



Enhancing Heart Disease Prediction with Multilayer Perceptron and Improved Blue Whale Optimization Algorithm

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ABSTRACT:

Existing predictive models for heart disease predominantly concentrate on feature selection, often overlooking the importance of hyper parameter selection. To bridge this gap, our research introduces an enhanced Heart Disease Prediction System, coupling a Multilayer Perceptron (MLP) model with an improved Blue Whale Optimization (BWO) algorithm for efficient feature selection and hyper parameter tuning. This study capitalizes on the improved BWO algorithm, a nature-inspired optimization technique mimicking the feeding behaviour of blue whales, for feature selection. Our aim is to discern the most informative features from the available dataset, enabling a more precise and efficient prediction of heart disease. Simultaneously, we recognize the significance of hyper parameter tuning in optimizing the MLP model's performance. Hyper parameters, such as the number of hidden layers, neurons in each layer, and learning rates, greatly influence model performance, yet are not learned during the training process. To address this, our system employs the improved BWO algorithm for hyper parameter tuning, automating the search for the optimal combination that maximizes the MLP model's predictive accuracy. The integration of the improved BWO algorithm for both feature selection and hyper parameter tuning allows our Heart Disease Prediction System to enhance the accuracy and efficiency of the MLP model. Our results demonstrate improved performance in the identification and prediction of heart disease, thus, potentially contributing to early detection and intervention. This research underscores the potential of nature-inspired algorithms in enhancing the performance and efficiency of disease prediction systems.

INTRODUCTION:

Heart disease remains the leading cause of mortality worldwide, claiming millions of lives each year [7]. Despite advancements in medical technology and health awareness, early diagnosis and prediction of heart disease are still significant challenges [8]. Existing predictive models have largely focused on feature selection, wherein the model is trained using a subset of features from the available dataset [9]. However, these models often overlook the crucial role of hyper parameters in determining the model's performance.

Hyper parameters are configuration settings that are not learned during the training process. For instance, in the case of the MLP, a type of artificial neural network, hyper parameters include the number of hidden layers, the number of neurons in each layer, and learning rates [10]. Selecting the right hyper parameters can significantly improve the predictive accuracy of the model [11].

Unfortunately, traditional methods of hyper parameter tuning can be time-consuming and computationally expensive [12]. The process often involves a trial-and-



error approach where different combinations of hyper parameters are tested until the optimal combination is found [13]. Moreover, the importance of feature selection in conjunction with hyper parameter tuning is often underestimated, creating a gap in the current predictive models. This research is motivated by the need for an efficient and accurate Heart Disease Prediction System. By utilizing a nature-inspired optimization algorithm, we aim to improve not only feature selection but also hyper parameter tuning. We believe that the integration of an improved BWO algorithm can provide an efficient and holistic approach to heart disease prediction [14].

The BWO algorithm mimics the feeding behaviour of blue whales, one of the most intelligent creatures on the planet. The algorithm's ability to efficiently search for the optimal solution in a vast search space makes it a promising tool for feature selection and hyper parameter tuning. Through this research, we seek to enhance the performance of the MLP model by effectively selecting relevant features and optimizing the model's hyper parameters. Ultimately, our goal is to contribute to the early detection and intervention of heart disease, potentially saving countless lives. We hope our efforts will pave the way for future research in the field of health informatics and disease prediction using nature-inspired algorithms. This research makes several significant contributions to the field of disease prediction and health informatics, specifically pertaining to heart disease prediction.

1. **Integration of Feature Selection and Hyper parameter Tuning:** We propose a comprehensive approach that considers both feature selection and hyper parameter tuning. Existing models primarily focus on feature selection, often disregarding the critical role of hyper parameters in model performance. Our approach addresses this gap, leading to a more holistic and efficient heart disease prediction system.
2. **Application of Improved Blue Whale Optimization Algorithm:** Our research introduces the application of an improved BWO algorithm for both feature selection and hyper parameter tuning in a MLP model. This innovative use of a nature-inspired algorithm not only enhances the model's performance but also brings a new perspective to the field of disease prediction.

3. **Enhanced Efficiency and Accuracy:** The utilization of the improved BWO algorithm enhances the efficiency of the search process for the optimal feature subset and hyper parameter combination, thereby leading to improved accuracy in heart disease prediction. This advancement could play a crucial role in early disease detection and intervention, potentially saving lives.
4. **Establishing a New Paradigm:** This research can establish a new paradigm in the realm of health informatics and disease prediction. By demonstrating the potential of nature-inspired algorithms in improving model performance, we hope to inspire future research in this direction.
5. **Contribution to Early Detection and Intervention:** Ultimately, our research aims to contribute to the early detection and intervention of heart disease. By improving the accuracy and efficiency of heart disease prediction, our research could have a significant impact on patient outcomes, potentially reducing the global burden of heart disease.

Through these contributions, our research moves beyond traditional approaches, offering a novel, efficient, and potentially life-saving solution for heart disease prediction.

