated by DL using mutation inside PSO. The main goal of this approach is to improve the area of search exploration by using probabilistic disturbances, which could lead to improved outcomes, especially for not convex optimization issues like tuning hyper parameters. To find superior approaches to prevent local minimum, the technique of optimization introduces diversity.

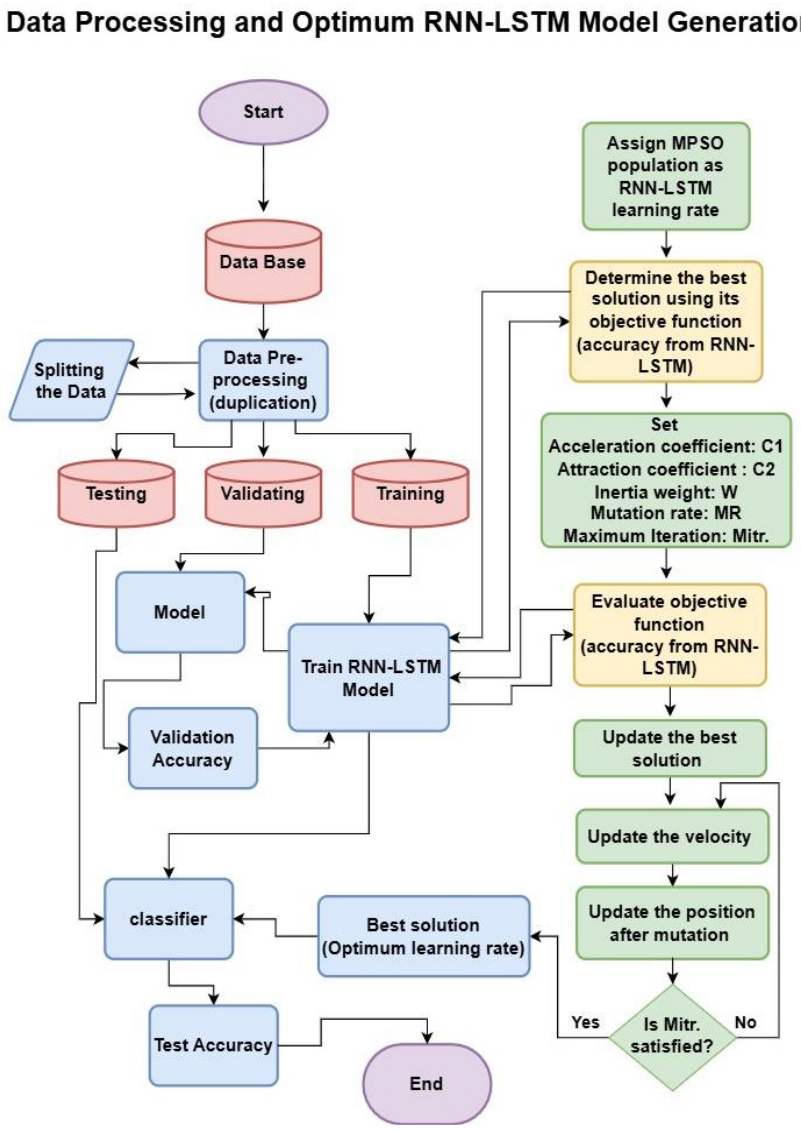

Fig. 5. Flowchart of the Proposed Methodology for Data Processing and Optimum RNN-LSTM Model Generation Using MPSO.

4. Simulation Results and Discussion

The simulations are executed on a Windows 10 Pro 64-bit Core i7 computer with 16 GB of RAM utilizing the MATLAB 2024a program. The evaluation of the proposed Optimal Hybrid RNN and LSTM architecture for the prediction of cardiac disease is detailed in this section. Conducting a thorough investigation of the parameter space is imperative due to the intricacy and numerous parameters associated with DL models. To ascertain the most effective configuration, an exhaustive series of experiments utilizing hybrid RNN and LSTM networks were executed. The subsequent pseudocode in Table 1 succinctly represents the fundamental elements of the experimental procedure:

Table 1. The proposed of proposed algorithm.

