

A Novel Heart Disease Prediction System using Deep Multi-Layer Perceptron and Optimal Feature Selection Mechanism

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Abstract: Diagnosis and prognosis of heart disease (HD) are essential medical tasks for a correct classification, which helps cardiologists to treat the patient properly. The current medical system is unable to obtain the entire information from the heart disease database. It is difficult for a physician to analyze and diagnose chronic disease because it is a challenging endeavor. Hence this paper proposes a novel weight and bias tune deep multi-layer perceptron for heart disease prediction (WBDMLP) with optimal feature selection using modified random forest (MRF). The proposed system comprised '3' phases such as data preprocessing, feature selection, and HD prediction. Initially the HD prediction data is collected from the Cleveland dataset and the missing value imputation and data normalization is applied on the dataset to preprocess the dataset. Following that, the feature selection was performed by using the MRF algorithm. Finally, the HD prediction is done based on WBDMLP approach and the parameters are tuned by Sobel sequence with Brownian random walk-based dragonfly optimization algorithm (SSBRWDOA). The results indicate that the proposed approach reaches 97.89% accuracy, which is relatively higher than existing methods.

Keywords: Heart Disease Prediction, Data Preprocessing, feature Selection, Machine Learning, Deep Learning

1. INTRODUCTION

The heart is the most vital organ in the body, as it employs a network of arteries, veins, and capillaries to transport oxygen-rich blood to various parts of the body [1]. HD can take many different forms, including coronary artery disease (CAD), cardiac failure, vascular disease, irregular heartbeat, and others. HD is a disorder when the blood vessels narrow or block, causing a myocardial infarction and discomfort in the chest [2]. According to the World Health Organization, HD accounts for 17.9 million deaths annually, making it the top cause of mortality globally [3]. There are many different types of heart disorders; the most prevalent type, coronary artery disease, can result in a heart attack. Other kinds of cardiac disease may harm the heart's valve or the heart itself, resulting in cardiac failure [4]. In high-income countries, poor diet, tobacco use, a high level of sugar, and obesity or body fat accumulation are all common risk factors for HD [5]. Specific behavioral issues must be examined in order to investigate a case of HD. The management of all of those heart patients relies on clinical studies based on medical histories and patient questions. Patients also undergo extensive tests, including those for blood pressure, glucose levels, vital signs, chest pain, ECG, maximum heart rate, and elevated sugar levels. On the plus side, effective treatment is possible if the disease is quickly and easily identified. All of these methods frequently lead to incorrect diagnosis, mechanical breakdowns, and delays in diagnostic testing [6].

Machine learning (ML) is now widely acknowledged to be playing a significant role in the medical sector [7]. As a supplement to established methods of disease diagnosis, ML approaches are gaining acceptance in the realm of healthcare. In reality, algorithms may be used to quickly and accurately process a sizable amount of data, allowing for the direct extraction of unexpected insights from observations [8]. Support vector machine (SVM), decision tree (DT), k-nearest neighbor (KNN), random forest (RF), AdaBoost, etc. are a few ML techniques that aid in the prediction of cardiac disease [9]. But it works well with a lot of data since medical data like patient histories and ECGs have a lot of data. As a result, some researchers concentrated on deep learning (DL) approaches for HD prediction. The DL is a subfield of ML that has a transformative capacity for accurately analyzing huge amounts of cardiac data at high speeds, extracting intelligent insights, and effectively addressing complex problems [10]. However, each method using DL is trained with its own feature space, and in some circumstances the features may contain noise that includes

both the same and unwanted data. In such instances, the training time is longer, and the false-positive rate is larger. To address this issue, an effective feature selection technique is required in order to deliver superior HD prediction results with optimized features [11]. Henceforth this paper proposes a novel DL approach with efficient feature selection to predict the HD. The objectives of the manuscript are outlined as follows:

- The missing values imputation and data normalization is performed to preprocess the dataset that improves the quality of the data for predicting the disease more accurately.
- Employing the MRF approach to choose the optimal features from the preprocessed dataset, aims to reduce the classifier' training time with minimal prediction loss.
- The proposed system uses a WBTDMMLP approach to predict the HD and the hyperparameters of the network are optimally chosen using SSBWDOA.

