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Article Title: **Advanced Heart Disease Prediction Model Using Dung Beetle-Based Feature Selection and Bi-LSTM Classifier**

Advanced Heart Disease Prediction Model Using Dung Beetle-Based Feature Selection and Bi-LSTM Classifier

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ABSTRACT

In the modern environment, it is quite difficult to detect Heart Disease (HD) through early-stage symptoms. Heart disease is the cause of mortality if the diagnosis is delayed including death occurs to prevent these issues. This paper proposes an innovative approach for the detection of heart disease from HD dataset, incorporating advanced techniques. Initially, data cleaning and data normalization is applied to the HD to eliminate or to find the duplicate values. Next, the images are segmented using K-means clustering, allowing for the separation of relevant regions associated with HD. Features are then optimized from the segmented HD using the Dung Beetle Optimization (DBO) algorithm, capturing optimized values for further analysis. Finally, a Bidirectional Long Short-Term Memory (BiLSTM) framework is proposed as a hybrid model to enhance the classification of HD images, leveraging both forward and backward temporal information to overcome challenges in disease analysis. The assessment of proposed work using python software reveals that the proposed framework with BiLSTM classifier ranks with improved accuracy of 91.56% when compared to the other techniques.

Keywords: Heart Disease, Data cleaning, Data normalization, K-Means clustering, Dung Beetle Optimization (DBO) algorithm, Bidirectional Long Short-Term Memory (BiLSTM).

1 Introduction

According to certain theories, Heart Disease (HD) is a collection of diseases that significantly affect the veins in the human heart. Doctors with extensive knowledge identify and analyse heart disease [1]. Therefore early identification is crucial to reduce the monetary and physical costs of heart disease to persons and organizations. Heart disease and stroke are the primary causes of Cardiac Vascular Diseases (CVDs), by WHO estimates that cause 23.6 million deaths overall by 2030 [2]. Whereas, the prevalence of chronic diseases is likewise rising in low and middle-income countries. Furthermore, some consumers find technology like Computed Tomography (CT) scans and electrocardiograms, which are essential for identifying coronary heart disease, to be too expensive and inconvenient. About 17 million persons have died as a result of the aforementioned cause alone [3]. Early preventative efforts have the potential to significantly lower the rates of one complicated disease in particular is heart disease, sometimes referred to as cardiovascular disease [4]. Few examples of cardiovascular diseases are atherosclerosis, coronary artery illness, heart beat abnormalities, congenital heart faults, and abnormalities of the heart valves. This result sometimes occurs as heart attacks, strokes, chest pain and heart failure [5]. Medical data increases every three years, according to data, statistics, hospital management, and clinical records, making the health sector a multibillion-dollar domain. Machine learning and data mining techniques are crucial for medical data analysis and knowledge extraction [6].

The primary goal of the approach is to use classifiers to effectively analyse cardiac disease in its early stages by classifying the important components of medical data. By using Machine Learning (ML) procedures to evaluate enormous amount of difficult medical data, healthcare professional's shows better anticipate cardiac problems [7]. An Artificial Intelligence (AI) based system that uses the random forest classifier to detect heart disease with greater accuracy. It is slow to process the data [8]. Moreover, to predict and validate the risks of heat-related diseases an SVM classifier for decision support as a cognitive approach is used. It is computational expense to predict the HD from the patient [9]

To detect heart disease some of the optimization technique is used. A Genetic Algorithm (GA) and Particle Swarm Optimization (PSO) optimized with Random Forest (RF) classifier (GAPSO-RF) to increase the accuracy of heart disease prediction. More time to process the data [10]. In order to help medical professionals to diagnose heart illness early, an Adaptive Genetic Algorithm with Fuzzy Logic (AGAFL) ideal is used to forecast heart disease. [11]. Moreover, a diagnostic system that uses an enhanced Extreme Gradient Boosting (XGBoost) classifier to predict cardiac disease. They optimized XGBoost's hyper parameters using Bayesian optimization, a very effective method for parameter optimization. As a result, performance is lower to predict the CVD from the patient affected [12].

For predicting HD a novel end-to-end deep learning approach that uses Convolutional Neural Networks (CNNs) to diagnose cardiac disorders using a single-channel ECG signal. It takes large data to train effectively it means small data are not trained effectively [13]. In order to categorize normal and abnormal heart disease and to attain more accuracy, a deep learning method known as CNN with Long Short Term Memory (LSTM) network is used. It is not predicted in the early stage it means it find as normal or abnormal only [14]. Moreover, SVM and Artificial Neural Network (ANN) methods are used to identify heart disease. It is highly expensive than the other methods [15].

2 Related work

Elsedimy *et al* [16] (2024) have proposed a Quantum-behaved Particle Swarm Optimization (QPSO) algorithm and Support Vector Machine (SVM) classification model to analyse and predict heart disease risk. PSO-SVM is an effective method to analyze heart disease and predict a patient's heart risk. To analyse heart disease from patient, the PSO-SVM model is used. The model is complicated to identify the heart disease. .