Pseudocode for the Optimum Hybrid RNN‑LSTM Algorithm
Input: Data set: UCI Dataset /Real Dataset. **Output:** Predict the person's normal and four types of heart disease. **Step1: Start.** **Step2:** Load dataset. **Step3:** Split to features and labels. **Step4:** Convert labels to categorical. **Step5:** Split the dataset into (training, validation, and test) sets. **Step6:** Normalize the features. **Step7:** Convert split datasets to arrays. **Step8:** Procedure RNN-LSTM model. # Initialization/ hidden units, no. of classes, max of epochs, batch size/. # Sequence input with 13 dimensions. # LSTM with 200 hidden units. # Fully connected layer with 5 layers. # SoftMax layer with SoftMax function. # Classification layer with cross entropy loss function. **Step9:** Run improved PSO algorithm to tunning RNN-LSTM learning rate value. # Initialization/ population as RNN-LSTM learning rate value, dimension, lower band, upper band, Max iteration, mutation Rate ($\boldsymbol{M_{rate}}$), acceleration coefficient, attraction coefficient, inertia weight/. # Evaluate the objective function as accuracy from RNN-LSTM model. # Apply PSO procedure. # Update position after mutation by eq. 4. # Return the best solution as a RNN-LSTM learning rate value. **Step10:** Model evaluation. # Predict Accuracy, Precision and Recall. **Step11: End.**

4.1 Performance evaluation

Evaluation metrics measure the efficacy of a model in addressing a certain problem description. Diverse assessment metrics are utilized based on the characteristics of the data and the specific problem under examination. Equations (5)-(11) encapsulate the performance criteria employed to assess the experimental findings of the models discussed in this work [33], [34], [35]. These metrics employ the subsequent foundational measures:

- A true positive (TP) indicates that the patient possesses cardiac disease, and the model accurately forecasts this condition.
- A true negative (TN) indicates that the patient is free of heart disease, and the model correctly identifies this condition.
- False positive (FP) signify that the patient is free of cardiac disease, although the model erroneously forecasts a positive diagnosis for the condition.
- A false negative (FN) denotes a scenario in which the patient possesses heart disease; however, the model erroneously forecasts a negative outcome.

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \tag{5}$$

$$Precision = \frac{TP}{TP+FP} \tag{6}$$

$$Sensitivity = \frac{TP}{TP+FN} \tag{7}$$

$$Specificity = \frac{TN}{TN+FP} \tag{8}$$

$$NPV = \frac{TN}{TN+FN} \tag{9}$$

$$MCC = \frac{(TP \times TN) - (FP \times FN)}{\sqrt{(TP+FP)(TP+FN)(TN+FP)(TN+FN)}} \tag{10}$$

$$F1\ score = \frac{2TP}{2TP+FP+FN} \tag{11}$$

4.2 Performance analysis

Table 5 illustrates the outcomes of the experiment conducted on the proposed MPSO-RNN-LSTM model, which was applied to the cardiovascular disease dataset to ascertain the presence of heart disease following hyperparameter optimization by PSO. Models were trained on data divided in a 60:20:20 ratio, achieving an accuracy of 98.36%, with high specificity, precision, and F1-score of 98.21%, 98.48%, and 98.48%, respectively, for data1. The accuracy for data2 is 98.75%, accompanied by high specificity, precision, and F1-score of 100%, 100%, and 96.97%, respectively.

Table 2. The classification benchmark metrics for proposed method.

Metric	Accuracy	Precision	Sensitivity	Specificity	NPV	MCC	F1 Score	Data
MPSO RNN-LSTM (Proposed)	98.36%	98.48%	98.48%	98.21%	98.21%	96.70%	98.48%	Data1
MPSO RNN-LSTM (Proposed)	98.75%	100%	94.12%	100%	98.44%	96.25%	96.97%	Data2

The performance of a binary classifier is illustrated by the receiver operating characteristic (ROC) curve. It illustrates the true positive rate in relation to the false positive rate across several classification criteria. The area under the ROC curve (AUC) is a scalar metric that quantifies the classifier's specificity and sensitivity, hence indicating its overall effectiveness. Fig. 6 and Fig. 7 illustrate that all models demonstrate a high AUC of 0.98 for UCI data and 0.97 for real data.

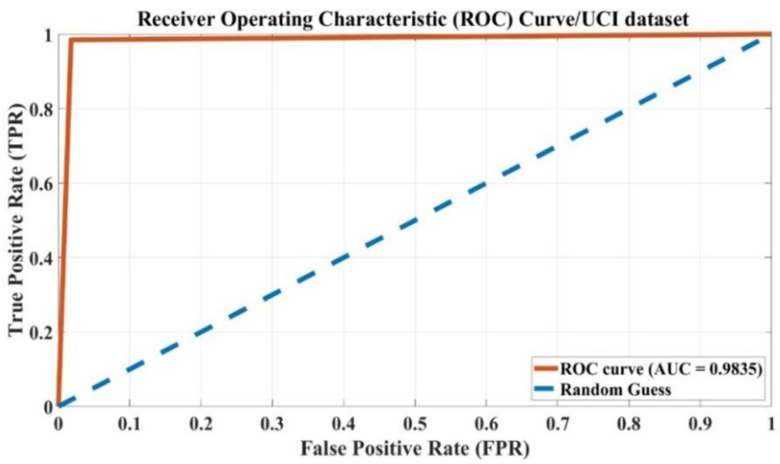

Fig. 6. Receiver Operating Characteristic Curve for Model Performance Evaluation on the UCI Dataset.