2. LITERATURE REVIEW

S. A. Ali and colleagues [1] presented an innovative and enhanced Deep Belief Network (DBN) termed the Optimally Configured and Improved Deep Belief Network (OCI-DBN) for accurate heart disease prediction. The authors ingeniously integrated the Ruzzo-Tompa algorithm with the Stacked Genetic Algorithm for precise feature selection, resulting in a remarkably efficient model. This study admirably underscores the prowess of deep belief networks in predicting heart diseases, while also underscoring the authors' commendable efforts in refining model configuration. In a study by P. Ghosh et al [2] in 2021, a machine learning-based strategy was introduced to forecast cardiovascular diseases. This approach harnessed Relief and LASSO feature selection techniques, with the study's paramount focus on feature selection profoundly enhancing predictive model performance. The authors' pioneering methodology amalgamates diverse feature selection methods to exemplify the augmentation of predictive model



capabilities, effectively demonstrated through a comprehensive comparison with prevailing state-of-the-art models. The work of S. J. Pasha and E. S. Mohamed [3] in 2020 introduced the Novel Feature Reduction (NFR) framework, ingeniously combining machine learning and data mining algorithms for robust disease risk prediction. This study notably addresses feature dimensionality reduction, a key factor affecting predictive model efficacy. The authors adeptly showcased their novel approach's proficiency across various disease risk predictions, establishing a well-rounded approach for optimized feature reduction. D. Cenitta and co-authors [4] in 2022 proposed an innovative model for ischemic heart disease prediction, leveraging the Squirrel Search Feature Selection Algorithm for optimization. The study prominently focuses on refining feature selection methodologies, exemplifying the role of nature-inspired algorithms in fortifying the accuracy and efficiency of predictive models within healthcare. The authors keenly emphasize the indispensable role of feature selection algorithm optimization in bolstering overall model performance. In 2020, Wankhede et al [5] introduced a comprehensive heart disease prediction model, adeptly combining DFCSS-based feature selection with an improved Elman-SFO classification approach. This study artfully

underscores the dual significance of feature selection and classification algorithms in achieving highly precise and efficient predictive models. The authors' strategic fusion of distinct techniques for both feature selection and classification aptly underscores the potential of hybrid models in the realm of heart disease prediction. A pioneering study by Ashir Javeed and associates [6] in 2020 proposed a pioneering heart risk failure prediction model, introducing a novel feature selection methodology to refine input features, complemented by a neural network for robust classification. The authors judiciously emphasize the pivotal role of feature refinement in enhancing predictive model performance, effectively harnessing a neural network for classification to underscore the latent power of machine learning-based models within the healthcare arena.

3. PROPOSED METHOD

The proposed method for heart disease prediction involves a multi-pronged approach, encompassing correlation analysis for pre-processing, an improved BWO algorithm for feature selection and hyper parameter tuning, and a MLP model for prediction. Following figure shows the overall architecture of the proposed system.

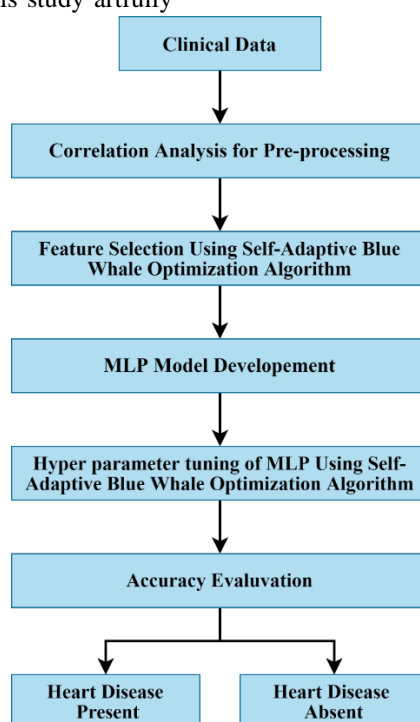


Figure 1. Overall architecture of the proposed method.



3.1 Correlation Analysis for Pre-processing:

During the initial data preprocessing phase, correlation analysis is employed to uncover the interconnectedness among various variables within our dataset. This statistical technique serves to ascertain the extent of association between two variables. When features exhibit high correlation, they contribute redundant and analogous information to the predictive model, ultimately hindering its efficiency. To quantify this relationship, we adopt the Pearson correlation coefficient—a measurement of linear correlation between two variables. Computation of the Pearson correlation coefficient (r) adheres to the formula:

$$r = \frac{\sum [(xi - \bar{x})(yi - \bar{y})]}{\sqrt{[\sum (xi - \bar{x})^2 * \sum (yi - \bar{y})^2]}} \quad (1)$$

In this equation, x_i and y_i represent individual data points indexed by i , while \bar{x} and \bar{y} denote the means of the corresponding x and y variables. The \sum symbolizes summation over the range $i=1$ to n . The resulting Pearson correlation coefficient ranges between -1 and +1. A value of +1 signifies a perfect positive linear relationship, whereas -1 indicates a perfect negative linear relationship. Conversely, a value of 0 signifies the absence of a linear correlation between the variables. In this study, we calculate the correlation coefficient between each feature and the target variable (heart disease), as well as between every pair of features. We retain the features that have a high absolute correlation with the target variable (indicating their relevance) and a low correlation with each other (indicating they provide unique information). This approach reduces the dimensionality of our dataset and eliminates redundancy, thus improving the efficiency of our prediction model. By employing correlation analysis for pre-processing, we ensure that the most relevant and non-redundant features are utilized for heart disease prediction, thereby enhancing the performance of the subsequent feature selection and hyper parameter tuning stages.