Deepika *et al* [17] (2022) have suggested a Multi-Layer Perceptron integrated with Enhanced Brownian Motion based on Dragonfly Algorithm (MLP-EBMDA) for CVD classification model for accurately predicting. MLP-EBMDA successfully tracks a patient's heart condition over time and accurately diagnoses heart issues. The model cannot adequately capture the structure and characteristics of the disease.

Srinivas and Katarya [18] (2022) have introduced a Hyper Optimized XG boost (HyOPTXg) an expert model that predicts heart illness. Using hyper-values, HyOPTXg improves as better classifiers that accurately diagnose and predict heart illness from the patient. It handles missing valves in the prediction stage and lack of limpidity happens in the diagnosis stage.

Mehmood *et al* [19] (2021) have proposed a Convolutional Neural Network designed for the finding of cardiovascular illness in a patient. CNN diagnoses heart disease in its early stages and predicts the patient's condition. Because it predicted early on for medical data, so the performance is good. It takes more time to detect the heart disease compared to the other method.

Vincent Paul *et al* [20] (2022) have invented a maximum-relevance-minimum-redundancy feature extraction method using a back propagation neural network, to detect a heart disease. A back propagation neural network properly diagnoses cardiac issues and predict a patient's heart issue throughout training time. It is prone to noisy data from HD and is time-consuming.

The main contributions of this study include

- Data cleaning and data normalization is utilized to effectively eliminate duplicate values from the input HD dataset, enhancing image quality for analysis.
- K-means clustering is employed to segment HD dataset, dividing the cluster for better feature extraction and analysis.
- Dung Beetle Optimization (DBO) Algorithm to optimize distinctive features from the segmented HD dataset, facilitating robust data representation.
- A BiLSTM-based framework is proposed, exactly addressing challenges in disease analysis for HD prediction.

3 Proposed method

For predicting the HD in early stage following methods are proposed. Firstly the input data is given to the preprocessing step were a data cleaning and normalization technique is applied to eliminate duplicate values from HD dataset and given to segmentation process.

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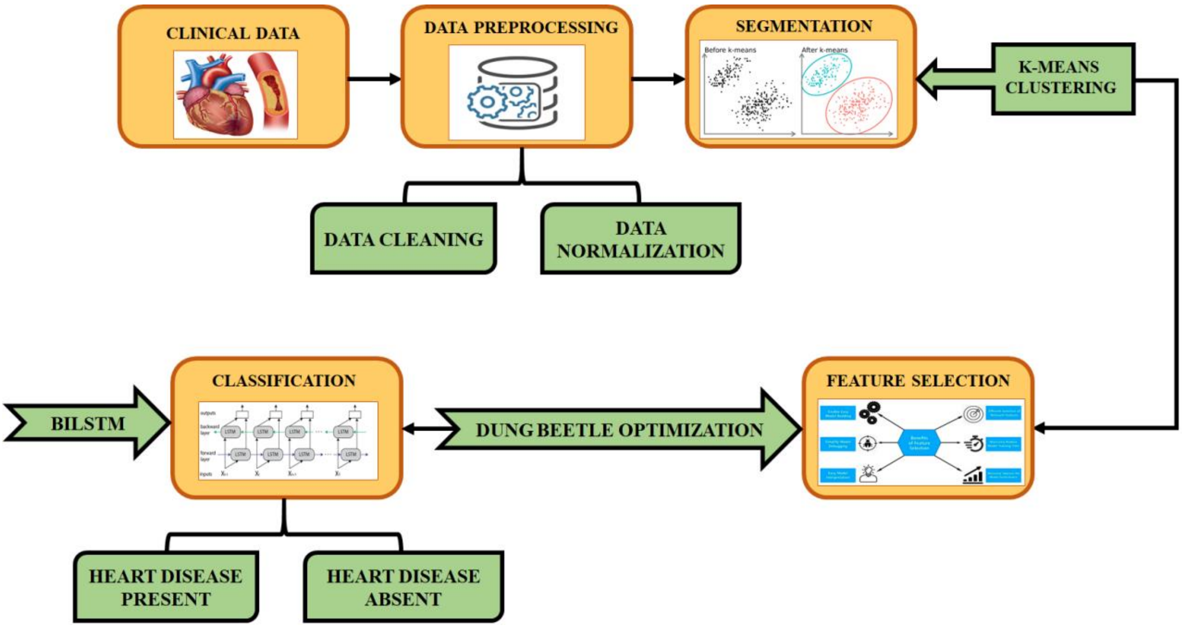

Figure 1: *Block diagram of proposed work*

Secondly the segmentation process uses the k-means clustering for segmenting or clustering the filtered HD and by using DBO algorithm a segmented HD features are optimized, that detects HD. Finally, the optimized HD is given to the BiLSTM to classify the HD. Then the classified HD gives better accuracy compared to the existing methods.