The rest of the manuscript is arranged as follows: surveys of recent works regarding our proposed system are described in section 2. Section 3 provides detailed explanations of the proposed methodology. Section 4 investigates the outcomes of the proposed and previous related methods. At last, section 5 concludes the proposed work with future directions.

2. RELATED WORK

Pratiyush Guleria et al. [12] recommended a cardiovascular disease prediction system using explainable artificial intelligence (XAI) approach. Once collecting the HD dataset, the features of the dataset were ranked using the T-test ranking model and the ranked features were retrieved using the neighborhood component analysis (NCA) model. Finally, the ensemble of ML models such as KNN, SVM, bagging, AdaBoost, Gaussian naïve bayes, and logistic regression were used to perform classification. Comparing all, the NB, RF and SVM attained better performance with an accuracy of 89% for HD prediction. **Ibrahim M. El-Hasnony et al. [13]** suggested a ML based HD prediction system using a multi-label active learning approach. The multilabel active learning approaches such as random, MMC, QUIRE, adaptive and AUDI were applied to the collected dataset that selected the most important data to query labels. The hyperparameters of the ranking classifiers were tuned using the grid search optimization approach. The system attained an f-measure and accuracy of $62.2 \pm 3.6\%$ and $57.4 \pm 4\%$, that showed its satisfactory outcomes in disease prediction. According to the findings, the system achieved accuracy and F-score of and, respectively, which was better than the existing methods.

Raniya R. Sarra et al. [14] developed a SVM based HD classification system with an efficient feature selection scheme. The system used Cleveland and Statlog datasets for training and testing. The χ^2 method was applied to select the features from the dataset and SVM was utilized to perform classification. The method attained an accuracy of 89.47% for disease prediction that was better than other models. **Rajkumar Gangappa Nadakinamani et al. [15]** presented an ensemble of ML frameworks for HD prediction. The system performed training on the Statlog and Hungarian datasets. The preprocessing and manual feature extraction phases were carried out to improve the data quality and extract the important features from the dataset. Finally, the extracted features were inputted to the ML classifiers say NB, JRIO, random tree, reduced error pruning tree, linear regression, J48, and M5P tree for disease classification. The outcomes proved that the random tree model obtained superior performance comparing all other existing models with minimal MAE and RMSE of 0.0011 and 0.0231. **Mohamed G. El-Shafiey et al. [16]** proffered a RF approach for HD prediction with a hybrid optimization-based feature selection. Initially the data was collected from the Statlog and Cleveland datasets. The feature extraction model was implemented using the multivariate statistical analysis once the collected dataset was normalized into a specific range of values. Then the hybrid genetic and particle swarm optimization was implemented to choose the relevant features from the extracted feature data. Finally, prediction was done based on an RF classifier that achieved an accuracy of 91.4% and 95.6% for the Cleveland and Statlog databases.

The majority of the aforementioned surveys use a variety of ML classifiers to improve the accuracy of the HD prediction system, although they are limited by the dataset's enormous amount of data. The DL has abruptly appeared and has taken the lead as the branch that accurately predicts HD. The capability of DL is to process complicated information, to identify the key characteristics of multidimensional data, and to more accurately categorize cardiac disease. The majority of the work, nevertheless, did not focus on the feature selection methodology to choose features

from the dataset. The removal of irrelevant information during feature selection helps the model perform better, be clearer to understand, and run faster, all of which are critical for classification. Thus, it is motivated to propose a novel weight and bias tuned deep multi-layer perceptron (DMLP) for HD prediction with optimal feature selection using MRF.

3. PROPOSED METHODOLOGY

This paper proposes a novel weight and bias tuned deep multi-layer perceptron for HD prediction with optimal feature selection mechanism. To begin, the HD data was collected from the Cleveland dataset and the collected data was pre-processed by performing missing value imputation and data normalization. Then optimal features from the preprocessed dataset are selected using the MRF. At last, the HD prediction is done by WBTDMPLP, in which the tuning of the network is performed using SSBRWDOA. The working process of the proposed approach is shown in fig. 1.