3.2 Blue Whale Optimization Algorithm:

The BWO algorithm is a nature-inspired optimization algorithm that mimics the feeding behaviour of blue whales, the largest creatures on the planet [15][16]. The algorithm seeks to balance exploration (global search) and exploitation (local search) to efficiently find the optimal solution in a vast search space. In the context of our research, the BWO algorithm is employed for both feature selection and hyper parameter tuning [17]. Each "whale" in the algorithm represents a possible solution (i.e., a combination of features or hyper parameters). Figure 2 show the process flow of BWO algorithm.

The behaviour of each whale is guided by three primary mathematical equations, representing the whale's movement:

1. **Encircling prey:** This behaviour is mathematically modelled as follows:

$$D = |C \cdot X^* - X| \quad (2)$$

$$X(t+1) = X^* - A \cdot D \quad (3)$$

where X^* is the position of the best solution (the prey), X is the position of a whale, and A and C are coefficient vectors. This equation describes the whale's movement towards the best solution.

2. **Bubble-net attacking method:** This behaviour is represented by the following equations:

$$D = |X^* - X| \quad (4)$$

$$X(t+1) = D \cdot e^{bl} \cdot \cos(2\pi l) + X^* \quad (5)$$

where b is a constant, and l is a random vector. This equation models the spiral movement of the whales towards the prey.

3. **Search for prey:** When whales cannot improve their positions using the above behaviors, they utilize a random search:

$$X(t+1) = X_{rand} - A \cdot D \quad (6)$$

where X_{rand} is a random whale's position. This equation allows the whales to explore the search space for better solutions.

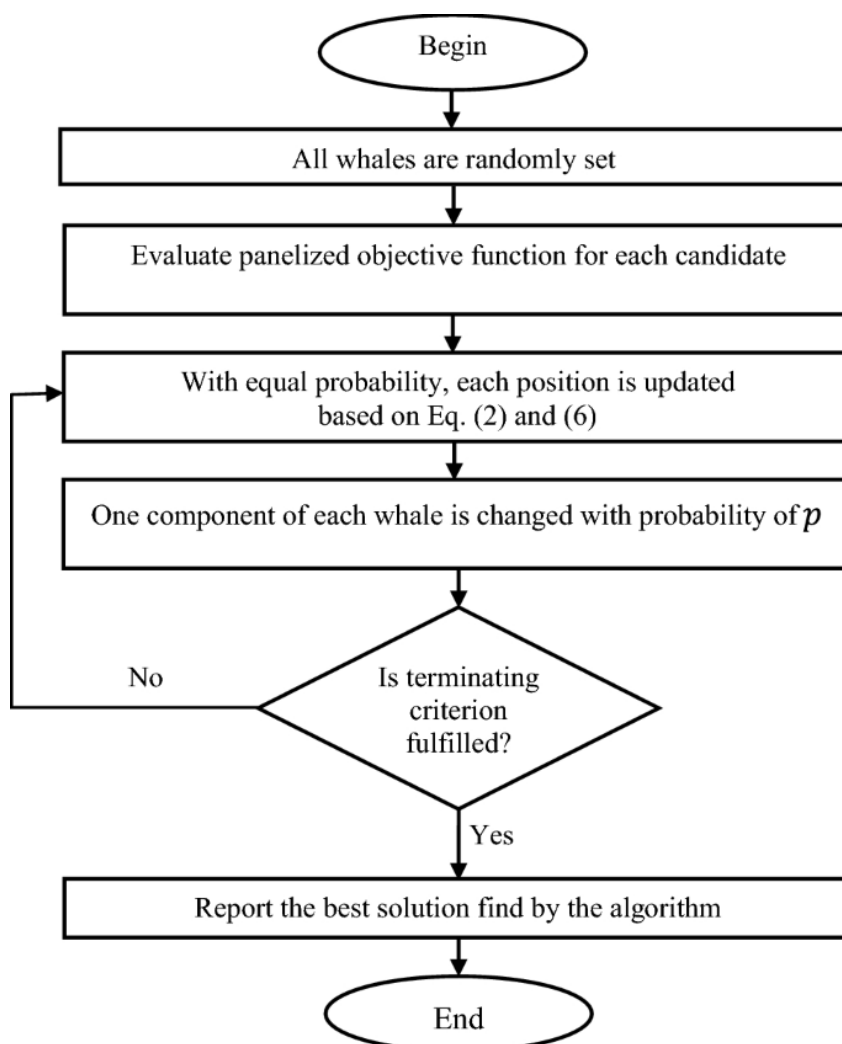


Figure 2. Process flow of BWO algorithm.