3.1 Data Pre-processing for HD prediction

The first step in the HD prediction is data pre-processing contains data cleaning and data normalization.

3.1.1 Data cleaning for HD prediction

The data cleaning is the process of eliminating any duplicate or missing values from the collected HD dataset. Additionally, unnecessary variables are eliminated, and the HD dataset is then utilized to train the model. Only when the missing value is of the Missing-At-Random (MAR) type are instances deleted, and rows with many missing entries in a single row are removed from the HD dataset.

3.1.2 Data normalization for HD prediction

The process of data normalization, which included mounting data into nominal data, also includes data transformation to HD dataset. Each value in the instances is scaled to an equal contribution as part of the normalizing procedure. The three main issues it addresses are outliers, which delay the training process of classifier design, and decreasing the bias of characteristics whose numerical influence is stronger in differentiating the corresponding class.

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3.2 Segmentation by K-Means clustering for HD prediction

K-Means Clustering is coming under unsupervised learning algorithm it is used to segment the clustering center. First, randomly initialize k points in the HD dataset called cluster centroids. The main objective of k-means clustering has three points one is grouping similar data points in HD; other is minimizing within cluster distance in HD and maximizing between cluster distances in HD. Evaluating a distance metric involves minimizing within-cluster distance. Furthermore, maximizing the distance between clusters is utilized to maximize the distance between them.

$$\text{Euclidean Distance} = \sqrt{(x1 - x2)2 + (y1 - y2)2} \tag{1}$$

$$\text{Centroid} = \frac{(x1+x2+x3)}{3}, \frac{(y1+y2+y3)}{3} \tag{2}$$

This formula can be extended to encompass n points as follows:

$$\text{Centroid} = \frac{(x1+x2+\cdots+xn)}{n}, \frac{(y1+y2+\cdots+yn)}{n} \tag{3}$$

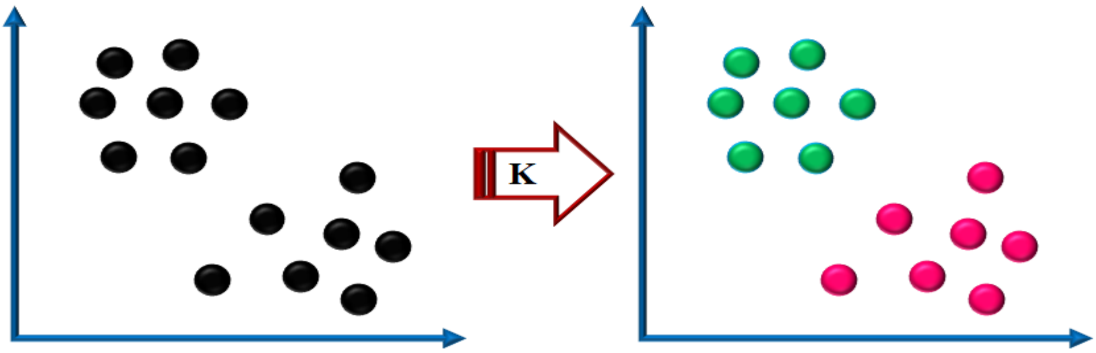

Figure 2: *K-means clustering operation*

K-means clustering operates on the basis of initialization, centroids, assignment, and outcome. Here, K points are selected from the heart disease detection dataset for initialization, and they also act as the initial cluster centroids in HD. The cluster centroids are used to assign HD and that HD experiences convergence when the centroids stop to change intensely.

3.3 Feature selection by Dung Beetle Optimization Algorithm for HD prediction

Based on the habits of dung beetles in HD, the Dung Beetle Optimization (DBO) algorithm is a swarm intelligence optimization method that divides the total population into four appropriate segments by imitating some of the behaviours associated with dung beetles in nature. The four appropriate types for DBO algorithm are as follows

3.3.1 Ball Rolling

In accordance with the positions of the celestial bodies, dung beetles must ensure that their pathway is a straightforward line when rolling the dung ball. Individuals in the algorithm travel in the designated direction across the exploration space instruction to mimic the dung beetle's behaviour. Individual dung beetles' paths are said to be influenced by the sun's intensity. The individual's position is altered by this process, as Equation (4) below illustrates.

$$X_n^{i+1} = X_n^i + a.k.X_n^{i-1} + b.\Delta x \tag{4}$$

$$\Delta x = \left|X_n^i - X^w\right| \tag{5}$$

Where $k \in (0,2)$ indicates the deflection coefficient, $b \in (0,1)$ indicates a natural coefficient, and X_n^{i+1} indicates the position of the n^{th} dung beetle at the i^{th} iteration; x indicate the grade of variation in light intensity, X^w worst location inside the current population and a denotes natural coefficient.

