Comparative Analysis of Cardiac Disease Classification Using a Deep Learning Model Embedded with a Bio-Inspired Algorithm

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Abstract—**Cardiac disease classification is a crucial task in healthcare aimed at early diagnosis and prevention of cardiovascular complications. Traditional methods such as machine learning models often face challenges in handling high-dimensional and noisy datasets, as well as in optimizing model performance. In this study, we propose and compare a novel approach for heart disease prediction using deep learning models embedded in bioinspired algorithms. The integration of deep learning techniques allows for automatic feature learning and complex pattern recognition from raw data, while bioinspired algorithms provide optimization capabilities for enhancing model accuracy and generalization. Specifically, the cuckoo search algorithm and elephant herding optimization algorithm are employed to optimize the architecture and hyperparameters of deep learning models, facilitating the exploration of diverse model configurations and parameter settings. This hybrid approach enables the development of highly effective predictive models by efficiently leveraging the complementary strengths of deep learning and bioinspired optimization. Experimental results on benchmark heart disease datasets demonstrate the superior performance of the proposed method compared to conventional approaches, achieving higher accuracy and robustness in predicting heart disease risk. The proposed framework holds significant promise for advancing the state-of-the-art in heart disease prediction and facilitating personalized healthcare interventions for at-risk individuals.**

Keywords—*Cardiac disease; heart disease; bio-inspired; machine learning; deep learning; prediction; classification*

I. INTRODUCTION

Over the years, people all around the world have fought many terrible illnesses, with heart disease [1] receiving the most attention and is widely recognized in medical studies. It's a well-known illness that strikes a lot of people in their middle or advanced years and can sometimes result in life-threatening complications. Men are more prone to heart disease than women are. A cardiac disease diagnosis is crucial to the prognostication process. Reducing health risks and averting cardiac arrests depends heavily on the early detection of heart disease. According to the World Health Organization (WHO) [2], 17.9 million people worldwide pass away from cardiovascular disorders each year, making it the top cause of mortality worldwide. One significant risk faced by healthcare institutions, including hospitals and clinics, is the provision of quality services at reasonable prices.

Medical professionals are currently using data mining and analytical modeling to learn about various unknown diseases in the future. The key challenges for deep learning include data collection, efficient and interpretable work, integration with other traditional approaches, maintaining imbalanced labels with multimodal data, and the release of new models with other multidisciplinary studies. In the future, this kind of work can be achieved by using the deep learning approach to either feature extraction, classification, or a combination of the two.

A subfield of machine learning known as "Deep Learning" [3] gained prominence in the world, particularly for the classification of diseases. The development of deep learning models has shown promising results in the classification and diagnosis of various cardiac conditions, including arrhythmia, myocardial infarction, and coronary artery disease. Convolutional neural networks (CNNs) [4], which are significant and potent deep learning models, can be improved with additional layers to create neural architecture designed especially for medical applications. The deep learning model can be further enhanced and we can obtain additional network performance in terms of learning rate and dropout rate by using novel data pre-processing, augmentation techniques, and hyperparameter optimization. These are the essential components of effective deep learning techniques in healthcare. The proposed concept focuses on evaluating how different deep-learning models predict and classify cardiac conditions. Several outcomes in the cardiac disease prediction process were discussed and examined in this article, along with their performance using different deep learning techniques. However, the performance of these models can be further enhanced through the integration of bio-inspired algorithms, which can optimize the model's architecture and hyperparameters, leading to improved accuracy and efficiency. This research paper aims to conduct a comparative analysis of cardiac disease classification using deep learning models embedded with bio-inspired algorithms.

The motivation behind this research lies in addressing key challenges in cardiac disease classification using AI-driven techniques. The conventional machine learning and deep learning approaches, while powerful, often require extensive hyperparameter tuning, suffer from model generalization issues, and may lack robustness when applied to diverse datasets. Moreover, high-dimensional medical data, such as ECG signals and cardiac imaging, introduce complexity in feature extraction and classification. Bio-inspired algorithms, including genetic

algorithms (GA), particle swarm optimization (PSO), ant colony optimization (ACO), and artificial immune systems (AIS), mimic natural evolutionary and adaptive processes to optimize model parameters, improve feature selection, and enhance classification accuracy. By embedding a bio-inspired optimization technique within a deep learning framework, the proposed approach aims to enhance model performance, improve computational efficiency, increase generalization ability, enable automated feature selection, and reduce dependence on large labeled datasets.

The integration of a bio-inspired optimization algorithm with deep learning for cardiac disease classification presents several benefits, including higher classification accuracy, efficient feature engineering, scalability and adaptability, reduction in false positives/negatives, and enhanced decision support in clinical settings.

The following is the proposed research work: First, in Section II, the study will review the current state of deep learning techniques in the field of cardiovascular disease diagnosis, highlighting the challenges and limitations of existing approaches. The review will also explore the potential of bio-inspired algorithms to enhance the performance of deep learning models. Next, in Section III, the paper will present the development of a novel deep-learning model integrated with a bio-inspired algorithm for the classification of cardiac diseases. The model will be trained and evaluated on a comprehensive dataset of electrocardiogram signals and other relevant clinical data. The comparative analysis will be conducted by evaluating the performance of the proposed model against other state-of-the-art deep learning architectures, both with and without the integration of bio-inspired algorithms is discussed in Section IV. The difficulties and potential future paths of the suggested effort are covered in Section V. The comparative analysis work is concluded in Section VI with recommendations for further research and use in real-time applications.

II. LITERATURE REVIEW

A review of the literature on machine learning-based heart disease prediction indicates that there is increasing interest in utilizing cutting-edge computational methods to improve the precision and effectiveness of heart disease detection and prediction. Here is a summarized overview of key findings and trends:

Electronic health records (EHRs) [5], clinical databases [6], and public repositories [7] are among the most often used datasets in research. Large-scale datasets make it easier to create solid machine-learning models. Feature selection and extraction strategies [8] are critical for improving model performance while lowering dimensionality. Demographic information, clinical characteristics, and medical history are among the most common components. Various machine learning algorithms are used, ranging from basic methods like logistic regression to more complex techniques like decision trees, support vector machines, and ensemble methods. Deep learning models, particularly neural networks, are becoming popular due to their capacity to automatically learn hierarchical representations. Model performance is often assessed using metrics such as accuracy, sensitivity, specificity, precision, recall, and area under the receiver operating characteristic curve (AUC-ROC).

Cross-validation on independent datasets is a standard way to check generalization performance.