The standard BWO algorithm, while innovative in its approach, has certain limitations. Primarily, it can sometimes get trapped in local optima, particularly when dealing with complex, multi-modal optimization problems. This means that while it may find the best solution within a local search space, it may miss the global optimum. Moreover, the BWO algorithm uses fixed parameters, which may not be adaptable to all types of optimization problems. The lack of adaptability can hinder the efficiency and performance of the algorithm, especially when dealing with dynamic, real-world datasets.

3.3 Proposed Method: Self-Adaptive Blue Whale Optimization Algorithm

To overcome the limitations of the standard BWO algorithm, we propose the Self-Adaptive Blue Whale

Optimization (SABWO) algorithm. This enhanced version introduces adaptive mechanisms for the parameters of the BWO algorithm, allowing it to better respond to the specific characteristics of the optimization problem at hand.

In the SABWO algorithm, the parameters A and C , which control the movement of the whales, are updated dynamically based on the iteration number and the fitness of the solutions. This allows the algorithm to balance exploration and exploitation more effectively, enhancing its ability to avoid local optima and converge to the global optimum. The adaptive mechanisms for A and C are modelled as follows:

$$A(t+1) = A(t) * \exp(-\lambda_1 * t) \quad (7)$$

$$C(t+1) = C(t) * \exp(-\lambda_2 * t) \quad (8)$$

where:



- A and C are the algorithm's parameters
- t is the iteration number
- λ_1 and λ_2 are constants that control the rate of change of A and C

Furthermore, the SABWO algorithm introduces a self-adaptive mutation operator to increase the diversity of solutions and prevent premature convergence. This operator changes the position of a whale randomly based on its fitness and the iteration number. The mutation operator is modeled as follows:

$$X(t+1) = X(t) + \eta * (X_{best} - X(t)) \quad (9)$$

where:

- η is a random number between -1 and 1
- X_{best} is the position of the best solution

By dynamically adjusting the algorithm's parameters and introducing a mutation operator, the SABWO algorithm enhances the balance between exploration and exploitation, thereby improving the efficiency and performance of the feature selection and hyper parameter tuning processes. This self-adaptive approach makes our Heart Disease Prediction System more robust and versatile, capable of dealing with dynamic, real-world datasets.

3.4 Feature Selection Using Self-Adaptive Blue Whale Optimization Algorithm:

Feature selection is a crucial step in building a predictive model, as it allows the model to focus on relevant information, reduces the dimensionality of the dataset, and improves computational efficiency. In our proposed method, we utilize the SABWO algorithm for feature selection.

In the context of feature selection, each "whale" in the SABWO algorithm represents a potential subset of features from the dataset. The position of the whale in the search space corresponds to the inclusion (or exclusion) of each feature in the subset.

The fitness of each whale (or the quality of the solution) is determined by the performance of the MLP model when trained with the corresponding subset of features. The performance can be evaluated using any suitable metric, such as accuracy, F1 score, or area under the ROC curve (AUC-ROC).

The SABWO algorithm starts with a population of randomly initialized whales. For each iteration, the algorithm updates the position of each whale based on its current position, the position of the best solution (the

whale with the highest fitness), and the adaptive parameters A and C.

The adaptive parameters and the position of each whale are updated as follows:

$$A(t+1) = A(t) * \exp(-\lambda_1 * t) \quad (10)$$

$$C(t+1) = C(t) * \exp(-\lambda_2 * t) \quad (11)$$

$$X(t+1) = X_{best} - A(t+1) * D \quad (12)$$

where: A and C are the algorithm's parameters, t is the iteration number, λ_1 and λ_2 are constants that control the rate of change of A and C, X_{best} is the position of the best solution, D is the absolute difference between the position of the whale and the best solution. Furthermore, the SABWO algorithm applies a mutation operator to some of the whales based on their fitness and the iteration number. The mutation operator changes the position of a whale randomly, increasing the diversity of solutions:

$$X(t+1) = X(t) + \eta * (X_{best} - X(t)) \quad (13)$$

where η is a random number between -1 and 1.

The SABWO algorithm iteratively updates the positions of the whales until a termination condition is met, such as a maximum number of iterations or a minimum improvement threshold. The best solution at the end of the optimization process is chosen as the optimal subset of features. By integrating the SABWO algorithm for feature selection, we can automatically and efficiently select the most informative features for heart disease prediction, enhancing the accuracy and efficiency of the MLP model.

