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A Machine Learning Approach for Accurate Diagnosis of Heart Disease: A Comparative Study

Hawkar Saeed Ezat [a], Ari Abdulla Rahim [b], Zana Azeez Kakarash [c]
Govar Abubakr Omar [d], Ahmed AL-SLEMANI [e,*]

[a] Kurdistan Institution for Strategic Studies and Scientific Research, Sulaimani, Iraq
[b] University of Halabja, Department of Physics, College of Science, Halabja, Iraq
[c] Kurdistan Technical Institute, Department of Information Technology, Sulaymaniyah, Iraq
[d] University College of Goizha, Department of Information Technology, Sulaymaniyah, Iraq
[e] Kalar Private Technical Institute, Department of Information Technology, Sulaymaniyah, Iraq

* Corresponding author

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ABSTRACT

Heart diseases are leading determinants of worldwide morbidity indices, underscoring the critical importance of accurate diagnostic assessments in facilitating timely therapeutic interventions and optimizing clinical outcomes. Traditional methods of diagnosis rely on clinical evaluations and laboratory tests, which may be subjective and prone to errors. In the present study, we suggest implementing a machine learning methodology to construct a prognostic framework for heart disease diagnosis by integrating demographic details, medical records, and laboratory information. In this study, a machine learning model for accurate disease diagnosis is used, using a LSTM recurrent neural network with its optimal hidden layer neuron obtained using a particle optimization algorithm. In this study, after preprocessing by normalizing the data and removing missing data, we reduced the number of unimportant features using principal component analysis in the next step so that we could classify the data more accurately using the recurrent neural network. In this research, we attained a precision level of 99.3%, surpassing the proposed technique by 1% when contrasted with the conventional method outlined in the foundational article.

Keywords: Machine Learning, Accurate Diagnosis, Heart Disease, Comparative Study

1. Introduction

Heart disease represents certain of the most widespread and incapacitating medical concerns internationally, influencing huge populations and ensuing in serious comorbidities and mortality [21]. Although medical technology and treatment options have advanced significantly, accurately diagnosing heart disease continues to be a complex and formidable challenge. Timely diagnosis is essential for effective treatment and better patient outcomes, as delays or incorrect diagnoses can lead to severe complications or even death [18, 13].

Conventional diagnostic approaches typically rely on clinical assessments, laboratory tests, and imaging techniques, all of which can be mentally demanding, prone to errors, and expensive [19]. The American Heart Association estimates that over 80% of coronary heart events can be prevented through early detection and treatment [7]. Nonetheless, the absence of accurate diagnostic tools and methodologies obstructs timely detection and treatment, placing a considerable strain on healthcare systems and society at large [8].

The emergence of machine learning as a distinct field of research has opened up new avenues for improving diagnostic accuracy across a broad spectrum of medical specialties [4]. Through the analysis of extensive datasets, machine learning models can reveal complex patterns and correlations between variables that may escape the attention of human healthcare professionals [22]. This method provides a more accurate, efficient, and cost-effective strategy for disease diagnosis, with the potential to transform heart disease diagnosis significantly [17, 9].

Training algorithms, categorizing synthetic intelligence, concentrate on tuition calculations to

* Corresponding author. e-mail address: ahmed.alslemani@ogr.sakarya.edu.tr
ORCID : 0000-0002-5668-9922

acquire information and formulate informed conjectures or selections [5]. The underlying principle is that automated systems can acquire understanding from information absent, requiring particular coding [1]. A particular algorithm class, neural networks, leverages complex webs of interconnected nodes (neuronal structures) to produce predictive outputs. Although they possess the ability to discern subtle patterns and correlations, they are also susceptible to the pitfall of overparameterization [11].

Diagnosing heart disease involves a multifaceted analysis of several factors, including demographic information, medical history, laboratory test results, and imaging studies [15]. The precision of diagnostic determinations is contingent upon the integrity of the data, the intricacy of the disease entity, and the proficiency of the attending healthcare specialist [20].

Machine learning has been applied in various medical disciplines, such as diagnosis, treatment planning, and personalized medicine [12]. These computational models can process large-scale datasets, recognize complex patterns, and enable informed predictions or decision-making [10].

There are several challenges associated with employing machine learning in heart disease diagnosis, including:

Data Quality: The efficacy of machine learning models is profoundly influenced by the integrity and reliability of the underlying data. Inaccurate predictions can arise from poor-quality data.