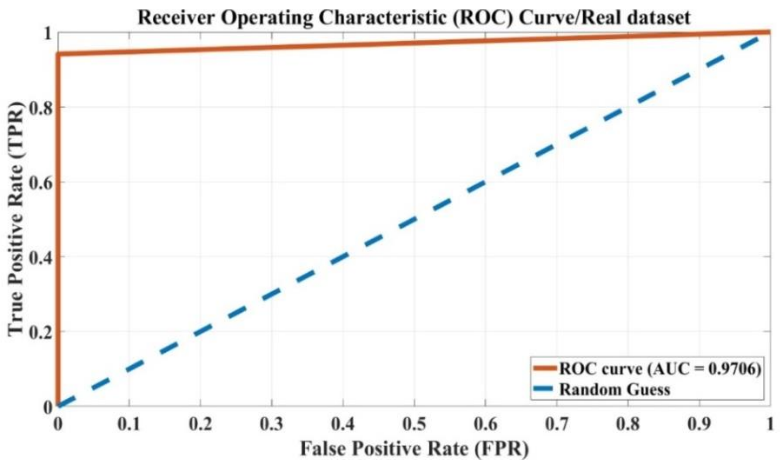

Fig. 7. Receiver Operating Characteristic Curve for Model Performance Evaluation on the Real Dataset.

Fig. 6 and 7 demonstrate the application of the confusion matrix in evaluating the efficacy of a model for classification. Fig. 6 depicts the anticipated values of True Positives (TP), False Positives (FP), True Negatives (TN), and False Negatives (FN) for the proposed MPSO-RNN-LSTM model. Each member in this confusion matrix denotes the count of instances for both the actual and expected classes corresponding to a specific set of labels. The matrix contains 65 true positives (TP) for heart disease classifications, 1 false positive (FP) labeled as "disease," 1 false negative (FN) categorized as "no disease," and 55 true negatives (TN) for various "heart disease" categories in data1. Fig. 7 depicts the projected values with optimal accuracy for three diagnostic categories in data2.

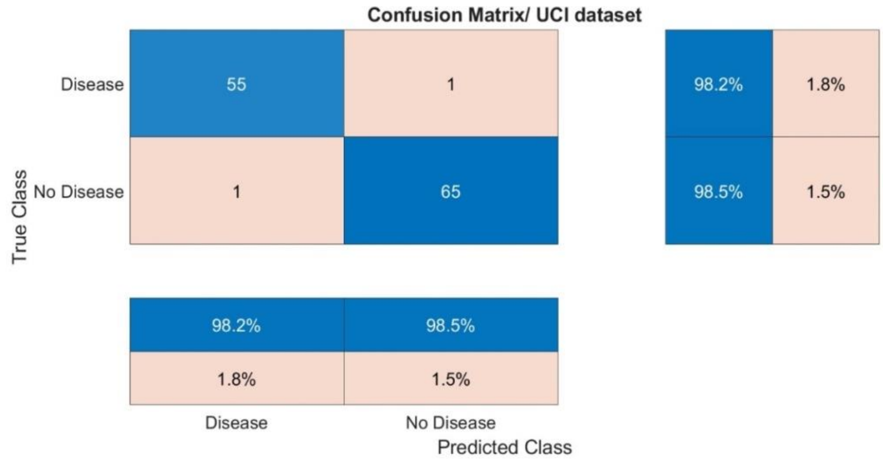

Fig. 8. Confusion Matrix for Classification Performance on the UCI Dataset (dataset1).