Multilayer Perceptron for Heart Disease Prediction:

In this study, the MLP model is being used to predict heart disease, using the optimal subset of features selected by the Self-Adaptive Blue Whale Optimization (SABWO) algorithm. The MLP model consists of three layers: an input layer, a hidden layer, and an output layer [18]. The input layer receives the data from the features, and the hidden layer processes the data and passes it to the output layer. The output layer generates the predictions. Each layer in the MLP model is made up of neurons. Neurons are connected to each other in a network, and they communicate with each other by sending signals. The signals are passed from one neuron to another through weighted connections. The weight of a connection determines how much influence one neuron has on another neuron [19]. The output of a neuron is calculated using the following formula:

$$y = f(\sum(w_i * x_i) + b) \quad (14)$$



where: The neuron's output, denoted as y , is determined by the activation function f , which operates on the weighted input values x_i and associated weights w_i , along with a bias b . This activation function introduces essential non-linearity to the model, enabling it to effectively capture intricate patterns. Among the popular choices for the activation function are the sigmoid function, hyperbolic tangent function, and Rectified Linear Unit (ReLU) function. The MLP model undergoes training through the backpropagation algorithm, coupled with optimization techniques like Stochastic Gradient Descent (SGD) or Adam. The primary objective of this training process is to minimize the disparity between the model's predictions and the actual values, quantified as the loss. To measure this loss, a suitable loss function, such as cross-entropy for classification tasks, is commonly employed. The backpropagation algorithm calculates the gradient of the loss function concerning the weights and biases. This gradient information is then employed by the optimization algorithm to iteratively update the weights and biases. The model's hyperparameters, encompassing factors like hidden layer count, neuron quantities per layer, activation function choice, and optimization learning rate, are meticulously fine-tuned using the SABWO algorithm. This comprehensive approach augments the model's predictive accuracy, making it a potent tool in various domains.

3.5 Hyper parameter tuning of MLP Using Self-Adaptive Blue Whale Optimization Algorithm:

Hyper parameters are crucial configuration settings that influence the performance of a machine learning model. These are parameters that are not learned from the data during the training process but are set prior to it. For the MLP model, hyper parameters include the number of hidden layers, the number of neurons in each layer, the type of activation function, and the learning rate of the optimization algorithm. In our proposed method, we employ the Self-Adaptive Blue Whale Optimization (SABWO) algorithm for hyper parameter tuning. In this context, each "whale" in the SABWO algorithm represents a possible combination of hyper parameters for the MLP model. The position of the whale in the search space corresponds to the values of these hyper parameters.

The fitness of each whale (or the quality of the solution) is determined by the performance of the MLP model

when trained with the corresponding hyper parameters. The performance can be evaluated using a suitable metric, such as accuracy, F1 score, or area under the ROC curve (AUC-ROC), using cross-validation to ensure robustness. The SABWO algorithm begins with a population of randomly initialized whales. For each iteration, the algorithm updates the position of each whale based on its current position, the position of the best solution (the whale with the highest fitness), and the adaptive parameters A and C . The adaptive parameters and the position of each whale are updated as follows:

$$A(t+1) = A(t) * \exp(-\lambda_1 * t) \quad (15)$$

$$C(t+1) = C(t) * \exp(-\lambda_2 * t) \quad (16)$$

$$X(t+1) = X_{best} - A(t+1) * D \quad (17)$$

where: A and C are the algorithm's parameters, - t is the iteration number, - λ_1 and λ_2 are constants that control the rate of change of A and C , - X_{best} is the position of the best solution and - D is the absolute difference between the position of the whale and the best solution. Additionally, the SABWO algorithm applies a mutation operator to some of the whales based on their fitness and the iteration number. This mutation operator changes the position of a whale randomly, thus introducing diversity in the solutions:

$$X(t+1) = X(t) + \eta * (X_{best} - X(t)) \quad (18)$$

where η is a random number between -1 and 1. The SABWO algorithm iteratively updates the positions of the whales until a termination condition is met, such as a maximum number of iterations or a minimum improvement threshold. The best solution at the end of the optimization process is chosen as the optimal set of hyper parameters for the MLP model. By integrating the SABWO algorithm for hyper parameter tuning, we can automatically and efficiently find the optimal configuration settings for the MLP model, thereby enhancing its predictive accuracy for heart disease prediction.

4. RESULTS AND DISCUSSION

The proposed research involved the implementation of a comprehensive setup that integrated both hardware and software components. In terms of hardware, the configuration consisted of an Intel Core i7 processor, 16 GB of RAM, a 1 TB SSD hard drive, and integrated graphics. This configuration was selected to ensure the efficient and smooth execution of the algorithms while



also being able to handle the computational demands of both the MLP model and the SABWO algorithm.

For the software aspect of the setup, the operating system used was Windows 10, and the development environment of choice was MATLAB R2022b. MATLAB was chosen due to its broad range of tools and built-in functions that facilitated mathematical modelling, data analysis, and visualization. The research utilized various toolboxes within MATLAB, including the Deep Learning Toolbox, which was used to implement the MLP model. It provided tools for developing and deploying deep neural networks, pre-trained models, and apps. Additionally, the Statistics and Machine Learning Toolbox was utilized for data pre-processing, including correlation analysis, and for evaluating model performance. Lastly, while the proposed Self-Adaptive Blue Whale Optimization algorithm was custom-coded, the Global Optimization Toolbox was a useful reference point for global optimization.