Dung beetles select to turn their bodies to change route and avoid obstacles in their route; this behaviour is similar to dancing to whatever happens in nature. This dung beetle behaviour is depicted in DBO as follows:

$$X_n^{i+1} = X_n^i + \tan \propto \left|X_n^i - X_n^{i-1}\right| \tag{6}$$

$$0 \leq \propto \leq \pi \tag{7}$$

3.3.2 Reproduction

To ensure a secure environment for their young, dung beetles must select a suitable oviposition spot when rolling the dung ball backbone of the shell. According to the above discussion, the algorithm models the region where females lay their eggs by eliciting a boundary selection strategy, it is described as follows:

$$LB_1 = \max(X^t.(1-T), LB) \tag{8}$$

$$UB_1 = \min(X^t.(1+T), UB) \tag{9}$$

Where X^t represents current narrow optimum, LB_1 and UB_1 is the lower and upper bounds of the spawning area, LB and UB are the lower and upper bounds of the exploration space, individually. As a result, during the iteration phase, the hatching balls' positions also vary. The procedure is stated as follows:

$$X_n^{i+1} = X^t + B_1.(X_n^i - LB_1) + B_2.(X_n^i - UB_1) \tag{10}$$

Where X_n^i location of the n^{th}hatching dung ball by t^{th}iteration, B_1 andB_2 stand two autonomous random matrices of 1.

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3.3.3 Small Dung Beetle

After successfully hatching, the young dung beetles go out in groups to seek for food, which also involves a range constraint. The following is the optimal foraging area for these little dung beetles:

$$\mathrm{LB}_2 = \max(\mathrm{X}^{\mathrm{tb}}.(1-\mathrm{T}), \mathrm{LB}) \quad (11)$$

$$\mathrm{UB}_2 = \min(\mathrm{X}^{\mathrm{tb}}.(1-\mathrm{T}), \mathrm{UB}) \quad (12)$$

Where X^{th} is the global optima, LB_2 and UB_2 signify the lower and upper bounds of the range.

3.3.4 Thief

Term "thieve" refers to dung beetles that steal dung balls from other members of their population. Consequently, the finest location to enter of food is probably the area aroundX^{-} during iteration phase, the thief dung beetles' location is restructured as follows:

$$\mathrm{X}_{\mathrm{n}}^{\mathrm{i}+1} = \mathrm{X}^{\mathrm{s}} + \mathrm{P.d.}\left(\left|\mathrm{X}_{\mathrm{n}}^{\mathrm{i}} - \mathrm{X}^{\mathrm{t}}\right| + \left|\mathrm{X}_{\mathrm{n}}^{\mathrm{i}} - \mathrm{X}^{-}\right|\right. \quad (13)$$

Where d designates a random vector of scope $1 \cdot D$conforming to the ordinary distribution, and P represents a constant.

3.4 Classification by Bidirectional LSTM for HD prediction:

BiLSTM is a classification technique under the neural network to classify the HD image. However, long-term memory issues arise because the original information will eventually be lost the HD image. Then this directly led to the development of the Long-Term Short-Term Memory (LSTM) model, which recalls long-term dependencies. When two hidden states are used in a bidirectional LSTM, the information travels both forward and backward. Information passes from the backward to the forward unidirectional LSTM. In principle, Bidirectional Recurrent Neural Network (BRNN) works by breaking down a typical RNN's neurons into bidirectional pathways. To comprehend Bi-LSTM by utilizing its elements and features: Long Short-Term Memory, or LSTM: An RNN type called LSTM was generated to get over the disadvantages of conventional RNNs in terms of identifying long-term dependencies in sequential data for HD.

- **Bidirectional Processing in HD:** Unlike traditional RNNs, which only analyse input HD sequences in one direction, Bi-LSTM methods the sequence in both directions instantaneously. The sequence is processed forward by one of its two LSTM layers and backward by the other. Each layer monitors its own hidden statuses and memory cells.

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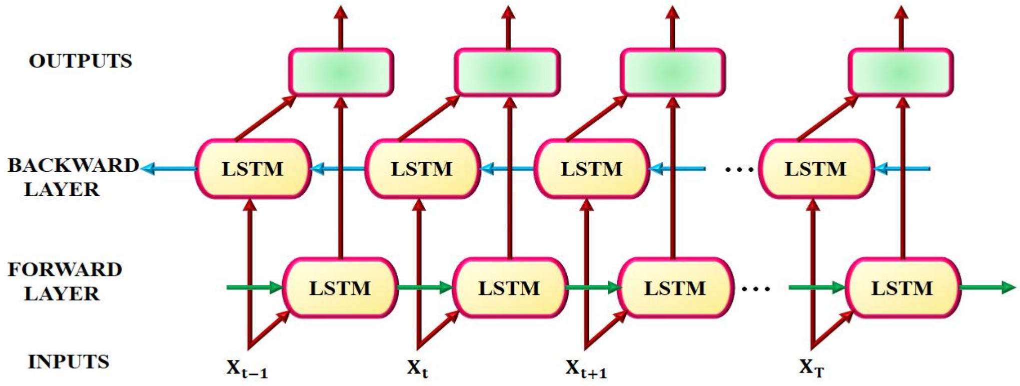