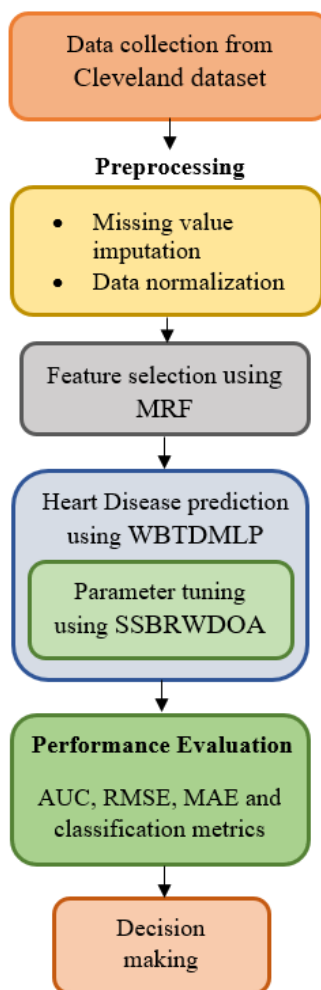


Figure 1: Structural framework

3.1 Data Preprocessing

Initially, the patient's HD related data is gathered from the Cleveland dataset that is available in openly available sources. Next, the data preprocessing is performed on the collected dataset. Data preprocessing is the way of transforming a training dataset into a visual format to improve quality performance of the data. In this work, there are two types of data preprocessing is performed on the collected dataset, namely, missing values imputation and data normalization. These are explained as follows:

Step 1: Missing values imputation

There are many missing data in the public datasets. Dealing with missing data is very important when preprocessing datasets since missing values lead to wrong decisions. The missing value of the dataset can be avoided by filling them with the mean value of the features in the entire column.

Step 2: Data normalization

Data normalization entails rescaling the data to a value between 0 and 1. It has no effect on the original data in the dataset and it is expressed as follows:

$$Norm_DataSet = \frac{\overline{OD}_s - \min(\overline{OD}_s)}{\max(\overline{OD}_s) - \min(\overline{OD}_s)} \quad (1)$$

Where, \overline{OD}_s indicates the original value in the dataset, $\min(\overline{OD}_s)$ and $\max(\overline{OD}_s)$ refers to the maximum and minimum data in the dataset.

3.2 Feature Selection

Feature selection is crucial because it eliminates duplicate and unnecessary features and minimizes the predictive model's training cost and time. Here, the MRF approach is applied to select the optimal features from the preprocessed dataset. The RF technique is one of the best tree-based feature selection methods, as measured by how successfully it increases node purity. There are nodes at the beginning of the trees that have the greatest decrease in impurity, and nodes at the end of the trees that have the least decrease in impurity. By cutting trees below a specific node, a subset of the most important features can be obtained. It combines all decision trees to produce the best possible result. It has strong predictive performance, minimal overfitting, and is simple to understand. Nevertheless, some low-quality decision trees will diminish the accuracy of RF. To enhance the accuracy of RF, the proposed system uses Cohen's kappa coefficient (CKC) for pre-pruning. This modification in conventional RF is named MRF algorithm. The steps of MRF are explained as follows:

Step 1: First, the preprocessed dataset of each tree is generated by bootstrap sampling: the total amount of instances in the preprocessed dataset is defined as \mathcal{Y} , and some samples are randomly selected from the dataset using a bootstrap sampling method.