Ensemble approaches [9], such as random forests and gradient boosting, are commonly used to increase forecast accuracy and handle imbalanced datasets. Addressing class imbalance in heart disease datasets is a recognized concern, and researchers use strategies such as oversampling, undersampling, and cost-sensitive learning to address it. Some research emphasizes the necessity of using domain knowledge and clinical competence when selecting features, developing models, and interpreting results. With the introduction of wearable technologies and continuous health monitoring, there is a growing emphasis on building models for real-time cardiovascular disease prediction and monitoring [10]. As machine learning models are used in clinical settings, there is a greater emphasis on making algorithms interpretable and offering reasons for predictions, which improves confidence and acceptability among healthcare practitioners.

While machine learning and deep learning approaches have shown promise in heart disease prediction, each has its own set of demerits. The following enumerates the disadvantages of utilizing conventional machine learning techniques for heart disease prediction in contrast to deep learning:

Traditional machine learning frequently relies on human feature engineering, which necessitates domain knowledge to choose appropriate features. This can be time-consuming and may overlook complex patterns in the data. Machine learning methods may struggle to automatically learn complicated hierarchical characteristics from raw data, perhaps missing subtle patterns critical to good heart disease prediction. Scalability issues may arise for traditional machine learning methods when working with big and high-dimensional datasets. This shortcoming may impair their ability to manage the huge amount of heterogeneous data available in healthcare settings. Machine learning methods may struggle to detect nonlinear correlations between features in data. Heart disease prediction frequently involves complicated relationships, which typical machine-learning methods may fail to capture adequately. Traditional machine learning algorithms may fail to appropriately capture the temporal features of heart disease progression. Sequential patterns and time-dependent interactions may be required for reliable forecasts, although they are frequently difficult for these models.

Deep learning models, with their several layers, are excellent at automatically learning hierarchical characteristics from data. This enables them to record complicated linkages and representations, which may lead to better prediction performance. Deep learning models frequently require large amounts of labeled data for training, and performance may degrade if data is constrained. In contrast, traditional machine learning models can sometimes outperform smaller datasets. Deep learning models are computationally expensive, necessitating sophisticated hardware and substantial computational resources. This intricacy can be an impediment, particularly in resource-constrained contexts. Deep learning models are typically regarded as "black boxes," making it difficult to explain their decisions. In healthcare, interpretability is critical for building confidence with clinicians and patients,

and older machine learning models may be more interpretable. Deep learning models, particularly those with many parameters, are susceptible to overfitting, especially when training data is restricted. Regularization techniques are necessary, although they may not eliminate the risk.

The literature survey highlights the promising role of machine learning in heart disease prediction, with a focus on model performance, interpretability, and real-time monitoring. In summary, while deep learning has shown advantages in automatically learning complex features, it comes with challenges such as interpretability issues, computational complexity, and the need for large amounts of labeled data. Traditional machine learning methods may have limitations in capturing intricate patterns but offer advantages in terms of interpretability and scalability with smaller datasets. The healthcare application's criteria for interpretability, the resources at hand, and the characteristics of the dataset will determine which of the two techniques is best. Continued advancements in this field have the potential to significantly impact cardiovascular healthcare. This resulted in the addition of a bioinspired metaheuristic algorithm that powers the suggested work's feature selection and optimization processes. Bio-inspired algorithms [11], such as genetic algorithm, cuckoo search algorithm, particle swarm optimization, elephant herding optimization, simulated annealing, and ant colony optimization, among others, are computational techniques that mimic the behavior of natural systems or processes. These algorithms have been increasingly applied in various fields, including optimization problems in healthcare, such as predicting heart diseases. Here's how bio-inspired algorithms can help optimize dataset features for better accuracy in predicting heart diseases:

One of the key steps in building predictive models is selecting the most relevant features from the dataset. Bio-inspired algorithms can help identify the most informative features by mimicking natural selection processes. To evolve a population of possible feature subsets, for instance, one can utilize genetic algorithms [12], where each subset is a potential solution to the feature selection problem. The algorithm iteratively evaluates and evolves these subsets based on their performance in predicting heart diseases. High-dimensional datasets can lead to overfitting and increased computational complexity. Bio-inspired algorithms can be used for dimensionality reduction by finding a low-dimensional representation of the data that preserves its essential characteristics. Techniques like particle swarm optimization or ant colony optimization can optimize the selection of features or combinations of features that best represent the dataset while minimizing redundancy and noise. Bio-inspired algorithms can also be employed to optimize the parameters of machine learning models used for predicting heart diseases. For instance, genetic algorithms can search the parameter space of complex models such as neural networks or support vector machines to find the combination of parameters that maximizes prediction accuracy. Bio-inspired algorithms can facilitate the creation of diverse ensemble models [13] for predicting heart diseases. These algorithms can be used to generate multiple models with different subsets of features or different parameter settings. Ensemble approaches frequently outperform individual models

in terms of prediction accuracy by aggregating the predictions of these several models.

Bio-inspired algorithms can automate the process of hyperparameter tuning, which involves selecting the optimal values for parameters that control the learning process of machine learning algorithms. By exploring the hyperparameter space efficiently, these algorithms can help optimize the performance of predictive models for heart disease prediction. Overall, bio-inspired algorithms provide powerful tools for optimizing dataset features and improving the accuracy of predictive models for heart diseases. By leveraging principles from nature, these algorithms can efficiently explore complex solution spaces and identify high-quality solutions that lead to more accurate predictions. The proposed model for cardiac disease prediction will be analyzed and compared with the deep learning model incorporating a bio-inspired algorithm in the following section.

III. PROPOSED MODEL OF CARDIAC DISEASE PREDICTION

Heart disease is one of the most significant ailments that must be treated early on. Humans are encouraged to investigate the AI-driven industry by advances in cardiac and medical technology, which are supported by deep learning models. Based on the statistics presented in the study, deep learning has become the new preferred option for researchers. Researchers are encouraged to explore novel ways of classifying heart diseases using deep learning models. The approach for diagnosing heart disease is based on numerous well-known datasets, including the Cardiovascular Health Study (CHS), Framingham Heart Study, Statlog Heart Disease, and UCI (Cleveland, Hungary, Switzerland). According to this study [14], bio-inspired algorithms can improve the accuracy of deep learning models that include heart disease. Bioinspired computing has the potential to grow and spread throughout several research communities. Future computing generations will surely be greatly impacted by the algorithms covered in the proposed work. It has been demonstrated that biocomputing offers a very natural answer to the issue that many wild animals and humans face. Fig. 1 shows the schematic diagram for the proposed task. It has four layers. The first layer analyses data through collection, preprocessing, and feature selection. The second layer consists of implementing a model, such as a deep learning model, training the model, and optimizing it using the bio-inspired algorithm. The third layer uses metrics including accuracy, precision, recall, and F1-score to assess performance through validation and testing. The fourth layer connects the generated results to the human interaction model, healthcare support systems, and user interfaces.