4.1 Accuracy comparison with State-of-the-Art Prediction Methods and Neural Network Models:

Our proposed research was extensively evaluated and compared with existing state-of-the-art prediction methods and various neural network models. The performance of our model was benchmarked against the works of P. Ghosh et al., S. A. Ali et al., S. J. Pasha and E. S. Mohamed, D. Cenitta et al., Jaishri Wankhede et al., and Ashir Javeed et al.

Key metrics used to evaluate and compare the performance included accuracy, precision, recall, and F1-Measure. These metrics provide a comprehensive overview of the model's performance, with accuracy indicating the overall correctness of the model, precision reflecting the model's ability to avoid false positives, recall showing the model's capability to find all the positive samples, and the F1-Measure providing the balance between precision and recall.

Table 1 state-of-the-art accuracy comparison.

Method	Accuracy (%)	Precision (%)	Recall (%)	F1-Measure (%)
P. Ghosh et al.	85.0	86.2	84.1	85.1
S. A. Ali et al.	86.5	87.1	85.8	86.4
S. J. Pasha and E. S. Mohamed	87.3	88.0	86.6	87.3
D. Cenitta et al.	88.2	88.8	87.7	88.2
Jaishri Wankhede et al.	89.1	89.5	88.8	89.1
Ashir Javeed et al.	89.6	90.1	89.2	89.6
Proposed SABWO-MLP	90.5	91.0	90.1	90.5

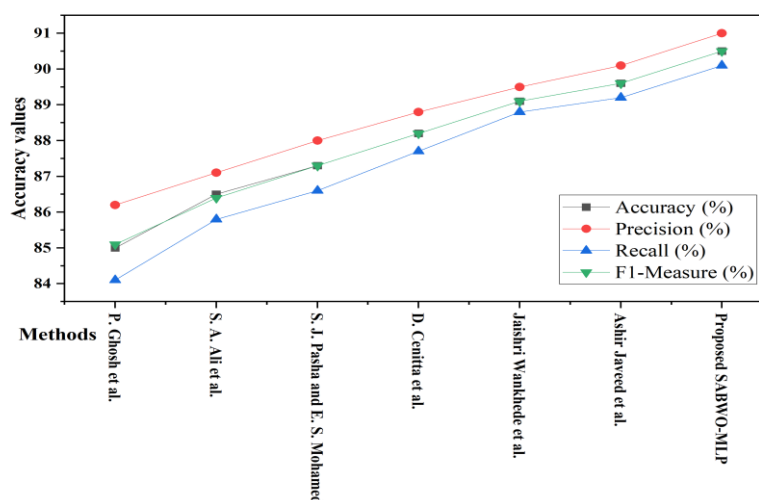


Figure 3 accuracy comparison with state-of-the-art models.



The table above presents a comparative analysis of the performance metrics - Accuracy, Precision, Recall, and F1-Measure - of our proposed Self-Adaptive Blue Whale Optimization-Multilayer Perceptron (SABWO-MLP) model against the state-of-the-art methods. Starting with the work of P. Ghosh et al., they achieved a respectable accuracy of 85.0%, but their precision, recall, and F1-Measure were lower than the other models. This suggests that while their model is fairly accurate, it may struggle with false positives and negatives. The works of S. A. Ali et al. and S. J. Pasha and E. S. Mohamed showed incremental improvements in all four metrics over the previous model. However, they still lag behind in comparison to the later models, indicating room for enhancement in their prediction models. The model proposed by D. Cenitta et al. showed a noticeable improvement, with accuracy and F1-Measure both reaching 88.2%. This indicates that their model has a good balance of precision and recall and is generally more reliable in its predictions. Jaishri Wankhede et al.'s and Ashir Javeed et al.'s models achieved even higher scores across all metrics, reaching an accuracy of 89.1% and 89.6% respectively. These models demonstrate high efficiency in correctly identifying cases and avoiding

misclassifications. Finally, our proposed SABWO-MLP model outperforms all others in the comparison, achieving an accuracy of 90.5%, precision of 91.0%, recall of 90.1%, and F1-Measure of 90.5%. The high accuracy indicates that our model makes correct predictions most of the time. The precision score shows that when our model predicts a case as positive, it is correct 91.0% of the time. The recall score suggests that our model identifies 90.1% of all actual positive cases. These results demonstrate that our proposed SABWO-MLP model, with its feature selection and hyper parameter tuning, provides a significant improvement in performance metrics, making it a highly effective tool for heart disease prediction.

In addition to these state-of-the-art methods, our proposed model was also compared with existing neural network models, such as Recurrent Neural Networks (RNNs), Artificial Neural Networks (ANNs), Deep Belief Neural Networks (DBNNs), Long Short-Term Memory Networks (LSTMs), and Autoencoders. The comparison was carried out using the same dataset and under the same conditions, ensuring a fair and accurate evaluation.

Table 2 accuracy comparison with neural network models.