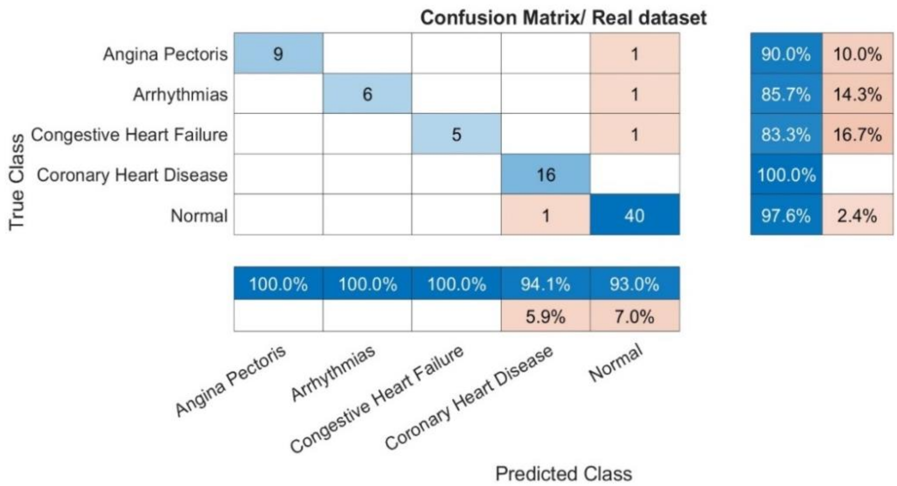

Fig. 9. Confusion Matrix for Classification Performance on the Real Dataset (dataset2).

The ablation study on Data1 and Data2 assesses the performance enhancements of the baseline RNN-LSTM model relative to the suggested MPSO-RNN-LSTM model, as shown in Table 3, Table 4 and Fig. 10. For Data1, the baseline RNN-LSTM model achieved an accuracy of 85.95%, precision of 86.06%, sensitivity of 86.06%, and specificity of 85.88%. In contrast, the proposed MPSO-RNN-LSTM model achieved an accuracy of 98.36%, precision of 98.48%, sensitivity of 98.48%, and specificity of 98.21%. These results highlight the substantial improvements in predictive performance, particularly in precision and sensitivity, which are critical for medical diagnosis. For Data2, the baseline RNN-LSTM model exhibited suboptimal performance, with an accuracy of 75.00%, precision of 66.84%, sensitivity of 93.60%, and specificity of 65.94%.

Table 3. Ablation study of datasets evaluation models for data1.

Model	Ablation Study		Performance Metrics			
	No-Optimization	Mutation-Optimization	Accuracy	Precision	Sensitivity	Specificity
Baseline Model (RNN-LSTM) [28]	✓		85.95%	86.06%	86.06%	85.88%
MPSO-RNN-LSTM (Proposed)		✓	**98.36%**	**98.48%**	**98.48%**	**98.21%**

Table 4. Ablation study of datasets evaluation models for data2.

Model	Ablation Study		Performance Metrics			
	No-Optimization	Mutation-Optimization	Accuracy	Precision	Sensitivity	Specificity
Baseline Model (RNN-LSTM) [28]	✓		75%	66.84%	93.6%	65.94%
MPSO-RNN-LSTM (Proposed)		✓	**98.75%**	**100%**	**94.12%**	**100%**

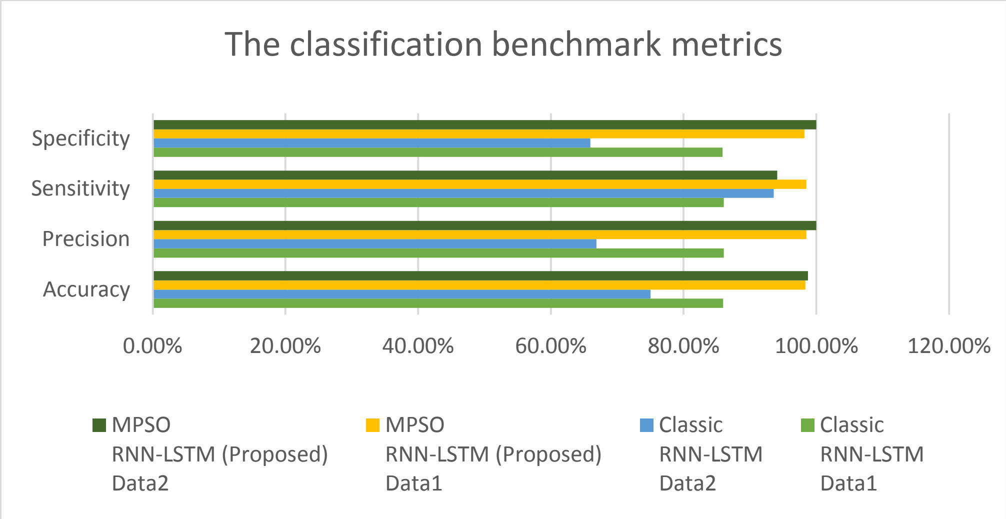

Fig. 10. Classification benchmark metrics of the proposed methodology in ablation study.