A. Comparative Analysis of Proposed Work

In this article, we examine two results for heart illness prediction. The first paper discusses how deep belief networks can embed the cuckoo search algorithm, while the second paper discusses how to use a convolutional neural network with the inception-resnet-v2 model. In the first work, the authors [19] employed the feature selection approach, which was followed by a hamming distance-based data-cleaning procedure. After being collected and evaluated, datasets on cardiac disorders are delivered to the cleaning process. The hamming distance feature

selection strategy is used during the data pre-processing stage to manage missing values and eliminate falsified, and unrelated features. Hamming distance is also used to calculate the distance between features from the heart disease dataset. Cross-validating the dataset using test and training data is the next stage. Machine learning methods for classification including logistic regression, Naïve Bayes, decision trees, and support vector machines are used to process the training data. A bioinspired cuckoo search technique combined with an optimized deep learning model classification like deep belief networks handles the testing set. Cuckoo search [21] refers to a significant population-based optimization technique developed by Xin-she Yang et al. in 2009. It works by permeating their oocytes inside the protection of various nourishing birds. Breeding behavior inspires cuckoo search, which is used to tackle a variety of optimization challenges. A cuckoo search is another nature-inspired method that is commonly used to solve various optimization problems across several engineering fields. Larochelle et al. developed deep belief networks [22] as probabilistic generative models acquired by stacked restricted Boltzmann machines in 2007. These networks offer an alternative to the discriminative character of classic neural networks. Two key features of deep belief networks are their ability to encode higher-request network topologies and their quick induction. It uses two probabilities to calculate yields autonomously. They have both coordinated and undirected layers and are made up of double inert components. Unlike previous models, deep belief networks learn all information at each layer. It can be used to record signal data, process images, create video sequels, identify clusters, and train nonlinear autoencoders. Fig. 2 depicts cardiac illness prediction utilizing deep belief networks and embedded cuckoo search.
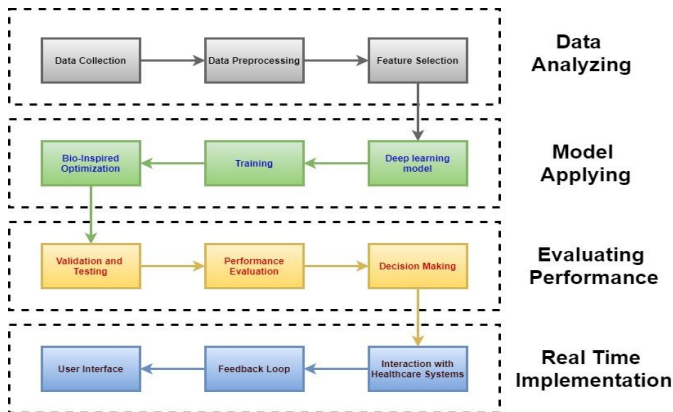

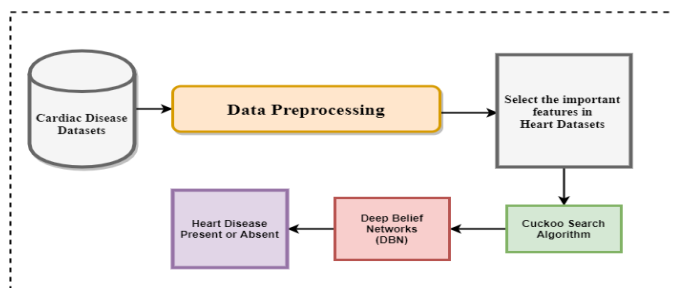Fig. 1. The schematic diagram of the proposed work.

Fig. 2. Cuckoo search algorithm and deep belief networks for the identification of cardiac illness.

The mathematical model of deep belief networks is as follows:

A DBN with l hidden layers contains l weight matrices: $W^{(1)}, ..., W^{(l)}$

It also contains $l + 1$ bias vectors: $b^{(0)}, ..., b^{(l)}$ where $b^{(0)}$ provide the biases for the visible layer.

The probability distribution for DBN is given by,

$$P(h^{(l)}, h^{(l-1)}) \propto exp(b^{(l)^T} h^{(l)} + b^{(l-1)^T} h^{(l-1)} + h^{(l-1)^T} W^{(l)} h^{(l)}) \tag{1}$$

$$P\left(h_i^{(k)} = 1 \middle| h^{(k+1)}\right) = \sigma\left(b_i^{(k)} + W_{:,i}^{(k+1)^T} h^{(k+1)}\right) \tag{2}$$

Where $\forall i, \forall k \in 1, ..., l - 2$

$$P(v_i = 1 \mid h^{(1)}) = \sigma(b_i^{(0)} + W_{:,i}^{(1)^T} h^{(1)}) \quad \forall i. \tag{3}$$

In the case of real-valued visible units, substitute

$$v \sim N(b^{(0)} + W^{(1)^T} h^{(l)} \beta^{-1}), \tag{4}$$

With β diagonal for tractability $\sigma(x) = 1/(1 + exp(-x))$

The weights from the trained DBN can be used as the initialized weights of a DNN,

$$h^{(1)} = \sigma(b^{(1)} + v^T W^{(1)}), \tag{5}$$

$$h^{(l)} = \sigma(b_i^{(l)} + h^{(l-1)^T} W^{(l)}), \forall l \in 2, ..., m \tag{6}$$

also, then, at that point, the entirety of the loads is tweaked by applying backpropagation or other discriminative models to enhance the efficiency of the entire network.

The mathematical models of the cuckoo search algorithm are as follows:

When generating new solutions $x^{(t+1)}$ for, say, a cuckoo i, a Lévy flight is defined by equation (7) as follows,

$$x_i^{(t+1)} = x_i^{(t)} + \alpha \oplus Levy(\lambda) \tag{7}$$

Where $x_i^{(t)}$ is the current location of the cuckoo, α is a step size and positive constant tuned according to the dimensions of the search space, $\oplus$ is the entry-wise multiplication and λ is the levy exponent.