Imbalanced Data: The diagnosis of cardiovascular disease often encounters a common challenge in the form of skewed datasets, where a substantial disparity exists between the prevalence of healthy subjects and those afflicted with the disease.

Feature Selection: Accurate diagnosis of cardiovascular disease necessitates the extraction of pertinent attributes from extensive datasets. Feature selection is crucial for reducing dimensionality and enhancing accuracy [14].

In this research, we propose a machine learning-based strategy to create a predictive model for heart disease detection by utilizing a combination of demographic data, medical history, and laboratory findings. Our objective is to demonstrate the practicality and effectiveness of this approach in improving the accuracy of heart disease diagnosis while alleviating the burden on healthcare systems.

1.1. Related works

Rajpurkar et al [2] conducted a study titled "Diagnosis of cardiovascular diseases using machine learning algorithms applied to electrocardiograms." The current work employed machine learning algorithms to analyze electrocardiogram (ECG) signals with the purpose of detecting cardiovascular diseases. The researchers discovered that their method could effectively diagnose cardiovascular illness with a precision rate of 93.2%.

A study titled "Classification based on deep learning of cardiac arrhythmias using ECG signals" was conducted by Shen et al [6] This research employed a sophisticated deep learning algorithm to accurately categorize cardiac arrhythmias based on electrocardiogram (ECG) signals. The researchers discovered that their method was able to classify cardiac arrhythmias with a precision of 95.1% accurately.

A comprehensive review by Liu et al. [24] investigated the potential of artificial intelligence in harnessing wearable sensor data for the diagnosis and prognosis of cardiovascular disorders. The researchers utilized machine learning algorithms to analyze data gathered from wearable sensors and successfully predicted the likelihood of cardiovascular illnesses with an accuracy of 88.2%. The review's outcomes underscored the promise of machine learning methodologies in discerning cardiovascular pathologies, emphasizing the necessity for continued investigation within this realm.

Maini et al. [25] proposed an unsupervised learning approach, employing clustering algorithms to categorize the Cleveland Heart Disease Dataset, thereby facilitating the identification of patterns and relationships within the data. The team created a range of predictive algorithms, encompassing decision trees, logistic regression, random forests, naive Bayes, and support vector machines, specifically identifying the most relevant variables for accurately identifying cardiovascular conditions. The research outcomes showed that Rapid Miner's performance consistently surpassed that of its counterparts, including models built using MATLAB and Weka, across various experiments. The artificial neural network (ANN) method was of particular significance, as it demonstrated exceptional speed and attained an accuracy of 90.74%.

In a separate investigation, Saboor et al. [26] deployed a suite of nine machine learning algorithms, comprising multinomial naive Bayes (MNB), random forests (RF), classification and regression trees (CART), linear discriminant analysis (LDA), extreme gradient boosting (XGB), support vector machines (SVM), AdaBoost (AB), extra trees (ET), and logistic regression (LR) on the optimized dataset following a thorough hyperparameter optimization process. The researchers undertook a series of preparatory steps, including data preprocessing and normalization. Then, they fine-tuned the model's hyperparameters to assess the validity of their approach using a widely employed dataset of cardiovascular disease. Among the various methods evaluated for diagnosing cardiac diseases, the SVM classifier stood out with an accuracy rate that can only be described as impressive-a staggering 96.72%.

Modepalli et al. [27] introduced an innovative machine-learning paradigm for predicting cardiac disease. Their methodology entailed applying data processing techniques, specifically regression and classification, to the Cleveland heart disease dataset, leveraging Random Forest, Decision Tree, and Hybrid

Model approaches. Notably, the hybrid model demonstrated a superior predictive capacity, achieving an overall accuracy of 88.7% in forecasting coronary heart disease, as evidenced by the experimental outcomes.

In their work, Kataria et al. [28] underscored cardiovascular pathology and affiliated risks while delineating diverse machine-learning methodologies for anticipated cardiologic infirmity. The research conducted a comparative analysis of supervised learning models employed in diagnostic trials. Among these models, the Logistic Regression classifier demonstrated superior performance, achieving an accuracy rate of 93.40%, surpassing all other classifiers evaluated.