Step 2: Construction of decision tree

Before constructing the decision trees, the CKC is used for pre-pruning to avoid overfitting. The CKC is a statistic that is used to measure inter-rater reliability for qualitative items, i.e. it measures the agreement between two items in the dataset and it is mathematically expressed as follows:

$$\Xi^* = \left(\frac{C_0 - C_{hp}}{1 - C_{hp}} \right) \quad (2)$$

Where, Ξ^* indicates the Cohen's kappa coefficient, C_0 indicates the relative observed agreement among items, and C_{hp} refers to the hypothetical probability of chance agreement. Then evaluate each feature's gain ratio in the splitting technique of each tree node, and the most optimal feature is selected as the splitting node. This procedure continues till a leaf node is formed. To conclude, d -training subsets trains the d -decision trees in the same way. The decision tree with optimal solutions is selected based on voting. These selected optimal features are fed into the classifier for further processing.

3.3 Heart Disease Prediction

Here, a WBTDMLP is utilized for HD prediction based on the selected features. The DMLP technique is a supervised artificial neural network that comprises input, hidden, and one output layers. Inputs addressed to hidden layers are directed to their activation functions. Then the activation functions' outputs are sent to further hidden layers, and the process continues for the number of hidden layers in the network. Finally, the output of the last hidden layer is given to the output layer, the result of which is utilized to make predictions. To improve the stability of network training, DMLP is frequently trained using a backpropagation technique. However, the random weights and bias initialization decreases the performance of the DMLP and it decreases the prediction rate and computational complexity. So, the proposed system uses the SSBRWDOA approach to optimally choose the weight and bias of the DMLP. In addition, the tanh and sigmoid activation structures are commonly used in MLP because they perform well in small to medium-sized systems. However, it does not solve the vanishing gradient problem. So, the proposed system uses a Hard-Swish Activation function (HSA) in the classification structure. These two modifications in conventional DMLP are termed WBTDMLP. Initially, the weighted sums of the inputs were calculated using equation (3).

$$Weighted_Sum = \sum_{p=1}^n \tilde{\omega}_{p,q} \overline{FS}_p + \tilde{\rho}_q \tag{3}$$

Where, n indicates the number of input nodes, $\tilde{\omega}_{p,q}$ refers to the p^{th} and q^{th} node's link weight in the input and hidden layer, $\tilde{\rho}_q$ represents the q^{th} hidden node's bias value, and \overline{FS}_p refers to the input selected feature set. Generally, the bias and weights of the network are randomly selected in the range of 0 to n-1, which increase the computational complexity and training time. Instead of randomly selecting these values, the weights and bias are optimally chosen by the SSBRWDOA algorithm. The dragonfly optimization (DFO) operates using dragonfly swarming behaviour. Dragonflies form dense groupings (swarms) for both hunting (static swarm) and movement (dynamic swarm). It has high computational efficiency and strong reliability, however, the performance of the DOA is affected by population initialization, because random initialization decreases the population diversity and leads to the problem of premature convergence. So, the proposed system uses Sobel sequence (SS) to increase the diversity of the population. The conventional DOA uses the levy flight strategy to model its random flying behaviour. However, it may fall into the local optimal solutions due to overflowing of search area and random flights interruption with larger searching steps. Hence, the proposed system uses Brownian Random Walk (BRW) strategy to explore the search space and avoid local optima issues. These SS and BRW strategy incorporations in conventional DOA are termed as SSBRWDOA. The process of SSBRWDOA is explained as follows:

First, initialize the population of dragonfly (i.e., random weight and bias value) using Sobel sequence.

$$\overline{B}_h = h_1 b_1, h_2 b_2, \dots, h_a b_h \tag{4}$$

$$b_h = n_1 b_{h-1} + n_2 b_{h-2} + \dots + n_a b_{a-1} + \left(\frac{b_{h-a}}{2a} \right) \tag{5}$$

Where, b_1 defines the binary function at h^{th} individual and n_a indicates the polynomial coefficient where $h > a$. After that, compute fitness of the individuals based on the classifier's accuracy. It is computed as follows:

$$FiFn = Max(AC_{cy}) \tag{6}$$

$$AC_{cy} = \frac{TP_{val} + TN_{val}}{TTL_{val}} \tag{7}$$

Where, TP_{val} indicates the true positive, TN_{val} refers to the true negative, and TTL_{val} denotes the total number of samples.