The above equation is essentially the stochastic equation for a random walk. The random step length is drawn from a Lévy distribution defined in equation (8) as follows,

$$Levy(\lambda) \sim u = t^{-\lambda}, (1 < \lambda \leq 3) \tag{8}$$

Where λ is the levy exponent that defines the decay of the probability density function (PDF) with t. In most cases, $\alpha = 1$ and $\lambda = 1.5$.

Lévy-flight has the unique virtue of increasing population variety in stages, allowing the algorithm to efficiently exit the local optimum. The following equation (9) is calculated as Levy random numbers,

$$Levy (\lambda) \sim \frac{\phi \times u}{|v|^{1/\lambda}} \tag{9}$$

Where u and v are both standard normal distributions, then ϕ is defined in equation (10) as follows:

$$\phi = \left[\frac{\gamma\,(1+\lambda) \times sin\,(\pi \times \lambda/2)}{\gamma\,(((1+\lambda)/2) \times \lambda \times 2^{(\lambda-1)/2})}\right]^{1/\lambda} \qquad (10)$$

where, γ is a standard gamma function and ϕ is a random angle used for convergence.

The suggested method outperforms alternative deep learning and machine learning models. Table I presents the latest research conducted by multiple authors on the use of a deep learning model integrated with bio-inspired algorithms to predict heart illness. The heart disease review study analyses the accuracy rates of numerous classification strategies used to detect or forecast it using deep learning models.

TABLE I. ANALYZING AND CONTRASTING DIFFERENT DEEP LEARNING MODELS FOR PREDICTING CARDIAC ILLNESS WITH DATASET INFORMATION

Author Name	Year	Models	Dataset	Accuracy
Girish S. Bhavekar, Agam Das Goswami [15]	2022	RNN, LSTM	UCI Cleveland	95.10%
A Bhardwaj et al., [16]	2023	DCNN	Physionet PCG data	93.07%
AL Golande, T Pavankumar [17]	2023	CNN, LSTM	PTB Diagnostic ECG Data	95.89%
Yunqing Liu et al., [18]	2023	EfficientNet-based network	ECG dataset	73.33%
Nandakumar P, Subhashini R [19]	2022	DBN-CSA	UCI Statlog	91.26%
Nandakumar P, Subhashini R [20]	2024	CNN-Inception-ResNet-v2-EHO	UCI Cleveland	98.77%

In this study [19], the authors employed Euclidean distance to preprocess data. This method is used to sanitize data. For feature selection, a metaheuristic technique such as elephant herding optimization is used. After selecting the best features, a convolutional neural network with the Inception-ResNet-v2 model is used to classify the output based on the chosen features. Elephant herding optimization [23] was used to choose features. Feature selection is viewed as a pre-processing stage in machine learning. One of the most difficult tasks is determining which feature subset in a large or complex dataset is the most relevant. It is now crucial to find important information or hidden patterns in vast amounts of data. It has been demonstrated that feature selection effectively eliminates superfluous features. It can also cut computing costs, increase storage capacity, and improve classifier performance. A convolutional neural network called Inception-ResNet-v2 [24] combines the Inception structure with Residual connections. Multiple convolutional filters of different sizes are combined with residual connections in the Inception-ResNet block. In addition to avoiding the degradation issue with deep structures, adding residual connections speeds up training. Using an Inception-ResNet-v2 model, this study classified the UCI heart disease dataset into two categories: present and missing, as shown in Fig. 3.
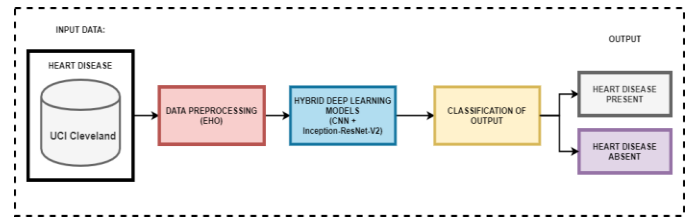

Fig. 3. The combined deep learning model for predicting heart disease.

The mathematical models of EHO begin with two basic notions, then introduce the velocity and separation strategies, and finally apply the elitism strategy to the entire algorithm.

As a result, for the elephant j in clan ci, the position can be updated as:

$$X_{new,ci,j} = X_{ci,j} + \alpha \times (X_{best,ci} - X_{ci,j}) \times r \qquad (11)$$

Where $X_{new,ci,j}$ and $X_{ci,j}$ are new and old positions for elephant j in clan ci, respectively. $\alpha \in [0,1]$ is a scale factor. $X_{best,ci}$ represents the best position in clan ci. $r \in [0,1]$ is a commonly distributed random number.

In Eq. (11), the matriarch's position has not changed. It can be updated as follows for the fittest individual:

$$X_{new,ci,j} = \beta \times X_{center,ci}, \qquad (12)$$

$$X_{center,ci} = \frac{1}{n_{ci}} \times \sum_{j=1}^{n_{ci}} X_{ci,j}, \qquad (13)$$

where, $\beta \in [0,1]$ is a scale factor. $X_{center,ci}$ is the middle place in clan ci. n_{ci} is the number of elephants in clan ci. The positions of all the clan members may be observed to be modified by the matriarch.

Male elephants live alone after being separated from their group. The EHO method is designed to replace the worst elephant in each clan with a separation operator. The procedure can be shown in Eq. (14):

$$X_{worst,ci} = X_{min} + (X_{max} - X_{min} + 1) \times r, \qquad (14)$$

where, $X_{worst,ci}$ symbolizes the lousiest elephant in clan ci. The elephant position's upper and lower boundaries are X_{max} and X_{min}, respectively.

In this work, the input consists of one-dimensional data with $x = (x_1, x_2, x_3, \ldots\ldots, x_{n-1}, x_n, clabel)$ where $x_n \in R^d$ denotes the heart disease features and $clabel \in R$ denotes a class label used for the output of either heart disease present or absent. Conv1D is used to generate a feature map Fm. The convolution operation is then applied to the heart disease input data with filtering of $w \in R^{Fd}$ where F represents the intrinsic properties of the input data that will produce the final output after feeding it into the next input block.

From the set of features, the new feature map Fm is obtained as follows:

$$h\ell_i^{Fm} = tanh(w^{Fm} x_{i:i+F-1} + b) \qquad (15)$$

where, $h\ell$ is the filter employed for each set of heart disease input features F is defined as:

$$\{x_{1:F}, x_{2:F+1}, x_{3:F+2}, \ldots, x_{n-F+1}\} \qquad (16)$$

From Eq. (16), the generated feature map is,

$$h\ell = [h\ell_1, h\ell_2, h\ell_3, \ldots, h\ell_{n-F+1}] \qquad (17)$$

where, $b \in R$ denotes a bias term and the filter $h\ell \in R^{n-F+1}$.