Shah et al. utilized supervised learning classification techniques on a pre-existing dataset of cardiovascular disease patients sourced from the Cleveland database within the UCI repository. This dataset consisted of 303 instances and encompassed 76 attributes. In their analysis, they concentrated on 14 pivotal qualities fundamental for illustrating the efficacy of erudition stratagems. Their inquiry culminated in the conclusion that the K-nearest neighbors (KNN) algorithm accomplished the maximum preciseness of 90.79% with more reduced fault quotients.

In a comparative study, Bharti et al. [30] assembled a range of machine learning and deep learning models to evaluate their performance on a supervised learning dataset related to coronary heart disease, characterized by 14 key features. The average accuracy achieved from deep learning methodology was 94.2%.

In another investigation, Ashish et al. [31] designed a rapid and precise computer-aided diagnostic system for coronary heart disease, leveraging the capabilities of support vector machine (SVM) classification and extreme gradient boosting (XGBoost) algorithms. Using the random forest approach for model training and evaluation, they discovered that the N2Genetic-nuSVM model, constructed from a meticulously curated Z-Alizadeh Sani dataset, demonstrated a high degree of precision in predicting clinical diagnoses of cardiovascular disease, achieving an accuracy rate of 93.08%.

2. Research Methodology

This research aims to improve the accuracy of cardiac disease diagnosis by leveraging the capabilities of data mining methodologies. Our objective is to categorize the preprocessed data using a recurrent LSTM neural network, after completing preprocessing activities such as normalization, deleting missing data, and lowering the dimensionality of unnecessary data. An advantage of utilizing this neural network is its capacity to save and recall information. This benefit guarantees that past network choices impact subsequent choices, resulting in enhanced accuracy during the training process and enabling the network to be effectively trained. This deep neural network consists of multiple layers, allowing it to select suitable features independently. We aim to optimize the network's performance by employing the particle swarm optimization algorithm to determine the optimal number of neurons in the hidden layers. This algorithm will be used in this research due to its suitable speed, high accuracy compared to algorithms like genetic algorithms, and ease of execution. Additionally, the proposed method is illustrated in Figure 1, and the steps used in this diagram are then explained.

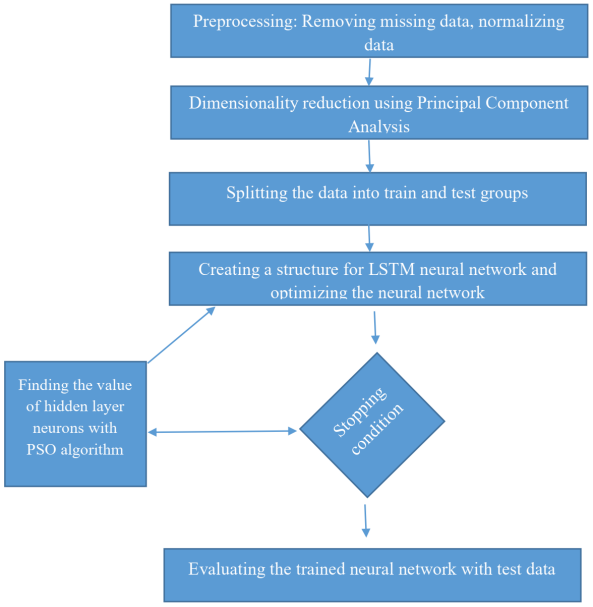

Figure 1. Diagram of the proposed method

3. Data Preprocessing

As shown in Figure 1, the first step after receiving data from the dataset is data preprocessing. Data preprocessing means preparing the data for final processing. This stage is one of the oldest but very sensitive stages in data mining because in some cases, if data preprocessing is not done correctly, even the strongest and deepest classifiers won't be able to classify with high accuracy. This stage includes steps such as handling missing data and normalizing the data. We will explain each of the mentioned steps as stages related to data preprocessing.

3.1. Processing data for missing values

In some cases, some data may be shown as missing due to noise or human errors in the dataset. Processing or removing this data is of utmost importance because if these data points are not removed from the dataset, the neural network won't be able to learn properly, and its accuracy will significantly decrease. Various methods have been proposed for removing this data, including replacing missing values with a constant or excluding all data from the decision-making process. However, these methods have their own specific problems. For example, if we fill the missing data with a constant value, sometimes the replacement value may have no logical relationship with the values of previous and subsequent samples, and the neural network may make mistakes during training. Or removing all this data may decrease accuracy in some cases because to remove all this data,

the entire column related to the data must be deleted, and the deleted column may be one of the important features of the sample, leading to lower accuracy naturally. Therefore, based on the reasons mentioned above, in this study, we intend to use the method of calculating the average value of neighboring data for processing missing data. For this purpose, initially using the software used, we find the 3 neighbors that are closer to the missing data in terms of Euclidean distance, and then the average value of these three neighbors determines the value of the missing data. This ensures that the replaced value has a logical relationship with the previous and subsequent features of each sample and that the neural network does not make mistakes during training.