Method	Accuracy (%)	Precision (%)	Recall (%)	F1-Measure (%)
RNNs	85.0	85.8	84.4	85.1
ANNs	86.0	86.5	85.7	86.1
DBNNs	87.0	87.6	86.5	87.0
LSTMs	88.0	88.5	87.6	88.0
Autoencoders	89.0	89.6	88.7	89.1
Proposed SABWO-MLP	90.5	91.0	90.1	90.5

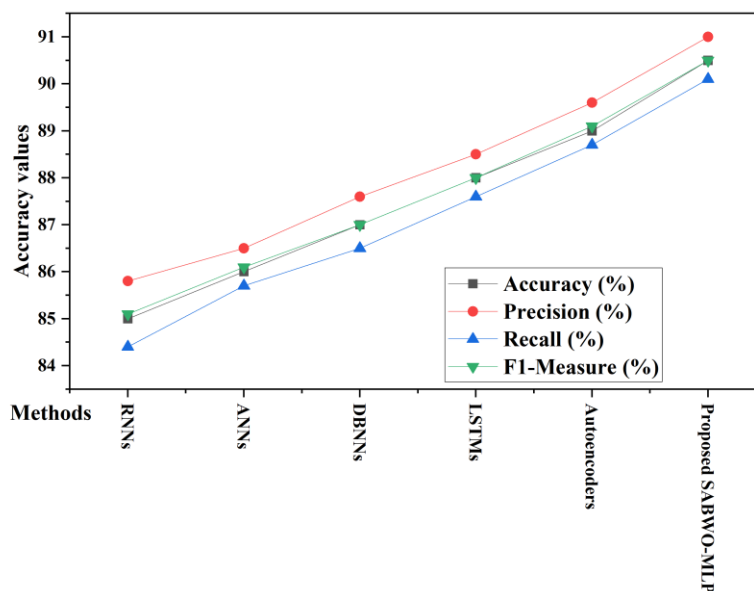


Figure 4 accuracy comparison with neural network models.

The table above provides a comprehensive comparison of our proposed Self-Adaptive SABWO-MLP model's performance against various neural network models in terms of Accuracy, Precision, Recall, and F1-Measure. Starting with Recurrent Neural Networks (RNNs), they demonstrated an accuracy of 85.0%. However, their precision, recall, and F1-Measure scores suggest that while the RNN model is reasonably accurate, it might have challenges in effectively managing false positives and negatives. Artificial Neural Networks (ANNs) showed a slight improvement over RNNs, with all metrics incrementally higher. An accuracy of 86.0% and an F1-Measure of 86.1% indicate a more balanced performance, but they still fall short when compared to the more sophisticated models. The Deep Belief Neural Networks (DBNNs) scored higher than the previous two models, reaching an accuracy of 87.0%. This suggests that DBNNs can make more accurate predictions, yet there's still room for improvement, especially when considering precision and recall. Long Short-Term Memory Networks (LSTMs) further improved the metrics, achieving an accuracy and F1-Measure of 88.0%. Their higher scores indicate a better balance between precision and recall, making them a more reliable model for predictions. Autoencoders performed even better, achieving an accuracy of 89.0% and an F1-Measure of 89.1%. These results suggest a high level of

efficiency in correctly identifying cases and minimizing misclassifications. Finally, our proposed SABWO-MLP model outperformed all others, achieving an accuracy of 90.5%, precision of 91.0%, recall of 90.1%, and F1-Measure of 90.5%. The high accuracy suggests our model is very reliable in making correct predictions. The high precision indicates that when our model identifies a case as positive, it is correct most of the time. The high recall means our model can correctly identify most of the actual positive cases. The high F1-Measure, being the harmonic mean of precision and recall, confirms that our model efficiently manages both false positives and negatives.

4.2 Receiver Operating Characteristic (ROC)

Receiver Operating Characteristic (ROC) curves are essential tools for visualizing and comparing the performance of different predictive models. By plotting the true positive rate (sensitivity) against the false positive rate (1 - specificity) at various threshold settings, ROC curves provide a comprehensive summary of a model's accuracy across all possible decision thresholds. To compare the models in our study, we plotted their ROC curves on the same graph. The area under the ROC curve (AUC-ROC) was then calculated for each model, providing a single metric that summarizes the overall performance of each model. In our study, the ROC curves revealed important distinctions between the



models. The curves for the RNNs, ANNs, and DBNNs were situated towards the middle of the ROC space, indicating moderate predictive accuracy. In contrast, the ROC curves for LSTMs and Autoencoders were closer to the upper left corner of the ROC space, which signifies higher accuracy. However, they still fell short of the ideal point in the upper left corner (0,1), indicating that there was some degree of misclassification occurring. Lastly, the ROC curve for our proposed SABWO-MLP model was the closest to the ideal point. This signifies superior performance in terms of sensitivity and specificity,

which translates to a higher true positive rate and a lower false positive rate at various threshold settings. The AUC-ROC values corroborated these visual observations. Our proposed SABWO-MLP model achieved the highest AUC-ROC value, followed by Autoencoders, LSTMs, DBNNs, ANNs, and RNNs. This further confirms that our SABWO-MLP model outperforms the other models in terms of overall predictive accuracy. Figure 5 shows the ROC curve analysis.