Then compute dragonflies' objective functions such as separation ($\overline{\overline{SE_k}}$), alignment ($\overline{\overline{AG_k}}$), cohesion ($\overline{\overline{CH_k}}$), attraction to food ($\overline{\overline{AF_k}}$), and distraction from enemy ($\overline{\overline{DE_k}}$). Separation is a tactic used by dragonflies to differentiate themselves from other agents. Alignment refers to individuals aligning their velocity to that of others in the neighborhood. The tendency of individuals to gravitate towards the center of the neighborhood's mass is referred to as cohesion. Attraction to food refers to how the food source draws those who fly towards it. And the inclination of individuals to flee from an opponent is defined as diversion from the enemy. This mathematical behavior is computed as follows:

$$\overline{\overline{SE_k}} = -\sum_{m=1}^L \overline{\overline{B}} - \overline{\overline{B_m}} \quad (8)$$

$$\overline{\overline{AG_k}} = \frac{\sum_{m=1}^L \tilde{v}_m}{L} \quad (9)$$

$$\overline{\overline{CH_k}} = \frac{\sum_{m=1}^L \overline{\overline{B_m}}}{L} - \overline{\overline{B}} \quad (10)$$

$$\overline{\overline{AF_k}} = \overline{\overline{B^+}} - \overline{\overline{B}} \quad (11)$$

$$\overline{\overline{DE_k}} = \overline{\overline{B^-}} + \overline{\overline{B}} \quad (12)$$

Where, L refers to the count of neighboring dragonflies, $\overline{\overline{B}}$ indicates the current individual' position, $\overline{\overline{B_m}}$ denotes the m ^{-th} neighboring agents' position, and, \tilde{v}_m denotes the m ^{-th} neighboring dragonflies' velocity, $\overline{\overline{B^+}}$ refers to food source' position, and $\overline{\overline{B^-}}$ denotes the position of enemy. Then update the dragonflies' using step and position vectors. The movement direction movement of the dragonflies are indicated using the step vector ($\Delta\overline{\overline{B}}$) which is calculated using equation (13).

$$\Delta\overline{\overline{B_{\phi+1}}} = \left(\alpha \overline{\overline{SE_k}} + \beta \overline{\overline{AG_k}} + \gamma \overline{\overline{CH_k}} + \kappa \overline{\overline{AF_k}} + \lambda \overline{\overline{DE_k}} \right) + \varpi \Delta\overline{\overline{B_{\phi}}} \quad (13)$$

Where, $\alpha, \beta, \gamma, \kappa,$ and λ indicates the weight vectors of the ($\overline{\overline{SE_k}}$), ($\overline{\overline{AG_k}}$), ($\overline{\overline{CH_k}}$), ($\overline{\overline{AF_k}}$), and ($\overline{\overline{DE_k}}$), ϕ refers to the iteration count, and ϖ denotes the inertia weight. The position vector of the individuals is updated using equation (14), once the computation of the step vector has been finished.

$$\overline{\overline{B_{\phi+1}}} = \overline{\overline{B_{\phi}}} + \Delta\overline{\overline{B_{\phi+1}}} \quad (14)$$

In DOA, a BRW function is taken into consideration to describe the random walk-in order to enhance the stochastic behaviour, arbitrariness, and exploration of the dragonflies as they fly about the search domain using random walk characteristics. The BRW is one of several physical phenomena where a quantity continually experiences minute random fluctuations. It is thought to be a Markov process with a continuous route and a Gaussian process that takes place continuously over time. It provides good global search capabilities and guards against problems with local optimization. By using BRW, the position of dragonfly is further updated as:

$$\overline{\overline{B_{\phi+1}}} = \overline{\overline{B_{\phi}}} + \Delta\overline{\overline{B_{\phi+1}}} \cdot BRW(\phi) \quad (15)$$