Figure 3: *BiLSTM for HD prediction*

- **Forward Pass in HD:** In the forward pass, the forward LSTM layer receives the input sequence (HD image) from the first to the last time step.
- **Backward Pass in HD:** The backward LSTM layer receives the input sequence in reverse order, from the last time step to the first, all at once.
- **Combining forward and Backward States in HD:** Following the completion of the forward and backward passes, at each time step both LSTM layers are combined.

These accesses regulate both the features and volume of HD data that is extracted. The input and forget gates are responsible for deciding which additional info be kept in the cell state and which elder info will be deleted. The output gate completes the network model's output after the cell state update is complete. This allows the Bi-LSTM output units to spontaneously absorb a illustration that incorporates both historical and future information.

4 Result and discussion

The aim of this work is improve the efficiency of various prospective DL algorithms and BiLSTM classifiers trained in order to create dualistic organization simulations that used as heart disease diagnosis tools. To assess the algorithms' performance, the heart disease dataset is utilized.

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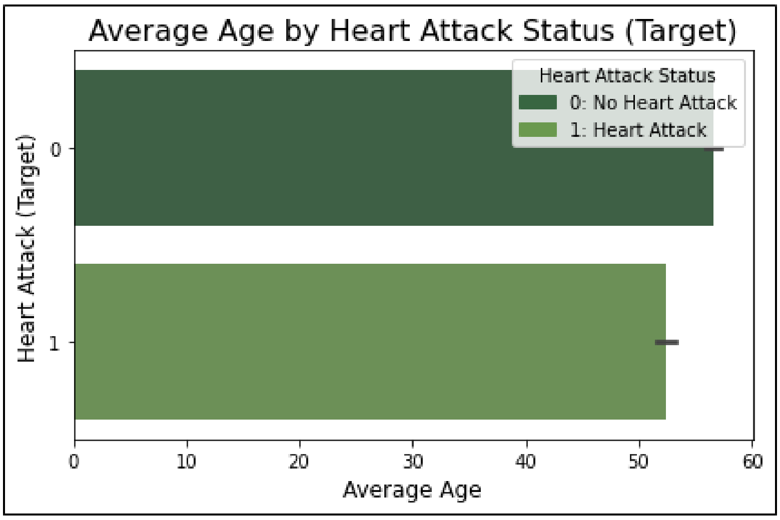

Figure 4: *Average age by heart attack status*

In this 0 means in HD dataset there is no heart attack and 1 means there is heart attack. It is imperative that the dataset are dealing with is roughly balanced and the target classes are around the same size. The ratio between the two classes is not quite 50%, as shown in Figure 4, but it is suitable to move on without shrinking or enlarging HD dataset.

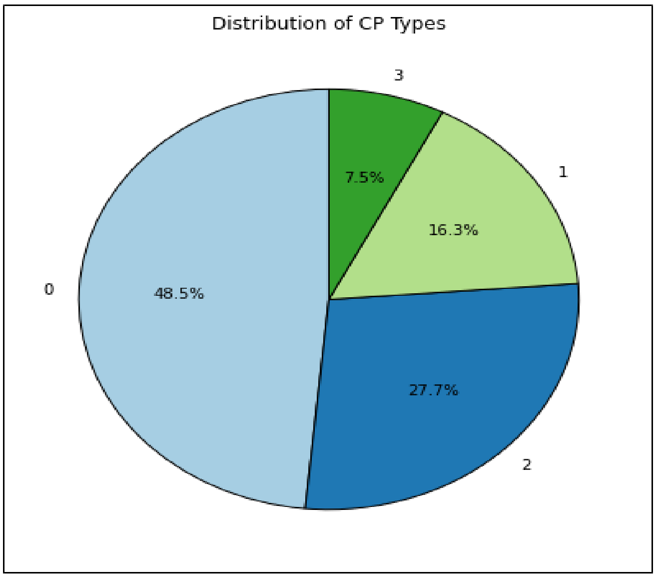

Figure 5: *Distribution of CP types*

In the above figure 5 distribution of CP types are plotted. Here value 0 for chest pain it is about 48.5%, value 1 for typical angina it is about 16.3%, value 2 for non-anginal pain it is about 27.7% and value 3 for asymptomatic it is about7.5%.