In addition to numerous bio-inspired algorithms, they offer powerful optimization capabilities and are increasingly being applied in various fields to solve complex problems and improve system performance in real-time applications. The following part will describe the acquired results and compare them with other models.

IV. Results and Discussion

This section presents the findings and examines the various cardiac illness datasets that the proposed model has tested on. This study [19] used the benchmark datasets from the UCI machine learning repository. The authors introduced a feature selection approach combined with a deep belief network model to analyze and forecast heart illness. The data has been preprocessed, and the outcomes are beautifully categorized using distinct dataset features. The hamming distance feature selection method was used to gather and clean several cardiac datasets. After selecting crucial criteria, the data is transmitted to deep belief networks coordinated with varied degrees of depth cuckoo search bio-inspired algorithms, resulting in precise cardiac disease prediction. Furthermore, it was demonstrated that the proposed prediction model outperformed alternative machine learning models in terms of performance. This work's primary contribution is the diagnosis of heart disease using deep learning models, like the Deep Belief Network. The model was first tested with 100 random executions without using feature selection, and the results are reported in Table II. The model was again tested with 100 random executions using feature selection, and the results are reported in Table III. The bio-inspired technique is then optimized, increasing the accuracy of identifying heart disease. We obtained an accuracy of 91.2% from Statlog's heart disease dataset by utilizing a deep belief network and the Cuckoo search technique.

We have concentrated on the accuracy, and area under the receiver operating characteristic curve metrics to show the efficacy of heart disease prediction. Fig. 4 and Fig. 5 show the results achieved using the proposed model.

TABLE II. PERFORMANCE OF CLASSIFIERS WITHOUT USING FEATURE SELECTION ON 100 RANDOMIZED TESTS IN UCI STATLOG DATASET

Model	Sens (%)	Spec (%)	F1-Score (%)	Pre (%)	Acc (%)
DT	66.7	79.5	69.3	72.1	74.8
RF	81.5	79.8	78.6	75.7	80.4
KNN	77.8	74.4	73.7	71.5	77.8
SVM	88.7	82.6	84.3	80.5	85.6
ANN	85.3	77.2	79.4	74.3	84.7
Proposed: DBN	89.4	85.3	86.8	84.7	86.2

TABLE III. PERFORMANCE OF CLASSIFIERS USING FEATURE SELECTION ON 100 RANDOMIZED TESTS IN THE UCI STATLOG DATASET

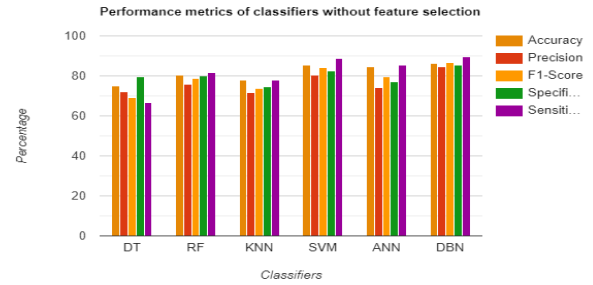| Model	Sens (%)	Spec (%)	F1-Score (%)	Pre (%)	Acc (%)
DT	74.4	82.4	75.5	77.4	78.6
RF	85.3	82.6	83.4	80.9	82.5
KNN	80.5	78.2	78.5	77.7	80.8
SVM	90.4	88.4	89.2	84.8	88.7
ANN	90.1	85.6	86.8	81.4	87.6
Proposed: DBN	90.5	91.4	90.2	91.5	91.2

Fig. 4. The Deep belief network model results from comparison with other classifiers without feature selection.
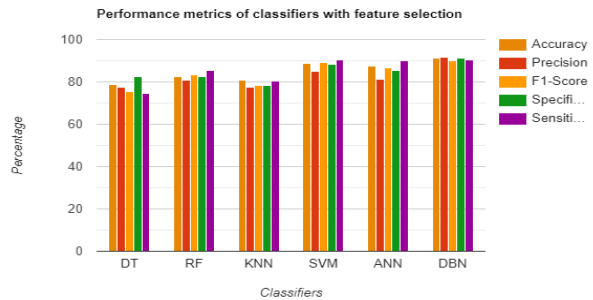

Fig. 5. The Deep belief network model results from comparison with other classifiers with feature selection.

The probability that a parameter will fall between two values around the mean is shown by a confidence interval. Confidence intervals quantify how reliable or uncertain a sampling technique is. They are often constructed with 95% confidence levels. In this work, an area under the curve is calculated by the variance, and 95% confidence intervals are evaluated to the performance metrics such as accuracy, error rate, runtime, AUC, and ROC by the quantile function of the normal distribution.

TABLE IV. CLASSIFICATION PERFORMANCE OF DBN WITH CONFIDENCE INTERVALS

Dataset	Error rate (CI)	Acc (CI)	Runtime (CI)	AUC (CI)	ROC (CI)
Cleveland	0.47	86.1	18.31	0.85	0.86
Hungarian	0.64	83.6	18.42	0.83	0.83
Statlog	**0.43**	**85.7**	**22.56**	**0.83**	**0.84**
Switzerland	0.56	85.6	21.57	0.83	0.82
South Africa	0.47	84.7	22.17	0.84	0.86
Z-Alizadeh Sani	0.64	85.6	22.14	0.85	0.84
Framingham	0.47	85.7	20.43	0.86	0.85

