

# Hybrid Model for Coronary Artery Disease Classification Based on Neural Networks and Evolutionary Algorithms

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The human body is a vital source of data such as images and signals. The signals are collected from different human organs and utilized in diagnosing different diseases. The designing and implementation of intelligent computer programs that try to emulate human intelligence are a sign of the integration of various sciences and areas of knowledge. The development of technologies associated with Artificial Intelligence (AI) techniques that are applied to medicine, represents a novel perspective, which can reduce costs, time, and medical errors. Coronary artery disease (CAD) killed many people in the world, it is considered the most common type of heart disease. This paper uses different evolutionary algorithms to optimize the neural network parameters to enhance the classification process of Coronary Artery Disease (CAD). A hybrid system that combines a Genetic Algorithm (GAs), Biogeography-Based Optimization (BBO) with neural networks (NNs) [GAsBBO-MLPNNs] is proposed to enhance the accuracy of CAD. This paper concentrates on the medical classification system for heart disease on CAD using the Z-Alizadeh Sani dataset as a benchmark. The proposed GAsBBO-MLPNNs outperformed other hybrid models such as; Biogeography-Based Optimization (BBO) and particle swarm optimization (PSO) methods combined with NNs, and previous works, where the method performance parameters result represented as 94.5%, 96.4%, and 94.8% accuracy, sensitivity, and specificity respectively.

**Keywords:** classification, heart disease, multi-layer perceptron neural network, genetic algorithms, particle swarm optimization, biogeography-based optimization

## 1. INTRODUCTION

Heart disease comprises a wide range of cardiovascular diseases. Types of heart disease include coronary artery disease (CAD) which is the most common type of heart disease, another type are Arrhythmia, heart failure, heart valve disease, heart muscle disease, congenital heart disease [1]. The plaque that accumulates in the inner surface of the coronary arteries causes the inner surface to become irregular and narrow. This plaque leads to blockage in the main arteries of the heart and reduces the blood flow to the heart muscle. Over time, this blockage can lead to a heart attack [2] There are many responsible factors for heart disease such as smoking, high blood pressure, family history, *etc.* These factors are used to decide by evaluating the test result of the patients. This process is difficult because it's not easy to consider the number of factors used in the evaluation process, as a result, the diagnosis of heart disease requires a high experience from scientists. However, recent research shows that artificial intelligence plays an important role in

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predicting and preventing different types of heart diseases [3]. Coronary heart disease (CHD) is a common type of heart disease that kills over 370,000 people every year [4].

For that, several tools and methods were proposed to develop an effective support medical decision support system. Moreover, day by a day, there is new methods and tools are continuing to be developed by the researcher in this field. The medical artificial intelligence (AI) in its conception depends on the structure of medical information and a set of other sciences, methods, and techniques that include computer science, the systemic analysis applied to medicine, statistics, logic, linguistics, decision-making theory, and modeling [5] AI in medicine has two main branches: physical and virtual. [6] The physical branch is represented by using robots to assist in surgeries and to assist elderly patients. While the virtual branch is represented by collecting information from electronic health records and signals to use it in control health management systems, and active guidance to the doctors in diagnosing diseases and making treatment decisions [6]. The researchers collect signals from different human organs and analyze them using various techniques such as neural networks, fuzzy logic, support vector machine, *etc.* to diagnose the diseases with high accuracy and less time. Some important signals are Electrocardiogram (ECG) and Electromyogram (EMG), in [7] the author uses an EEG signal to diagnose Alzheimer's disease.

Neural Networks (NNs) are paradigms computationally based on mathematical models with the ability of strong pattern recognition. They are calculation algorithms based on an analogy of the nervous system, which tries to imitate the human ability to learn, making it learn to identify patterns of association between inputs (predictive variables) and their dependent states (outputs). Neural Networks (NNs) are the widest classification technique used, where the systems can learn through training numbers of neural networks then combine their results, and it can generalize the results from the training data [8]. Evolutionary Algorithms (EAs) represent a simulation strategy to solve complex problems based on the theory of natural evolution and the theory of genetic variation. Thus, they try to find a set of values given function. EAs can be used efficiently to optimize the NNs parameters [9].