3.2. Data normalization

After processing the missing data, in the next step, we normalize the data and limit the values of the features of each sample to a specific range. Data normalization ensures that the values of all considered features for each sample are within a specific range. This ensures that when the neural network is training, all data have an equal impact on the training process, and no data has priority over another. The relationship used in this process for normalizing the data is shown in equation 1.

$$X_{norom} = \frac{x - x_{min}}{x_{mix} - x_{min}} \quad (1)$$

4. Removing Unimportant Data and Data Partitioning

The subsequent phase involves separating the dataset into two distinct groups: one for testing and another for model training. The training data will be used to adjust the parameters of the neural network. For this purpose, this dataset along with the specific label of each data sample is provided to the neural network so that the network can adjust its weights and bias values considering the features of each sample and its label. This procedure involves modifying the network weights and biases, a process known as training. Following the training phase, the neural network is then assessed using test data in the subsequent step. We aim to use 70% of the available data for training and 30% for evaluating the neural network. The data division chart is shown in Figure 2.

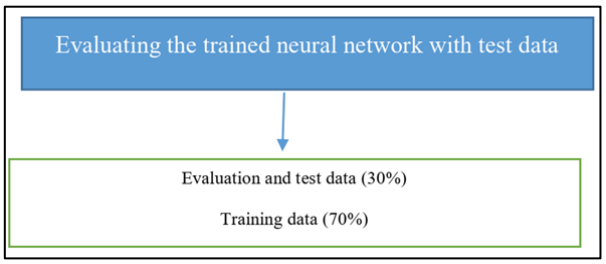

Figure 2. Data partition diagram

5. Classifying the data using an optimized LSTM neural network with Particle Swarm Optimization algorithm

Our current research efforts are concentrated on applying a Long-Short-Term Memory (LSTM) neural network architecture to classify and analyze refined data. The development of the LSTM neural network was motivated by the need to overcome the issue of vanishing gradients in traditional recurrent neural networks, which was achieved by substituting the intermediate RNN layer with a dedicated LSTM layer. The most important feature of LSTM is its ability to learn long-term dependencies, which was not possible with traditional recurrent neural networks. To predict the next time step, updating weight values in the network is necessary, requiring the retention of information from earlier time steps. A recurrent neural network can only learn a limited amount of short-term dependencies, but sequences of long-term dependencies like 1000 time steps cannot be learned using RNN, whereas LSTM can accurately learn these long-term dependencies. In LSTM, three gates must be considered for adjustment, reading, erasing, and writing. The input gate scales a known method between 0 and 1; if the decision is made to close the gate, no input is received. The output gate is crucial as it may decide to close the output and have no output memory. The forget gates are used to delete previously held information.

The LSTM neural network has various components that are described in detail in the following section:

Input: The relationships in this section are based on Equation 2.

$$Z_t = g(W_z X_t + R_z Y_{t-1} + b_z) \quad (2)$$

In equation 2, g, b_z, x_t, y_{t-1} at time t, the input, output at time t-1, bias, and activation functions are considered. Later, the dimensions and weights in this section are arbitrary.

Input gate: The reason for creating this gate is to control the input reading and have the ability to read from the input. The equation for this section is based on equation 3.

$$i_t = \sigma(W_i X_t + R_i Y_{t-1} + P_i \cdot C_{t-1} + b_z) \quad (3)$$

In equation 3 σ, b_z, y_{t-1}, x_t, the input at time t, output at time t-1, bias, memory cell at t-1, and activation functions are considered. The variables that control the reading values of the memory cells are denoted by pi.

Memory cells: This cell is constructed from self-feedback. The equation for this cell is based on equation 4.

$$c_t = z_t \cdot i_i + C_{t-1} \cdot f_t) \quad (4)$$

As expressed in equation 4, the outputs of the input gates at time t, denoted by it, the input section's

production at time t, represented by zt, the previous memory cells ct-1, and the outputs of the forget gates are all considered. The core innovation of LSTM revolves around this cell. To control the reading, writing, and erasing values of this cell, 3 gates are created.