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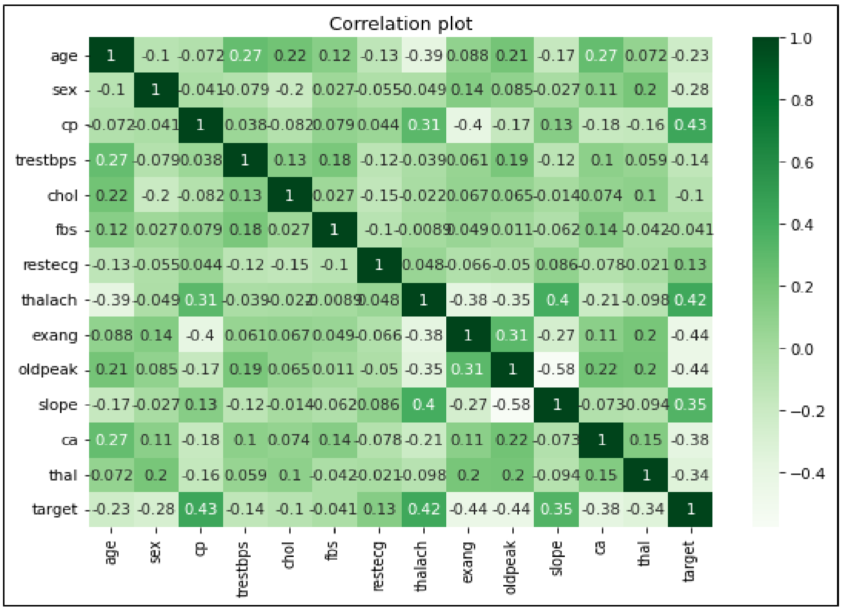

Figure 6: *Correlation plot for HD*

To determine the correlation between different categories correlation matrix is used. The feature in the heart disease dataset is analysed with highest correlation. Figure 6 for Age, chol, restecg, thalach, exang, slope, sex, cp, trestbps, ca, thal target the correlation matrix is analysed.

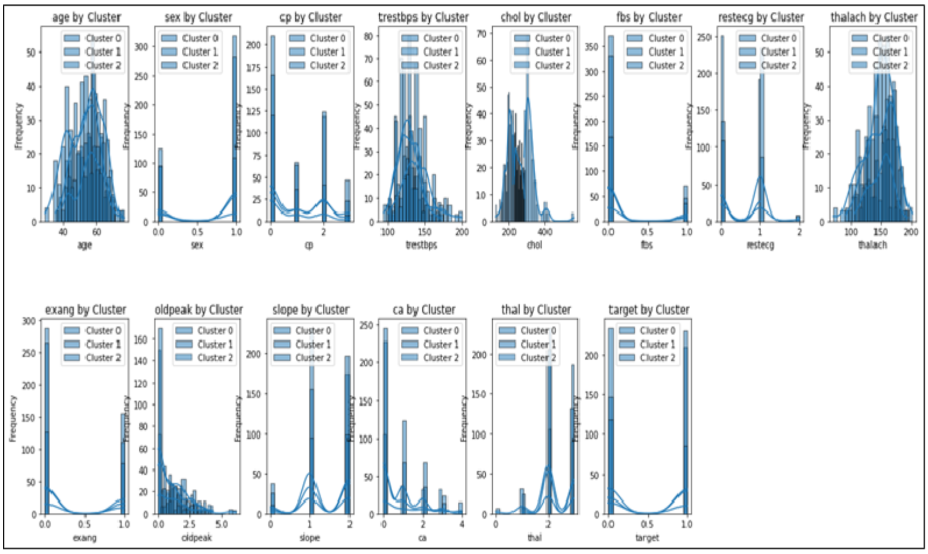

Figure 7: *K-means clustering for HD*

In above figure 7 the 14 categories are calculated using K-Means clustering .It shows the values for three clusters as cluster 1, cluster2, and cluster3. Figure 7 shows the histogram for every attribute in the dataset. A histogram displays an attribute's distribution observe from the

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histograms that the distribution range of each attribute varies. Therefore, it must be very helpful to normalize the input attribute (features) before feeding data into machine-learning models.

Figure 8: *Data distribution across clusters*

In figure 8 the data distribution across clusters is calculated for cluster0, cluster1 and cluster3 and the number of data points for each cluster is from 0 to 500.The cluster0 varies from 0 to 450, cluster1 varies from 0 to 380 and cluster2 varies from 0 to 200.