Fig. 11 illustrates the training progress graph of the learning network for UCI Dataset 1. The graph illustrates the trends in model accuracy and loss across 100 epochs, with iterations reaching 1700 because of a greater number of iterations per epoch (17). The training accuracy curve (solid blue line) exhibits a gradual increase, stabilizing around 100%, whereas the validation accuracy (dashed black line) attains a final value of 96.45%, suggesting robust generalization. The training and validation loss curves exhibit a consistent decline throughout the iterations, with the training loss (solid orange line) stabilizing at a low level. The validation loss closely matches the training loss, indicating minimal overfitting and effective model convergence. The training duration was 21 seconds on a single CPU, utilizing a learning rate of 0.001, and a total processing time of approximately 4 minutes, demonstrating efficient resource utilization. The model demonstrates effective learning and strong performance, attaining high accuracy and stable loss metrics in both training and validation sets. Fig. 12 illustrates the training progress of the network for Real-time Dataset 2, detailing the model's learning behavior across 100 epochs, with accuracy and loss curves presented for both training and validation set.

The training accuracy, indicated by the solid blue line, shows a steady increase, stabilizing close to 100%, signifying effective learning. The validation accuracy, indicated by the black dashed line, shows a consistent improvement and stabilizes at 97%, demonstrating robust generalization with limited overfitting. The loss curves provide additional evidence for these findings. The training loss, represented by the solid orange line, exhibits a smooth decrease over iterations and stabilizes at a low value, indicating effective model convergence. The validation loss exhibits a comparable trend, closely mirroring the training loss during the entire process. The correspondence between the training and validation metrics underscores the model's robustness and stability. The training was completed in 17 seconds on a single CPU with a constant learning rate of 0.001 and a total processing time of approximately 3 minutes, highlighting the efficiency of the configuration. The high validation accuracy and consistent loss values demonstrate that the model is well-trained, generalizes effectively to new data, and maintains low error rates.

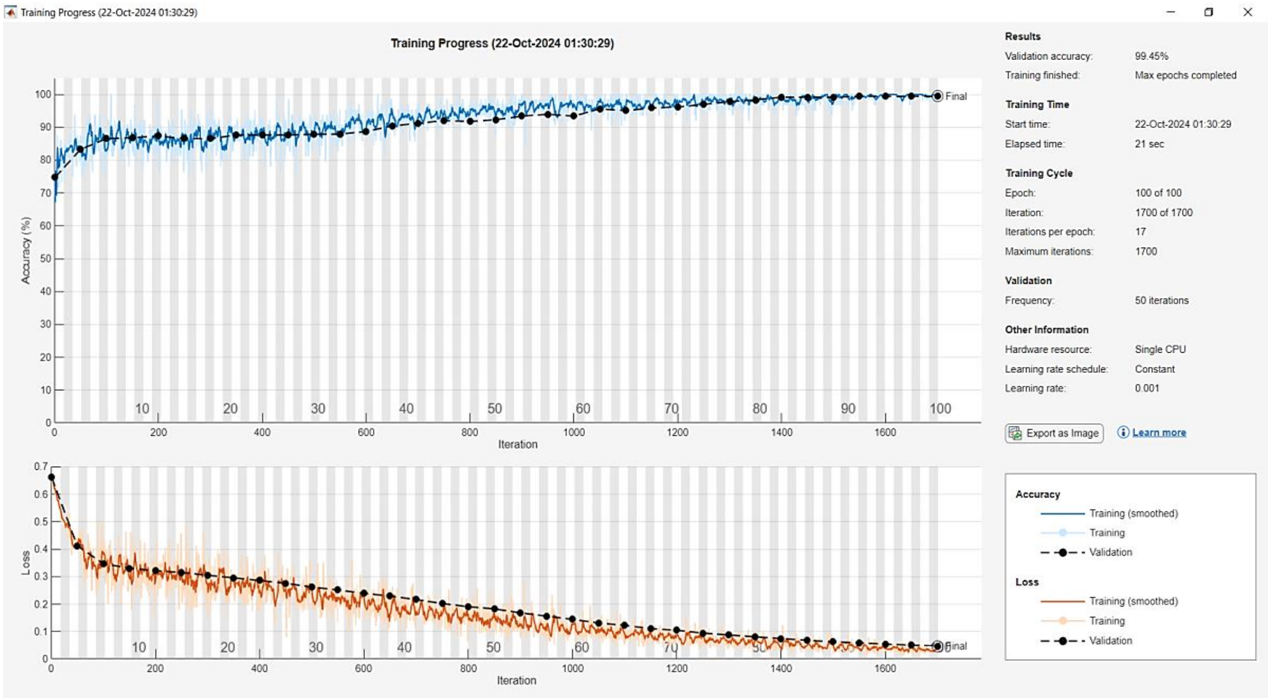

Fig. 11. Training Progress Graph for Dataset 1 - Model Performance Over Epochs.