Forget gates: The equation for these gates is based on equation 5.

$$f_t = \sigma(W_f X_t + R_f Y_{t-1} + P_f \cdot C_{t-1} + b_f) \quad (5)$$

In equation 5, σ, y_{t-1}, b_f, x_t the input at time t, output at time t-1, bias, the memory cell at t-1, and activation functions are considered. The variables that control the reading values of the memory cells are denoted by p-f.

Output blocks: The equation for these blocks is based on equation 6.

$$y_t = h(c_t) \cdot o_t \quad (6)$$

In equation 6,c_t, o_t represents the output of the output gate, and the value of memory cells at time t is taken into account. In the recurrent neural network, the output is a function of the state, but in LSTM, the output is a function of the memory cell values.

Output gates: The equation for these blocks is based on equation 7.

$$o_t = \sigma(W_o X_t + R_o Y_{t-1} + P_o \cdot C_t + b_o) \quad (7)$$

In equation 7, σ, c_t, x_t, y_{t-1}, the input at time t, output at time t-1, bias, the memory cell at t, and activation functions are considered. The variables that control the reading values of the memory cells are denoted by po.

In LSTM, gradient explosions don't happen because the functions are between zero and one and their derivatives are also between zero and one. The training algorithm for these types of networks, like the old recurrent neural network, is done using error backpropagation methods.

As mentioned, the most important layer in an LSTM neural network, which is responsible for processing the data, is the hidden layer of this network called the LSTM layer. This study aims to enhance the neural network's performance by determining the ideal neuron count in the LSTM layer. This will be achieved by applying the Particle Swarm Optimization algorithm. The reason for using this algorithm for optimization is its simplicity in implementation and convergence speed. This algorithm converges less on local optima due to its search and exploration features. The algorithm's functionality enables it to exhaustively explore the entire range of potential values for the number of neurons in the hidden layer. Subsequently, through an iterative process, it identifies the optimal value that yields the minimum error for the neural network.

Figure 3 illustrates the sequential steps involved in the Particle Swarm Optimization algorithm, which is utilized to optimize the performance of the long-s-term memory neural network.

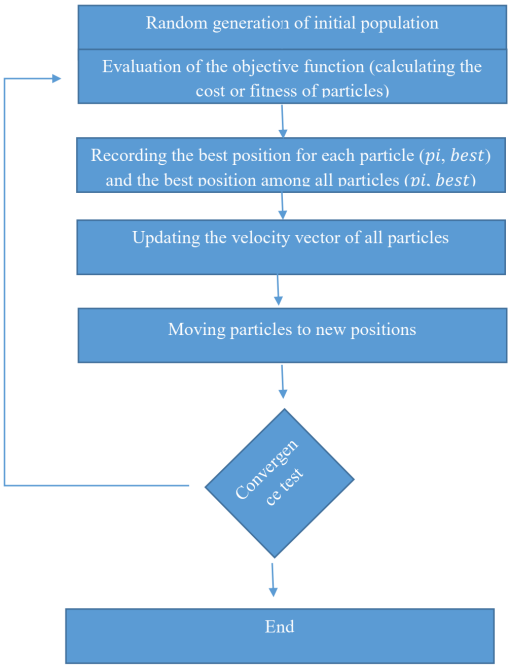

Figure 3. Graphical Representation of the Particle Swarm Optimization Process for Optimizing the Number of Neurons in Hidden Layers Within Neural Network Architectures.

The algorithm's particle structure is defined by the number of neurons comprising the neural network's hidden layer, and the initial population is constituted by a set of particles, with each particle embodying a specific neuron count for the hidden layer. This algorithm assesses the particles' values in each iterative cycle by applying a cost function, where the neural network's error serves as the evaluative metric. At each iteration, the fitness score is determined by reassessing the neural network's classification error, which is achieved by dynamically adjusting the number of neurons in the hidden layer. This process is mathematically formalized in Equation 8, which defines the cost function.

$$MSE = \frac{1}{2}\sum_{i-1}^{n}(y_i - y_i')^2 \quad (8)$$

After calculating each particle's fitness value, the particles will subsequently converge towards the particle exhibiting the highest fitness value in the next iteration. The equations for updating the speed and movement of particles for updating by the Particle Swarm Optimization algorithm are then provided.