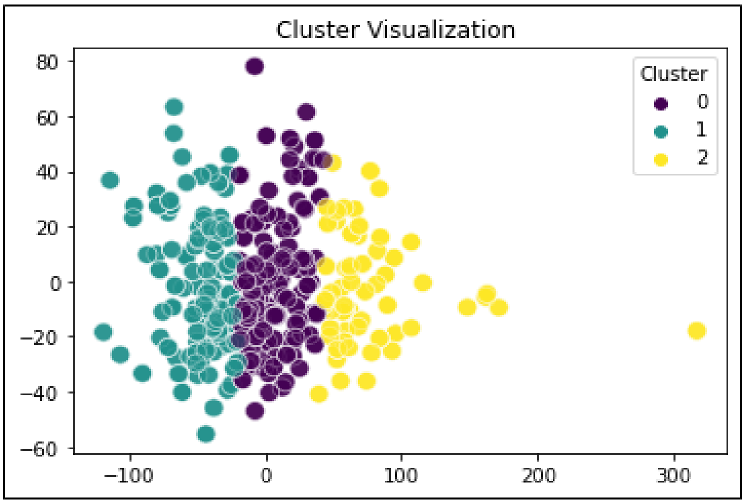

Figure 9: *Cluster visualization*

In the above figure 9 the cluster visualization shows the values for clster0, cluster1 and cluster2. Here cluster 1 is placed in between -100 to 0, cluster 0 is placed in the center of the centroid as 0 and cluster 2 is placed on 0 to 200 and above 300.

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4.1 Evaluation metrics

Using various evaluation metrics the future framework to training data from HD dataset is evaluated. And these metrics are accuracy, precision, recall, F1 score and AUC. By following equation each metrics are defined as

$$Accuracy = \frac{(TN+TP)}{TP+TN+FP+FN} \tag{14}$$

$$Precision = \frac{(TP)}{(TP+FP)} \tag{15}$$

$$Recall = \frac{(TP)}{(TP+FN)} \tag{16}$$

$$F1 - score = \frac{(2*\text{Precision}*\text{Recall})}{(Precision + Recall)} \tag{17}$$

At last, the simulation performance across different classifications is evaluated using the AUC, which describes the connection between the TP and FP proportions.

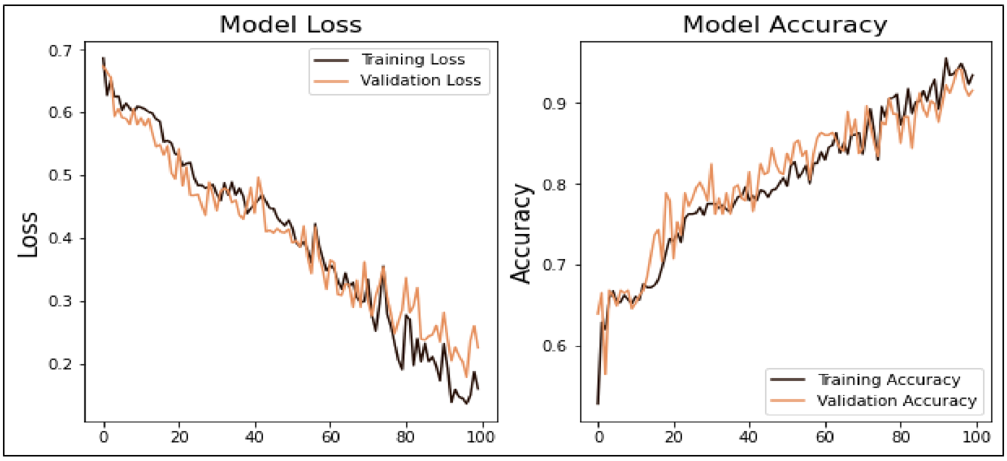

Figure 10: *Model loss and model accuracy*

The Model Loss graph figure 10 shows a reliable decline in both training and validation loss, representing improved learning and reduced error. The Model Accuracy graph illustrates increasing accuracy of 91.56%, with the model achieving high performance and minimal overfitting.

4.2 Confusion matrix

Heart disease detection is predicted using confusion matrix. 0 for no heart attack and 1 for heart attack the true label and predicted label are predicted from the two stages. Figure number

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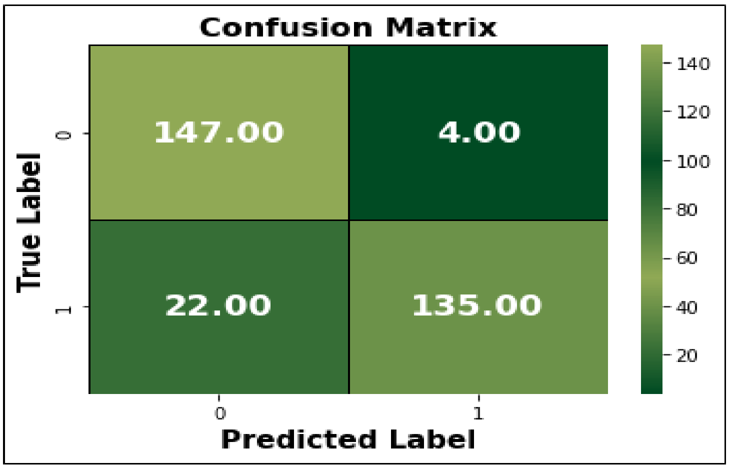

Figure 11: *Confusion matrix for HD prediction*

The confusion matrix in figure 11 calculates the model's performance in predicting no heart attack and heart attack. It shows high accuracy for the proposed BiLSTM than the other methods. Overall, the model demonstrates robust performance with strong classification accuracy across all categories.