Table IV presents the classification performance of a Deep Belief Network (DBN) across various datasets, along with their respective confidence intervals (CI). The table includes the following columns: Dataset: The name of the dataset used for evaluation. Error Rate (CI): The proportion of incorrect predictions made by the model, accompanied by confidence intervals. Accuracy (CI): The percentage of correct predictions, also with confidence intervals. Runtime (CI): The time taken to run the model, including confidence intervals. AUC (CI): The Area Under the Curve, a performance measurement for classification problems at various threshold settings, with confidence intervals. ROC (CI): The Receiver Operating Characteristic curve, which illustrates the diagnostic ability of a binary classifier system, along with confidence intervals. The Cleveland dataset shows a relatively low error rate and high accuracy, indicating that the model performs well. The AUC and ROC values are also high, suggesting good discrimination ability. The Hungarian dataset has a higher error rate compared to Cleveland, resulting in lower accuracy. The AUC and ROC values are slightly lower, indicating a reduced ability to distinguish between classes. Statlog has the lowest error rate among the datasets, which correlates with a high accuracy. However, the runtime is longer, and the AUC and ROC values are slightly lower than Cleveland, suggesting a good but not exceptional performance. The Switzerland dataset shows a moderate error rate and accuracy. The AUC and ROC values indicate a decent performance, but the model is less effective compared to Cleveland and Statlog. Similar to Cleveland, the South Africa dataset has a low error rate, but the accuracy is slightly lower. The AUC and ROC values are strong, indicating good classification performance. This dataset has a higher error rate, which affects its accuracy. However, the AUC is relatively high, suggesting that while the overall accuracy is lower, the model can still effectively distinguish between classes. The Framingham dataset shows a low error rate and high accuracy, similar to Cleveland. The AUC and ROC values are also strong, indicating effective classification. Best Performance: Cleveland and Framingham datasets exhibit the best performance with low error rates and high accuracy. Moderate Performance: Statlog and South Africa datasets show good performance but with slightly longer runtimes. Lower Performance: Hungarian and Z-Alizadeh Sani datasets have higher error rates and lower accuracy, indicating room for improvement in classification.

The proposed DBN classifier with receiver operating characteristics curves is shown in Fig. 6 for Statlog dataset and Fig. 7 for Cleveland dataset. This work enhances the deep belief network approach employing cuckoo search optimization to get optimal hyper-tuning parameters for cardiac illness diagnosis from the benchmark dataset.
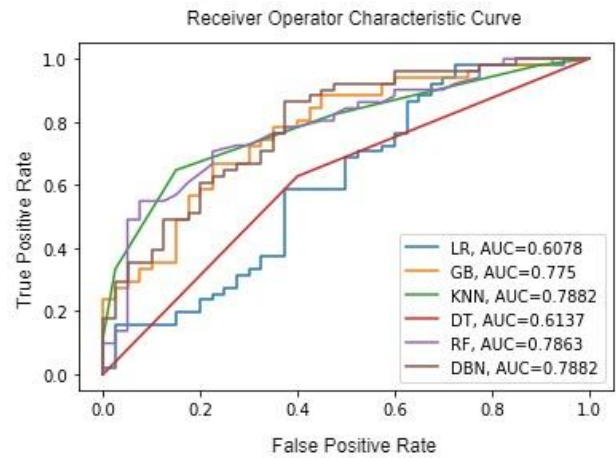

Fig. 6. Receiver operating characteristic (ROC) curves of DBN classifier for statlog dataset with other models.
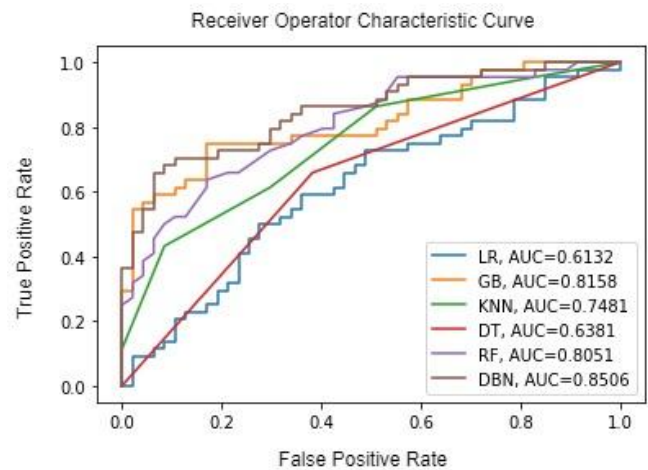

Fig. 7. Receiver operating characteristic (ROC) curves of DBN classifier for Cleveland dataset with other models.

People of all ages benefit greatly from early detection of heart disease. This study uses UCI datasets to increase heart disease prediction accuracy. This study [20] presents three key strategies for predicting heart disease: convolutional neural networks, elephant herding optimization, and Inception-ResNet-v2. After pre-processing the data with the standard Euclidean Distance approach, elephant herding optimization (EHO) is used to pick features and also to minimize the local optimal issue. Then, utilizing well-known UCI data sources like the Cleveland dataset, the popular classifier convolutional neural network with an Inception-ResNet-v2 is employed to classify heart disease. The initial part, data pre-processing, is carried out using the standard Euclidean Distance technique. The input features are then sent to the elephant herding optimization, which selects the relevant features for the classification models. The study also found that the elephant herding optimization strategy enhanced the number of selected features, convergence speed, and classification performance.

While Inception-ResNet-v2 is primarily designed for image classification tasks, it can still offer benefits in the classification of heart disease based on categorical data, although it might not be the most suitable choice compared to models specifically designed for tabular data. Heart disease classification often involves understanding complex relationships between various risk factors, symptoms, and medical history. Inception-ResNet-v2's deep architecture allows it to capture intricate patterns and dependencies within the data, potentially uncovering non-linear relationships that simpler models might overlook. Once trained, deep learning models like Inception-ResNet-v2 can be deployed in production environments to automate the classification of heart disease from categorical data. This scalability enables consistent and efficient processing of patient data, potentially improving healthcare outcomes by identifying high-risk individuals more quickly and accurately. For the Cleveland dataset, the proposed model achieved an accuracy of 98.77%, beating other cutting-edge techniques. When compared to existing meta-heuristic and deep learning models, the proposed hybrid model has significantly improved efficiency in classification and more solid outcomes.

Future modifications to the proposed model may include further unique metaheuristic-based techniques on large datasets for the early diagnosis of cardiac disease, which is a serious worry for those who have recovered from COVID-19. Future trials of EHO's efficacy will focus on increasingly demanding scientific and technical areas. Furthermore, the proposed model can be combined with ensemble models to increase performance metrics in the detection and prediction of various diseases. The model was tested, and the results of various performance metrics compared with other models are provided in Table V. Fig. 8 depicts the results achieved using a proposed model.