If the number of particles is equal to m, the current position T of particle i is represented as $X_i = (x_{i1} . x_{i2} . \ldots x_{in})^T \in S$. The speed of particle i is determined using an n-dimensional vector $V_i = (v_{i1} . v_{i2} . \ldots v_{in})^T \in S$. In order to update the state of particles towards the optimal solution, the speed of the particle must be evaluated first. According to the basic Particle Swarm Optimization algorithm, the update in iteration t+1 is obtained based on 9.

$$v_{id}(t+1) = v_{id}(t) + c_1 r_1(t)[pbest_{id}(t) - x_{id}(t)] + c_2 r_2(t)[gbest(t) - x_{id}(t)] \quad (9)$$

As expressed in equation 9, $pbestid\ (t)$ denotes the optimal position attained by particle i in the d-dimensional space at iteration t, while gbest (t) represents the globally optimal position achieved by all particles at iteration t. The parameters c1 and c2 are positive constants, while r1 and r2 are random variables uniformly distributed between 0 and 1.

Once the movement of particles is determined, the new position of particles is evaluated using Equation 10.

$$X_i(t+1) = x_{id}(t) + \ v_{id}(t+1) \quad (10)$$

Then, a new position for all particles in a search space with the obtained fitness values of gbest and pbest is updated, and this process will continue until the optimal point in the search space is reached. In this process, upon reaching a certain number of iterations, the algorithm's termination condition will be determined. Upon the culmination of the algorithm's search process, the optimal neuron count for the hidden layer, which yields the minimum error for the neural network, will be identified and reported.

5. Results of the Proposed Method

5.1. Dataset

As can be seen from specific features listed in Table (1), this study utilizes the Hungarian dataset, publicly available from the UCI repository, to validate the proposed approach. Comprising 490 samples, each characterized by 14 distinct features, this dataset provides a comprehensive basis for evaluation.

Table 1. Features of the Hungarian dataset.

No.	Features
1	Age
2	Gender
3	The classification of chest pain is categorized into four distinct types: 1) Typical angina, 2) Atypical angina, 3) Non-anginal pain, and 4) Asymptomatic.
4	Blood pressure at rest measured in millimeters of mercury (mmHg) during hospitalization
5	Cholesterol levels
6	Number of cigarettes smoked per year
7	Blood sugar level
8	Family history
9	Resting electrocardiogram readings in one of the presented conditions Three categories: (1): A value of 0 corresponds to a normal condition, while ST-T wave abnormality is signaled otherwise. (2): A value is assigned to indicate abnormality, specifically when the segment is less than 0.05 mV ST. (3): A value of 2 is assigned to signify the presence of left ventricular (LV) hypertrophy, as determined by ST-T criteria, as well as a corresponding indication of 1.
10	Maximum heart rate achieved
11	The presence or absence of exercise-induced angina is denoted by a binary value, where 0 represents no and 1 represents yes.
12	ST-segment depression during exercise concerning baseline
13	The slope of S-T segment
14	Exercise test duration in minutes

5.2. Evaluation Metrics

The proposed methodology's performance will be comprehensively evaluated using a suite of metrics, comprising accuracy, coverage, precision, and F-score, to provide a detailed understanding and interpretation of the resulting outcomes. The relationships related to these metrics are provided below, along with a brief explanation of each metric's usage.

Table 2. Metric Relationship

Metric Name	Column A (t)
Accuracy	$= \frac{TP + TN}{TP + FP + FN + TN}$
Precision	$= \frac{TP}{TP + FP}$
Recall	$= \frac{TP}{TP + FN}$
F-score	$= \frac{2 * \text{Precision} * \text{Recall}}{\text{Precision} + \text{Recall}}$

• Accuracy is defined as the rate of correct predictions returned by our model.

• Recall can be defined as the rate of positive samples returned by the model.

• Precision can be defined as the rate of correct responses provided in each target class.

• The F-score, a metric that balances precision and recall, can be mathematically formulated as their harmonic mean. In particular, the F1-score is a weighted average of precision and recall, with a perfect score of 1 and a worst-case score of 0.

5.3. Analysis and examination of the obtained results

The Particle Swarm Optimization algorithm was utilized to determine the optimal number of neurons in the LSTM hidden layer, with the specifics of the optimization algorithm employed being summarized in Table 3.