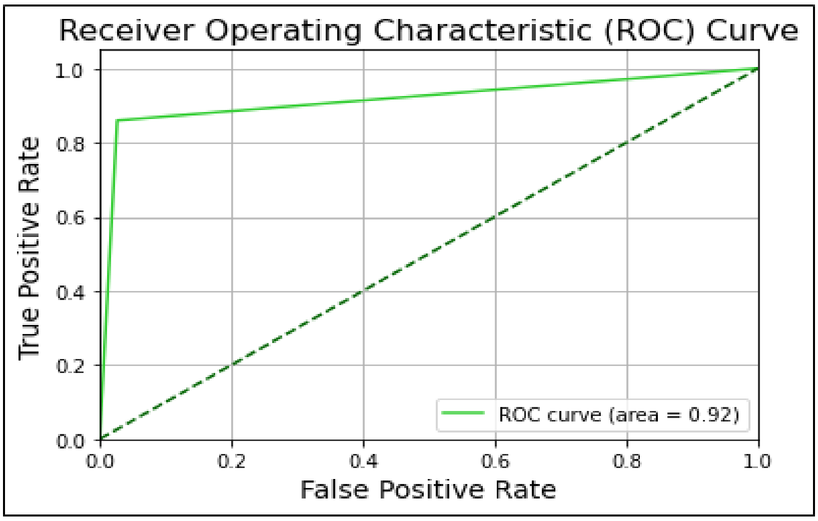

Figure 12: *ROC curve for HD prediction*

In above figure 12 the ROC curve shows the true positive rate and false positive rate. The ROC curve for heart disease prediction is about 92%.

4.3 Comparison for the proposed method

In contrast, several other studies [2, 21, and 22] unnoticed the time series component of the training data and just used baseline data. Using the proposed BiLSTM it gives higher

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accuracy of 91.56% than the existing method MLP-PSO, RF, and MLP is compared in table 1.

Table 1: *Comparison for proposed accuracy*

Study	Method	Accuracy
Al Bataineh *et al.*[21]	MLP-PSO	84.61 %
Rani *et al.* [22]	RF	86.6 %
Bhatt *et al* [2]	MLP	87.28 %
Proposed Approach	BiLSTM	91.56 %

Comparison of precision and recall for HD prediction

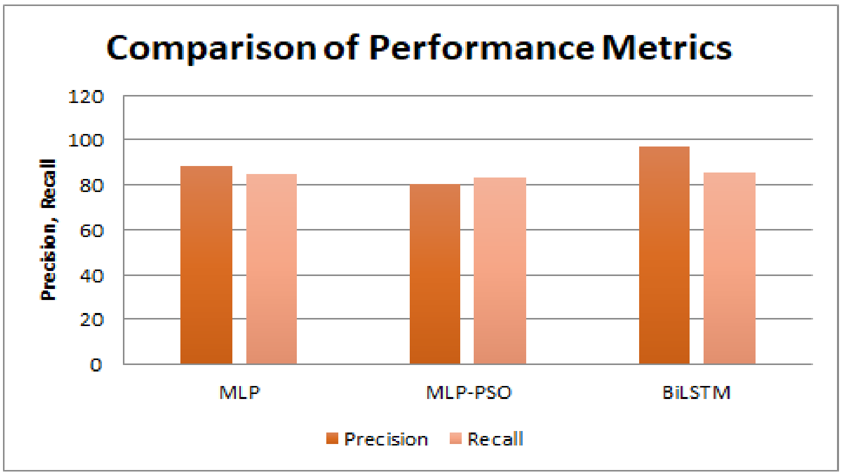

Figure 13: *Performance metrics is plotted for precision and recall*

In the above figure comparisons of performance metrics is plotted for precision and recall. For the existing MLP the precision value is 88.92% and recall is 84.85%, MLP-PSO the precision value is 80.8% and recall is 83.3%, and for proposed method precision is 97.12% and recall is 85.99% respectively.

5 Conclusion

The proposed work demonstrates a robust framework for HD diagnosis using HD data, leveraging advanced techniques like BiLSTM to significantly enhance accuracy and reliability. The integration of advanced preprocessing techniques, such as eliminates unwanted data and duplicate ensures that the input images are optimized for feature extraction. Further to enhance the precision of identifying cluster regions in the images K-means clustering for segmentation is used. Additionally, the features are optimized using Dung Beetle optimization algorithm and multi-dimensional analysis of the input data, capturing crucial patterns for effective classification in heart disease analysis. Using the proposed technique BiLSTM with prediction accuracy of 91.56% is achieved which is high

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when compared to the previous technique. This robust framework not only facilitates early and precise HD detection but also provides an accessible and efficient solution for clinical applications, aiding in timely treatment and better patient outcomes.

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