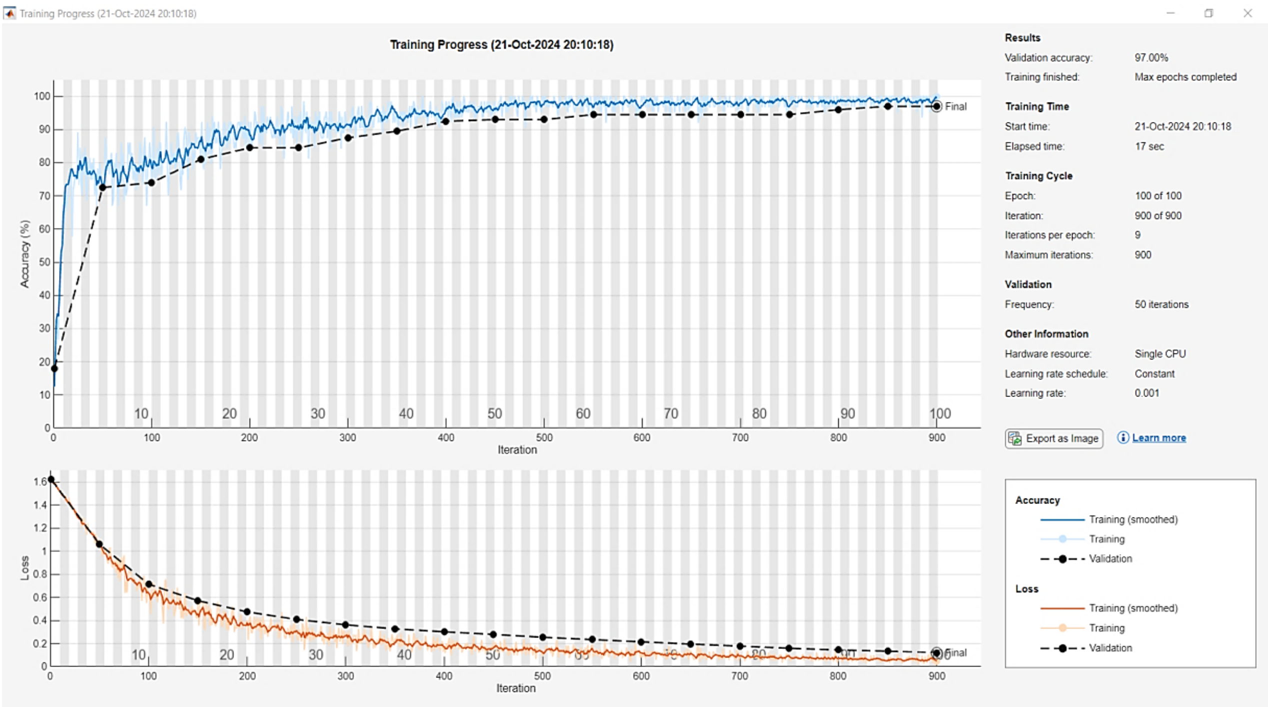

Fig. 12. Training Progress Graph for Dataset 2 - Model Performance Over Epochs.

4.3 *Comparative with existing methods*

The comparative analysis of heart disease prediction proposed method for Dataset 1 is illustrated visually in Fig. 13. Table 5 details the methodologies, and this evaluation highlights the various levels of accuracy that each technique achieved. An obvious contrast of the methods' results is made possible by using separate bars to indicate their accuracy. Fig. 14 shows the results of a comparison of Dataset 2 for approaches used to predict cardiac events. Table 4 provides the results of the accuracy evaluations of the various approaches. The graphical representation of bars makes it easy to compare the predicted effectiveness of different heart disease approaches for Dataset 2. Forecasting heart disease over various datasets has been the subject of numerous research that has tested various techniques. On Dataset 2, Al-Taie et al. [7] achieved accuracy rates between 83% and 94.5 percent using a variety of classification techniques, such as MLP, Random Forest, SMO, and Bayes Net. Similarly, Saleh et al. [6] assessed J48, Naïve Bayes, REPTREE, and 1BK on Dataset 2, reporting accuracies between 85% and 94.5%. Dileep et al. [19] evaluated a plethora of techniques on Dataset 1, spanning DNN, Regression tree, SVM, Logistic regression, KNN, gated recurrent unit, CNN, Ensemble, and DBN, with accuracy ranging from 75.40% to 94.78%. Kumar et al. [36] achieved an accuracy of 89% using CNN+LSTM on Dataset 1, while Safa et al. [18] applied DSTV-FAM to Dataset 1, achieving a remarkable accuracy of 97%. Naresh et al. [37] implemented Improved ANN on Dataset 1, resulting in an accuracy of 96.6%.