Table 3. Optimization Algorithm Specifications

Objective of optimization	Determining the ideal neuron count in the LSTM network's hidden layer
Algorithm objective function	MSE
Initial population count	15

Number of iterations	12
Population member basis	Particles represented by their corresponding hidden layer neuron counts

Through the application of the Particle Swarm Optimization algorithm, the optimal neuron count for the LSTM hidden layer was determined to be 25, which was attained after 12 iterative cycles. Furthermore, the parameters of the neural network used for classifying the data are presented in Table 3.

Table 4. Specifications of the LSTM Recurrent Neural Network

Number of input layer neurons	12
Number of hidden layer neurons	25
Number of fully connected layer neurons	2
Activation function	Softmax
Output layer neurons	2
Epoch count of the algorithm	250
Batch size value	1000
Training algorithm of the network	adam

According to Table 4, the input layer is configured with 12 neurons, as each sample is represented by a 12-dimensional feature vector that is input into the neural network. Furthermore, the hidden layer of this network is composed of 25 neurons, as determined by the optimization algorithm, and the output layer is fully connected with 2 neurons, which correspond to the two output classes.

Figure 4 illustrates the training process of the LSTM neural network for 250 epochs or 1000 iterations (each consisting of 400 iterations).

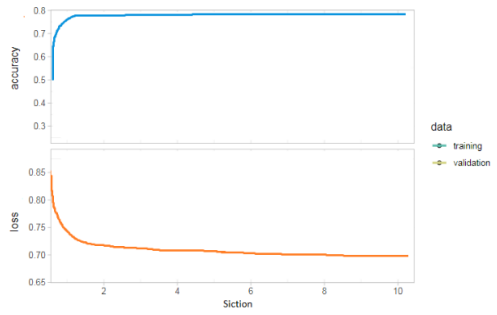

Figure 4. The procedure for training the LSTM recurrent neural network

In Figure 4, the neural network's accuracy is shown for each iteration using a blue-colored graph, while the classification error for each iteration is represented using a red-colored graph, which decreases with the reduction of training error. With each iteration, the accuracy increases and the error decreases, reaching an accuracy of 99.8% for the training process at iteration 250. Subsequently, after the network has learned from the data, the final model's accuracy was evaluated using test data as input and the obtained data was utilized. The model's performance will be evaluated and presented primarily through a confusion matrix and a receiver operating characteristic (ROC) curve.

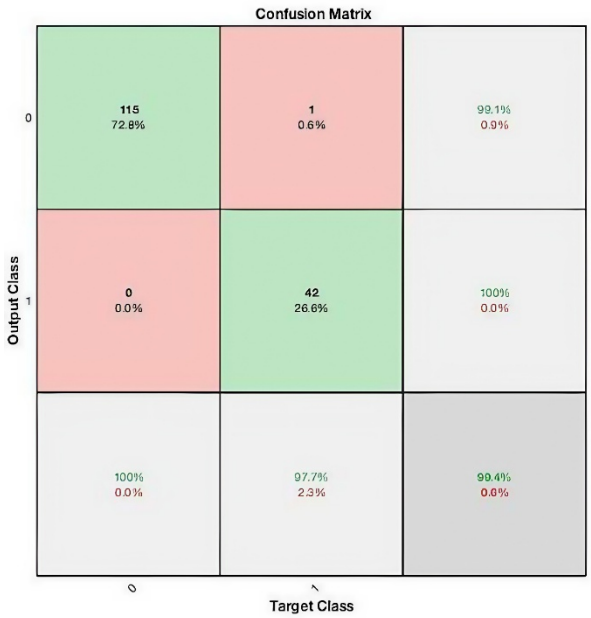

Figure 5. Test data classification outcomes presented in a confusion matrix format

Figure 5 illustrates a confusion matrix that categorizes outcomes into two distinct classes: label 1, which represents individuals afflicted with heart disease, and label 0, which corresponds to healthy individuals. This matrix displays metrics including correct positives, correct negatives, incorrect positives, incorrect negatives, and the overall level of accuracy. Green squares indicate the rate of correct diagnosis, while red squares indicate classification errors. The concepts of each element in this matrix are explained in Table 5.

Table 5. Concept of each element in the confusion matrix

True positive detection = 72.8%	False positive detection = 6%	Accuracy = 99.1%
False negative detection = 0%	True negative detection = 26.6%	Negative prediction rate = 100%
Coverage = 100%	Specificity = 97.7%	Overall accuracy = 99.4%

Additionally, Figure 6 shows the ROC curve which represents the classification performance. The curve illustrates the balance between the true and false positive rates, with curves above the diagonal line signifying superior classifier performance and accuracy. The optimal point on this curve is at coordinates (1.0).