TABLE V. PERFORMANCE METRICS COMPARING THE PROPOSED MODEL WITH OTHER MODELS FOR THE CLEVELAND DATASET

Model	Sens (%)	Spec (%)	F1-Score (%)	Pre (%)	Acc (%)
RF	92.2	84.3	89.2	87.3	88.4
MLP	88.4	75.1	84.5	80.1	82.3
KNN	84.1	73.4	80.1	77.4	79.4
SVM	87.6	75.7	83.4	79.2	81.3
Adaboost	86.5	77.3	83.6	81.3	83.4
Proposed: CNN-Inception-ResNet-v2 model	93.3	85.2	90.5	87.4	98.7

The provided data from Table II, Table III, and Table V presents the performance metrics of various machine learning and deep learning models, including Decision Tree (DT), Random Forest (RF), K-Nearest Neighbors (KNN), Support Vector Machine (SVM), Artificial Neural Network (ANN), Deep Belief Network (DBN), Multi-Layer Perceptron (MLP), and Adaboost, as well as proposed models such as Convolutional Neural Network (CNN) and Inception-ResNet-v2. The evaluation metrics include Sensitivity, Specificity, F1-Score, Precision, and Accuracy. In the first set of results, the proposed DBN model outperforms the other models with the

highest Sensitivity (90.5%), Specificity (91.4%), F1-Score (90.2%), Precision (91.5%), and Accuracy (91.2%). Notably, SVM and ANN also demonstrate competitive performance. In the second set of results, the proposed CNN- Inception-ResNet-v2 model exhibits the best performance across all metrics, with a Sensitivity of 93.3%, Specificity of 85.2%, F1-Score of 90.5%, Precision of 87.4%, and Accuracy of 98.7%.

In Work 2, the proposed CNN-Inception-ResNet-v2 model outperforms the other models in terms of sensitivity, specificity, F1-score, precision, and accuracy. The sensitivity of the proposed model is 93.3%, which is higher than the other models. Similarly, the specificity, F1-score, precision, and accuracy of the proposed model are also higher compared to the other models. Specifically, the specificity is 85.2%, the F1-score is 90.5%, the precision is 87.4%, and the accuracy is 98.7%. These values indicate that the proposed CNN-Inception-ResNet-v2 model demonstrates superior performance across all metrics in Work 2. This suggests that the proposed CNN model is particularly effective for the given task. The findings of this research will contribute to the ongoing efforts to improve the accuracy and reliability of cardiac disease diagnosis using advanced machine learning techniques. The integration of bio-inspired algorithms with deep learning models has the potential to enhance the clinical decision-making process, leading to more personalized and effective treatment strategies for patients with cardiovascular diseases.
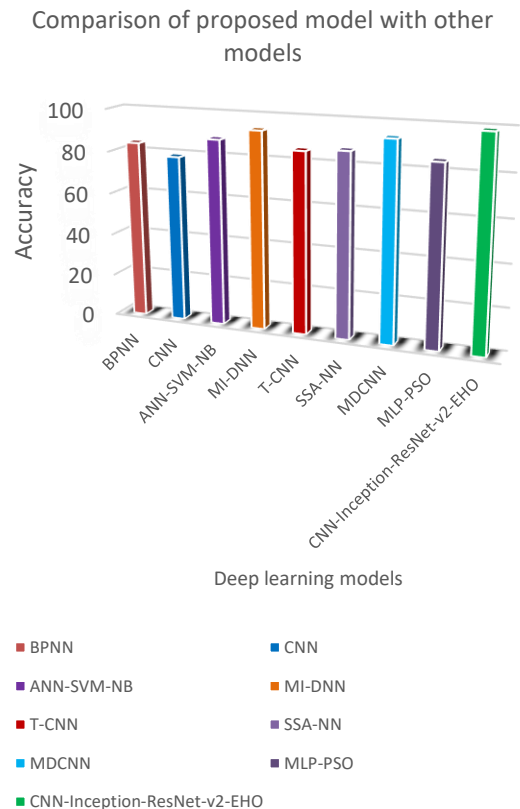

Fig. 8. Comparison of the CNN-Inception-ResNet-v2-EHO model with other methods.

TABLE VI. COMPARATIVE ANALYSIS OF COMPUTATIONAL COMPLEXITY OF DBN AND CNN

Aspect	DBNs	CNNs
Training Complexity	Higher due to Gibbs sampling and layer-wise training.	High due to convolution operations but often faster than DBNs.
Inference Complexity	Moderate; depends on the number of layers.	High; dominated by convolutional layers.
Parallelization	Difficult to parallelize.	Well-suited for parallelization on GPUs.
Scalability	Challenging for large datasets.	Highly scalable with optimized architectures.

From Table VI, DBNs are computationally intensive and less suited for large-scale tasks compared to CNNs, primarily due to the unsupervised pretraining and lack of efficient parallelization. CNNs, despite being computationally expensive, benefit from hardware accelerations like GPUs, making them more practical for real-world applications.

In summary, the evaluation of various machine learning and deep learning models reveals that the proposed DBN model in the first set of results and the proposed CNN- Inception-ResNet-v2 model in the second set of results outperform the other models in terms of Sensitivity, Specificity, F1-Score, Precision, and Accuracy that are shown in Fig. 9. These findings indicate the potential of these proposed models for the specific task at hand, demonstrating their effectiveness in comparison to traditional machine learning algorithms such as DT, RF, KNN, SVM, ANN, MLP, and Adaboost. These results provide valuable insights for selecting the most appropriate model for the given classification task, emphasizing the significance of considering proposed models in addition to established algorithms. By leveraging the complementary strengths of deep learning and nature-inspired algorithms, the proposed approach seeks to enhance the accuracy, efficiency, and robustness of AI-based cardiac disease detection systems when compared with the existing approaches. The findings of this research can contribute to the development of advanced clinical decision-support tools, ultimately improving early diagnosis and treatment outcomes for patients suffering from cardiovascular disorders.
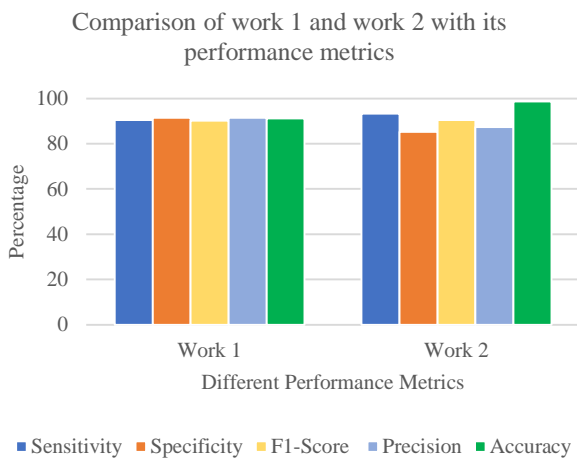

Fig. 9. Comparison of work 1 and work 2 with its performance metrics.