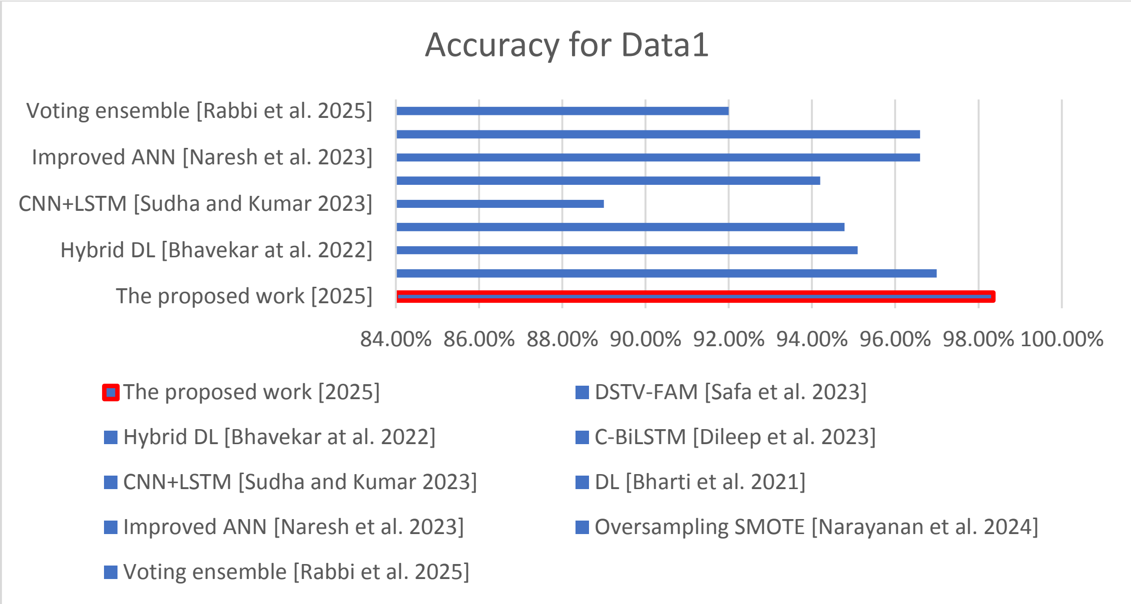

Fig. 13. Comparing the suggested method's accuracy to that of other studies that have used equivalent datasets1.

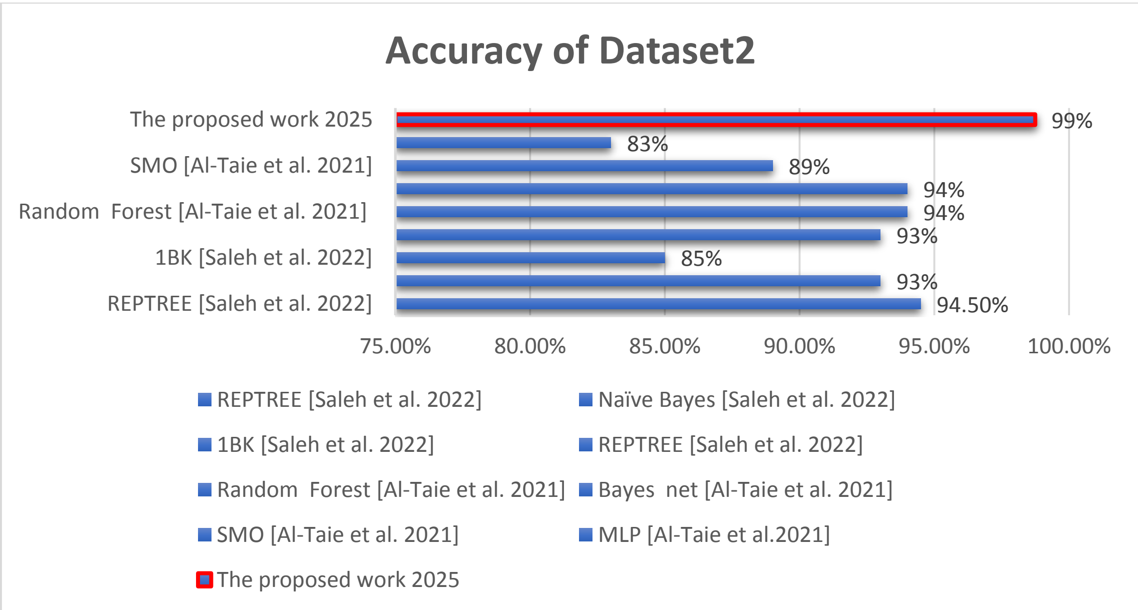

Fig. 14. Comparing the suggested method's accuracy to that of other studies that have used equivalent datasets2.