Where, the Brownian random walks ($BRW(\phi)$) obeys a Gaussian distribution with zero mean and time-dependent variance, i.e. ($BRW(\phi) \sim S(0, \psi^2(\phi))$), where, S indicates the number of steps exists in the solution and $\psi^2(\phi)$ refers variance of BRW and it is computed as:

$$\psi^2(\phi) = |dv_0|^2 \phi^2 + (2\hat{F})\phi \quad (16)$$

Where, dv_0 indicates the drift velocity of the system and $\hat{F} = l^2 / (2\tau^*)$ refers to the diffusion coefficient related to the step length l over a short time interval τ during each jump. This process is continued until the optimum solution is found (i.e., optimum weight and bias). Once optimal weight and bias are obtained by SSBRWDOA, the equation (3) is recomputed as follows:

$$Weighted_Sum = \sum_{p=1}^n \tilde{\omega}_{p,q}^{**} \overline{FS}_p + \tilde{\rho}_q^{**} \quad (17)$$

Where, $\tilde{\omega}^{**}$ and $\tilde{\rho}^{**}$ indicates the optimal weight and bias values. The output (\overline{OU}_p) of each neuron in the hidden layer is calculated as follows:

$$\overline{OU}_p = \Omega^* \left(\sum_{p=1}^n \tilde{\omega}_{p,q}^{**} \overline{FS}_p + \tilde{\rho}_q^{**} \right) \quad (18)$$

Where, Ω^* indicates the HSA function. It is a new novel activation function and it is formulated as follows:

$$\Omega^* = 2 * \overline{FS} * \max \left(0, \min \left(1, \left(\varepsilon \overline{FS} * 0.2 + 0.5 \right) \right) \right) \quad (19)$$

Where, ε indicates either a trainable parameter or a constant. As $\varepsilon \rightarrow \infty$, the hard-sigmoid component approaches 0 to 1. Finally, the back-propagation concludes the training process to propagate the computed loss back from the output to the input.

4. RESULTS AND DISCUSSION

Here, the performance of the proposed WBTDMLP with optimal feature selection using MRF is analyzed with the existing approaches. The system was implemented in the working platform of Python with 12 GB of GDDR5 VRAM, and Intel Xeon Processor with two 2.20-GHz cores and 13 GB RAM.

4.1 Dataset Descriptions

To test the proposed model, the proposed system uses Cleveland's heart samples from the UCI repository. The Cleveland dataset has 303 data instances, comprising 13 features, and 1 target variable. The collection includes 138 normal instances and 165 abnormal instances. Here we are using 70% of the data for training and 30% of the data for testing.

4.2 Performance Analysis

In this section, the efficiency of the proposed WBTDMLP is investigated against the conventional DMLP, KNN, SVM, and DT methods. To assess the outcomes of the proposed mode, some evaluation metrics are used such as accuracy, precision, recall, f-measure, Area under Curve (AUC), Root Mean Square Error (RMSE), and Mean Absolute Error (MAE). Figure 2 shows the outcomes of the proposed model with existing methods in terms of accuracy, precision, recall, and f-measure.