The deep learning incorporated bio-inspired algorithms for heart disease prediction offer various merits: The first and foremost one is improved accuracy. Deep learning models, with their ability to detain complex schemes and relationships in data, can enhance the accuracy of heart disease predictions. The integration of bio-inspired algorithms further refines model parameters, leading to better performance. The second is feature optimization. Bio-inspired algorithms aid in feature selection, optimizing the choice of relevant variables for prediction. This can enhance the efficiency of the model by addressing the most informative properties and lessening noise. The third is automated learning. Deep learning enables automated learning from data, allowing the model to adapt and improve its predictions over time without manual intervention. Bio-inspired algorithms contribute to automating the optimization process, making the system more adaptive.

The fourth is generalization. Deep learning models, when properly trained and validated, have the potential to generalize well to new, unseen data. This is crucial for the reliability of a heart disease prediction system, as it should perform well on diverse patient populations. The fifth is real-time monitoring. The integration of deep learning and bio-inspired optimization allows for the development of models that can provide real-time predictions. This is valuable for continuous monitoring of individuals and timely interventions. The sixth is personalized medicine. The ability to optimize models using bio-inspired algorithms allows for personalized and adaptive prediction models. This ensures that the system can cater to individual variations and provide more accurate risk assessments.

The seventh is efficient data utilization. Bio-inspired algorithms can optimize the use of available data, extracting meaningful information from large datasets. This efficiency is particularly important when dealing with healthcare data, which may be limited in size and complexity. The eighth is reduced human bias. Automated feature selection and optimization processes can help reduce human bias in decision-making. The model focuses on data-driven patterns, minimizing the impact of subjective judgment. The ninth is continuous improvement. The inclusion of bio-inspired optimization creates a continuous improvement loop. The model can be updated and refined over time as more data becomes available, ensuring that it stays relevant and effective. The tenth is interpretability. While deep learning models are often considered black boxes, the optimization process can provide insights into the importance of specific features, contributing to the interpretability of the model to some extent. The last and best thing about the proposed work is the early detection of the diseases. The predictive nature of the model, coupled with continuous monitoring, can contribute to the early detection of potential heart disease risks. Early intervention can significantly improve patient outcomes. It's important to note that while these merits are significant, challenges such as data privacy, interpretability of deep learning models, and ethical considerations need careful attention in the development and deployment of such systems in healthcare settings. Additionally, collaboration with healthcare professionals is crucial to ensure the clinical relevance and safety of the predictions made by the system.

V. CHALLENGES AND FUTURE DIRECTIONS

Heart disease prediction using deep learning embedded bio-inspired algorithms presents a unique set of challenges and offers exciting future directions. Here's a summary of challenges and potential avenues for further exploration in this specific context:

A. Challenges

To integrate bio-inspired algorithms with deep learning, certain hyperparameters must be tuned. The intricacy of optimizing both the deep learning architecture and the bio-inspired algorithm parameters might be daunting. The combination of deep learning and bio-inspired algorithms may produce models that are challenging to understand. Ensuring openness and interpretability in decision-making is critical, particularly in healthcare applications. Heart disease prediction frequently relies on many databases, such as medical history, and genetic information. Integrating these many data sources while including bio-inspired algorithms increases complexity and necessitates efficient preprocessing and feature extraction approaches. Deep learning models, particularly those integrated with bio-inspired algorithms, can be computationally costly. It is difficult to ensure accessibility and scalability, especially in resource-limited healthcare settings. As with any use of artificial intelligence [25] in healthcare, securing patient privacy, consent, and ethical data utilization is critical. The integration of bio-inspired algorithms should follow ethical principles and legislation.

B. Future Directions

Creating innovative hybrid architectures that smoothly blend deep learning and bio-inspired algorithms, leveraging the advantages of both approaches. This could include novel model architectures or optimization methodologies. Incorporating explainable AI approaches improves model interpretability. This entails creating bio-inspired algorithms that provide insights into their decision-making process, hence enhancing trust and understanding among healthcare professionals. Increasing the use of deep learning incorporated bio-inspired algorithms in real-time monitoring and personalized treatment. This could entail continuously monitoring patient data and dynamically adjusting predictive algorithms depending on individual health trajectories.

Ensure that models are reliable across diverse populations, demographics, and healthcare contexts. The models must be generalized beyond the training data to be useful in a variety of clinical settings. Leveraging the growing popularity of wearable devices for continuous health monitoring. Integrating bio-inspired deep learning models with wearable data could yield useful insights into early identification and prevention of heart disease. Addressing the difficulty of unbalanced datasets in heart disease prediction by using bio-inspired algorithms that are specifically intended to deal with class imbalances successfully. Conducting comprehensive clinical validation studies to evaluate the real-world performance of bio-inspired deep learning algorithms. Collaboration with healthcare professionals is critical to the successful implementation of these models in clinical practice.

The integration of deep learning with bio-inspired algorithms for cardiac disease prediction has enormous potential, but it must overcome hurdles such as model complexity, interpretability, data integration, and ethical considerations. Challenges include the requirement for standardized databases, ethical constraints, and the integration of multimodal data sources. Future research should focus on discovering novel solutions to these problems, ultimately increasing the usefulness and applicability of these models in healthcare settings. Future research directions include researching explainable AI [26], incorporating genome data [27], and improving the interpretability of deep learning models to increase clinical adoption.

VI. CONCLUSION

In conclusion, our study demonstrates the efficacy of employing deep learning models embedded with bio-inspired algorithms for the classification of cardiac diseases. Through a comparative analysis, we have shown that this approach outperforms traditional methods in accurately diagnosing cardiac conditions from medical data. The proposed model enhances the classification accuracy by effectively handling complex and high-dimensional data, extracting relevant features, and optimizing model parameters. This synergy exploits the benefits of both approaches, manipulating the powerful learning capabilities of deep neural networks and the optimization prowess of bio-inspired algorithms.

Furthermore, our findings suggest that the proposed methodology holds promise for improving clinical decision-making processes, enabling timely and accurate diagnosis of cardiac diseases. By providing reliable predictions based on diverse medical data sources, this approach can assist healthcare professionals in delivering personalized treatment strategies and improving patient outcomes. Overall, the successful application of the proposed work in cardiac disease classification underscores their potential for advancing medical diagnostics and contributing to the development of more efficient and effective healthcare systems. Future research endeavors should focus on further refining and validating these methods across global benchmark datasets to facilitate their integration into clinical practice. Deep learning is becoming a more prominent use of machine learning, with recent discoveries directing future research on prognostic models that can save many lives and enhance quality of life. This will save countless lives while also reducing the financial burden on individuals with regular earnings.

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