Furthermore, Bharti et al. [38] utilized DL, K-neighbors, logistic regression, random forest, and decision tree on Dataset 1, with accuracies ranging from 80.3% to 94.2%. Beyond that, combined DL [17] attained 95.1%. and recently, Narayanan et al. [20] employed ML approaches utilizing the Synthetic Minority Oversampling Technique (SMOTE) for oversampling, achieving a maximum accuracy of 96.6%, sensitivity of 90%, and specificity and precision of 100% through the Random Forest method. Rabbi et al. [15] demonstrate that the VEMLA\achieved 92% accuracy on the Cleveland Heart Disease dataset, while the bagging ensemble machine learning algorithm (BEMLA) achieved 97% accuracy on both the Framingham Heart Disease and Indicators of Heart Disease (2020) datasets. Contrarily, the proposed study (2025) utilized Optimal RNN-LSTM on Datasets 1 and 2, attaining outstanding accuracy levels of 98.36%, 98.75%, respectively. This result highlights how well our suggested technique performs in consistently estimating cardiovascular disease over different datasets.

Table 5. provides an assessment of the cardiovascular disease prediction system taking the most current findings into account.

Author [ref]/Year	**Datasets**	**Methods**	**Accuracy**
Safa et al. [18]/2021	Dataset1	DSTV-FAM	97%
Bharti et. al. [36]/2021	Dataset1	Logistic regression K neighbors SVM Random forest Decision tree DL	83.3% 84.8% 83.2% 80.3% 82.3% 94.2%
Bhavekar et al. [17] /2022	Dataset1	Hybrid DL	95.1%
Naresh et al. [35]/2023	Dataset1	Improved ANN	96.6%
Dileep et al. [19]/2023	Dataset1	Regression tree SVM Logistic regression KNN Gated recurrent unit CNN Ensemble DBN DNN C -BiLSTM	75.40% 78.79% 81.38% 82.80% 81.46% 85% 88.54% 90% 91.24% 94.78%
Kumar et al. [34]/2023	Dataset1	CNN+LSTM	89%
Mohapatra et al. [16]/2023	Dataset1	MLP	92%
Narayanan et al. [20]/2024	Dataset1	Oversampling SMOTE	96.6%
Rabbi et al. [15]/2025	Dataset1	Voting ensemble machine learning algorithm (VEMLA)	92%
Proposed study/ 2025	**Dataset1**	**MPSO- RNN-LSTM**	**98.36%**
Al-Taie et al. [7]/ 2021	Dataset2	Random Forest Multilayer Perceptron Sequential Minimal Optimization Bayes Net	94% 83% 89% 94.5%
Saleh et al. [6]/2022	Dataset2	J48 Naïve Bayes REPTREE 1BK	94.5% 93% 93% 85%
Proposed study/ 2025	**Dataset2**	**MPSO- RNN-LSTM**	**98.75%**

5. Conclusion

Cardiovascular disease represents a significant global health challenge, necessitating the development of accurate and efficient predictive models to mitigate its impact. This study introduces an optimal learning technique specifically designed for predicting heart disease, aiming to enhance predictive performance and support early diagnosis and risk assessment. By improving the accuracy of heart disease prediction, the proposed methodology seeks to facilitate superior patient care and reduce the incidence of heart-related complications. The study proposes a model-based optimal RNN-LSTM as a robust method for the effective prediction of heart diseases. The suggested MPSO-RNN-LSTM model utilized a recognized open-access dataset and many cross-validation procedures to assess the methodology and quantify the overall accuracy of the heart disease diagnosis system. In comparison to baseline algorithms and state-of-the-art algorithms, the performance of MPSO-RNN-LSTM was significantly superior, achieving 98.36% accuracy, 98.48% sensitivity, 98.21% specificity, 98.48% precision, a 98.48% F1 score, and a 98% AUC for data1, as well as 98.75% accuracy, 94.12% sensitivity, 100% specificity, 95.00% precision, a 96.97% F1 score, and a 97% AUC for data2. Moreover, the study illustrated that the proposed system is adjustable by a learning rate optimization via the PSO method. This research has substantially advanced the domain of machine learning and deep learning prediction applications by presenting novel insights and methodologies.

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Authors’ Profiles

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