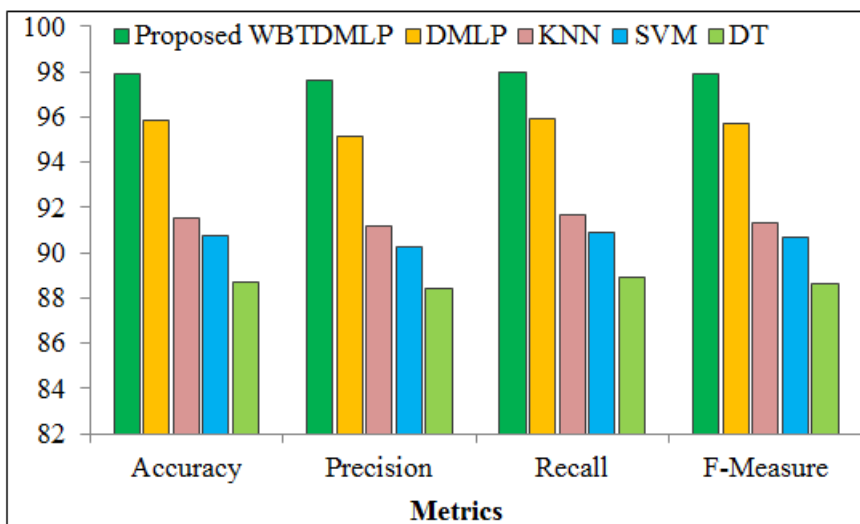


Figure 2: Results analysis of the proposed model

The results clearly shows that the WBTDMLP is the best algorithm for predicting HD, because, it attains better accuracy, precision, recall, and f-measure arte than the existing methods. For example, the existing DMLP offers 95.87 % accuracy, 95.17% precision, 95.93% recall, and 95.68 f-measure, the existing KNN offers 91.56 % accuracy, 91.16% precision, 91.66% recall, and 91.35% f-measure, the existing SVM proffers 90.79% accuracy, 90.29% precision, 90.89% recall, and 90.67% f-measure, and the existing DT provides 88.68% accuracy, 88.45% precision, 88.89% recall, and 88.61% f-measure, which are low-attained values for prediction of HD, but our proposed approach reaches 97.89% accuracy along with 97.61% precision, 97.98% recall, and 97.94% f-measure, which higher than all existing methods. This shows the effectiveness of the proposed approach. Next, table 1 also shows the outcomes of the proposed approach with respect to the AUC, RMSE, and MAE metrics. Herein also, the proposed system has a less error value (RMSE and MAE) and maximal AUC values than the existing methods. For example, first consider the AUC metric, the proposed one has maximum AUC of 0.96, but the existing DMLP, KNN, SVM, and DT have AUC of 0.94, 0.93, 0.89, and 0.86, respectively. Similarly, the proposed one has lower RMSE and MAE of 0.0198 and 0.0009, which is lower when compared to the existing methods. Thus, the overall results show that the proposed work outperformed state-of-the-art methods. The reason is the proposed approach uses MRF based feature selection approach which increases the prediction rate and computational efficiency. Also, the HD prediction is done by WBTDMLP approach, here the weight and bias are optimally chosen by SSBRWDOA, so it decreases the training time and computational complexity.

Table 1: Efficiency analysis of the proposed model

Techniques	AUC	RMSE	MAE
Proposed WBTDMLP	0.96	0.0198	0.0009
DMLP	0.94	0.0231	0.0011
KNN	0.93	0.0309	0.0022
SVM	0.89	0.0521	0.0031
DT	0.86	0.0743	0.0049

5. CONCLUSION

In this paper, a novel weight and bias tune deep multi-layer perceptron for HD prediction with optimal feature selection using modified random forest is proposed. The system comprises three phases, namely, data preprocessing, feature selection, and HD prediction. The experimentation is done by using the Cleveland dataset to assess the proposed work’s performance. The metrics utilized for assessing the proposed work are accuracy, precision, recall, f-measure, AUC, RMSE, and MAE metrics. The proposed work’s outcome is investigated against the conventional DMLP, KNN, SVM, and DT approaches. Here, the proposed work achieves maximum accuracy of 97.89% with minimal 0.0198 RMSE and 0.0009 MAE. Thus, the experimental result evidently appears to prove that the performance of the

proposed model is better as compared to an existing state of art mechanism. In future the proposed work will be prolonged to an efficient dimensionality reduction approach to solve the class imbalance problem and the proposed work's performance is tested with more dataset.

COMPLIANCE WITH ETHICAL STANDARDS

Conflict of Interest: I, Nithya Shree A.P, declares no conflicts of Interest to disclose.

Ethical Approval: This article does not contain any studies with human participants or animals performed by any of the authors.

CONFLICT OF INTEREST

I, Nithya Shree A.P, declares no conflicts of Interest to disclose.

COMPETING INTERESTS

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Not Applicable

RESEARCH INVOLVING HUMAN AND/OR ANIMALS

This article does not contain any studies with human participants or animals performed by any of the authors.

INFORMED CONSENT

Not Applicable.

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