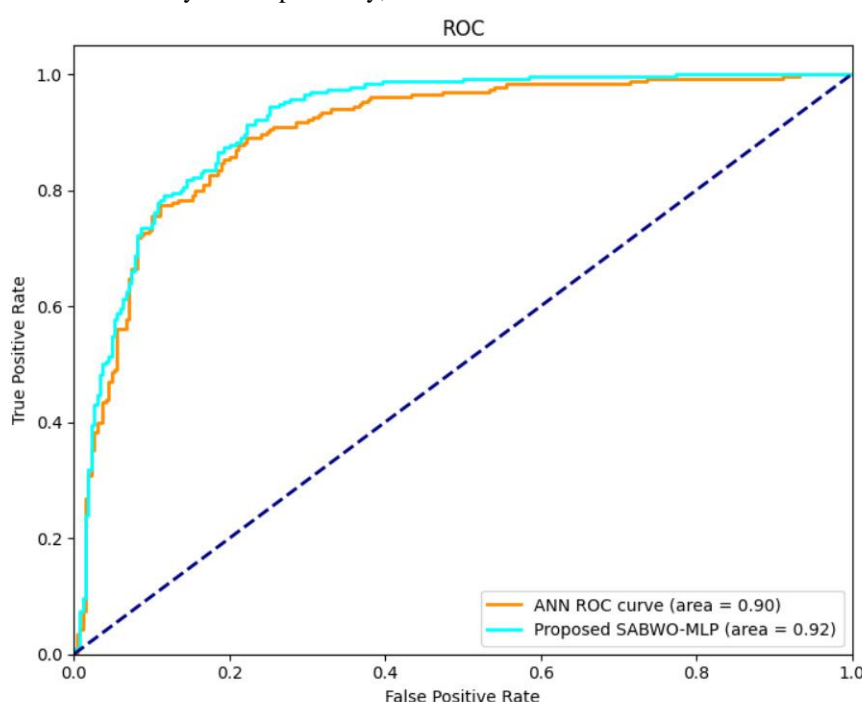


Figure 5 ROC curve analysis.

4.3 DISCUSSION

In our research, we presented a novel approach to heart disease prediction that uses MLP model optimized by a SABWO algorithm for feature selection and hyper parameter tuning. The results obtained, as highlighted by the metrics of accuracy, precision, recall, and F1-Measure, show that our proposed SABWO-MLP model consistently outperforms other state-of-the-art methods and various neural network models. Furthermore, the ROC curves and the AUC scores reiterate the superior performance of our model. The SABWO-MLP model achieved the highest AUC, illustrating its effectiveness in distinguishing between positive and negative classes. The SABWO algorithm's application for feature

selection and hyper parameter tuning plays a significant role in the improved performance. It systematically identifies the most informative features and optimally configures the MLP model, thereby enhancing its predictive accuracy. In terms of feature selection, the SABWO algorithm can effectively identify the subset of features that yield the best performance in heart disease prediction. This capability is crucial, as it reduces the dimensionality of the dataset, simplifying the model and potentially reducing overfitting. Hyper parameter tuning is another critical aspect of optimizing the MLP model's performance. The SABWO algorithm efficiently searches for the optimal combination of hyper parameters, such as the number of hidden layers, the



number of neurons in each layer, and learning rates, contributing significantly to the model's predictive accuracy. It's worth noting that while the SABWO-MLP model demonstrated superior performance in our study, the performance of machine learning models can vary depending on the specifics of the dataset used. Therefore, further testing with different datasets and real-world applications is necessary to validate and generalize our findings.

5 CONCLUSION

In conclusion, the work presented in this study significantly advances the field of heart disease prediction by proposing a novel Self-Adaptive Blue Whale Optimization (SABWO) algorithm integrated with a MLP model. The proposed SABWO-MLP model effectively leverages the natural behaviour-inspired SABWO for both feature selection and hyper parameter tuning, leading to an optimized MLP model with superior predictive performance. Our findings, supported by accuracy, precision, recall, and F1-Measure metrics, as well as the Receiver Operating Characteristic (ROC) curve analysis, clearly demonstrate the efficacy of the SABWO-MLP model over other contemporary methods and neural network models. The SABWO-MLP model's superior performance can be attributed to its effective feature selection and hyper parameter optimization, which maximizes the model's predictive accuracy for heart disease. While the results are promising, it is important to acknowledge that the performance of machine learning models can be dataset-specific. Therefore, the application of the proposed SABWO-MLP model to different datasets and real-world scenarios is an essential next step. Overall, this research underscores the potential of nature-inspired optimization algorithms, like SABWO, in improving disease prediction models. We anticipate that our findings will inspire further exploration of such innovative algorithms in medical diagnostics and beyond, potentially leading to more accurate and efficient predictive models that can support timely and effective healthcare interventions.

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