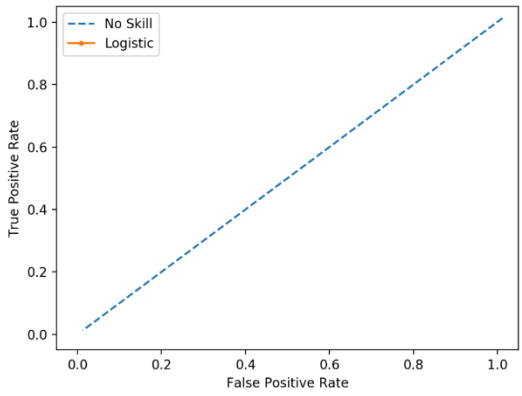

Figure 6. Test Data Performance Characteristic Curve

To evaluate the test data results from different aspects, a bar chart shown in Figure 7 is used. The graph comprehensively evaluates the model's performance on the test data, showcasing the calculated values for multiple metrics, including accuracy, precision, recall, and F-measure.

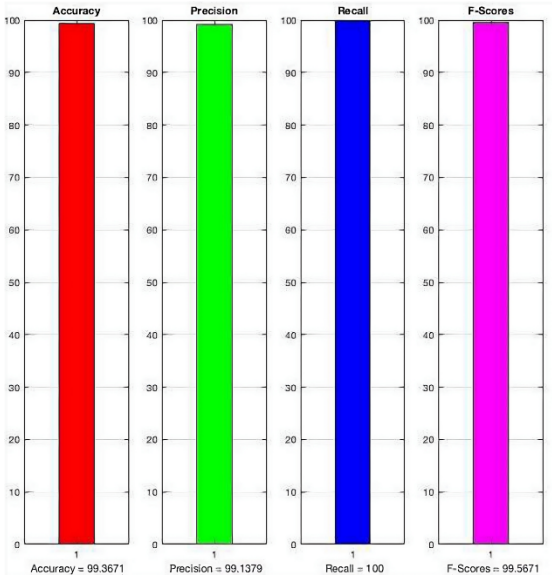

Figure 7. Test Data Performance Characteristic Curve

Table 6 juxtaposes the assessment metrics acquired for the proposed approach against those of other established methodologies outlined in the foundational study.

Table 6. Comparison of Existing Methods in the Baseline Article with the Proposed Method

Method	Accuracy	Precision	F
Naive Bayes	83.4%	88.8%	83.4%
Decision Tree	77.6%	84.6%	77.6%
Baseline Article	98.5%	98.2%	97.3%
LSTM+PSO	99.3%	99.1%	99.56%

As depicted in Table 6, the outcomes of the proposed technique surpass those of all alternative methods despite the uniform utilization of the dataset across all methodologies. The experimental outcomes demonstrate that the proposed methodology surpasses the baseline paper and other approaches in terms of accuracy, yielding significantly improved results. The reason for this improvement can be considered as follows: in the proposed method, preprocessing has been done correctly, and the classification used in the proposed method is a deep and highly accurate classification that has been optimized using the particle swarm optimization algorithm. This increased the classification power.

6. Conclusion

The primary goal of this research was to develop an advanced monitoring system for the accurate diagnosis of heart disease, focusing on minimizing misclassification errors and improving overall precision. A Long Short-Term Memory (LSTM) neural network was employed, while a Particle Swarm Optimization (PSO) algorithm was used to determine the optimal number of neurons in the hidden layers. During the preprocessing phase, the data was normalized, and missing values were appropriately handled. Principal Component Analysis (PCA) was then applied to remove irrelevant features, ensuring more accurate classification by the recurrent neural network. The proposed approach achieved an impressive precision of 99.3%, surpassing the results reported in the foundational paper.

Despite the high accuracy of the proposed model, there are still opportunities for further improvement and expansion. Future research could explore more advanced data processing techniques, such as transfer learning, to enhance model performance across diverse datasets. Additionally, integrating LSTM with other neural network architectures, such as transformers, could further improve accuracy and stability. Moreover, implementing the proposed system in real-world clinical environments and evaluating its performance under practical conditions would be a crucial step toward its real-world applicability.

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