This paper aims to improve the accuracy of heart disease prediction using a Hybrid model of NNs and EAs [10]. Three optimization algorithms in which biogeography-based optimization (BBO) [11], genetic algorithms (GAs) [12], and particle swarm optimization (PSO) [13] were combined with NNs that are proposed to address this problem. In this paper, all the experiments were performed on the Z-Alizadeh Sani dataset, where the process starts with using the dataset as input and applying the preprocessing method such as feature selection and data normalization. These selected features are used as input data to improve the classification accuracy of heart disease by combining EAs with NNs. In this paper, a hybrid Genetic Algorithm – Biogeography-Based Optimization Based Neural Network (GAsBBO-MLPNNs) was proposed to improve the accuracy result in an international CAD Z-Alizadeh Sani dataset.

The paper is organized as follows. Section 2 will introduce a set of previous works within the same research field. Section 3 will illustrate the algorithmic foundations of the proposed approach, dataset description, the preprocessing phase, implementation platform, system parameters, and the performance metrics will be presented in Section 4. The experimental Result will be presented and discussed in Section 5. Conclusions and future works will be discussed in Section 6.

## 2. RELATED WORKS

The purpose of this research is the creation of a model to classify and to provide predictive analysis on the diagnosis of coronary artery disease through using artificial intelligence techniques. The main objective of applying artificial intelligence techniques to classify international CAD datasets is to help medical specialists process the non-linear data automatically and find the correct diagnosis. In previous years, many researchers have used different artificial intelligence techniques to predict and diagnose CAD. Alizadehsani *et al.* [15] proposed a data mining method for the diagnosis of CAD on the Z-Alizadeh Sani dataset. They performed a comparison study between four algorithms: Naïve Bayes, Sequential Minimal Optimization (SMO) classifiers, and Neural Network. Also, they created three features which are left anterior descending (LAD), left circumflex artery (LCX), and right coronary artery (RCA) to improve the performance of the proposed methodology. The highest accuracy which has been achieved is 92.09% by using the SMO, Alizadehsani *et al.* [16] used a support vector machine (SVM) to improve the prediction of CAD, the proposed “feature engineering method” uses the result of three classifiers, *i.e.* LAD, LCX, and RCA in the training dataset. The proposed applied to the Z-Alizadeh Sani dataset which extended to 500 records. It has achieved accuracy, sensitivity, specificity, 96.40%, 100%, and 88.1%, respectively for detecting CAD. Chen *et al.* [17] used big data mining and cloud computing in the “Disease Diagnosis and Treatment Recommendation System” (DDTRS). The proposed consisted of two modules: a Density-Peaked Clustering Analysis (DPCA) algorithm to identify the link between disease and symptoms based, and a disease diagnosis and treatment recommendation module. The result shows that the proposed provides a high-quality recommendation with a low latency response.

Sahoo *et al.* [18] proposed a process that uses NNs and SVM to extract features from four types of ECG signals. These features are used to diagnosis the cardiac abnormalities: Normal, left bundle branch block, right bundle branch block paced beats. They achieved a high prediction performance and average accuracy of 96.67% and 98.39% in NNs and SVM. Shadmand *et al.* [19] proposed a system that used an ECG signal to classify the heartbeats of the patients using Block-based Neural networks (BBNNs). They used the PSO algorithm to optimize the BBNNs input parameters to overcome the variation in ECG signal from one person to another, the proposed provides a classification accuracy of 97%. Herry *et al.* [20] proposed an adaptive non-harmonic model and synchrosqueezing transform (SST) to describe the ECG pattern on the MIT-BIH database to enhance the detection of a heartbeat between normal and abnormal arrhythmia. They achieved a positive predictive value compared with other prediction algorithms using many more features. Arabasadi *et al.* [21] used NNs and GAs to predict cardiovascular disease. It can detect CAD without the need for an invasive diagnostic method. The proposed identified the initial data using a genetic algorithm, and increase the performance of the neural network by 10% through enhancing the primary weight used in it. They achieved an accuracy of 93.85%, a sensitivity of 97%, and a specificity of 92% in predicting coronary artery disease diagnosis. Acharya *et al.* [22] used two- and five-seconds ECG signals to diagnose CAD using convolutional neural networks (CNNs). The proposed differentiates between normal and abnormal ECG using deep CNNs and helps the doctors in making a reliable decision making of CAD using ECG signals. The proposed achieves a diagnose accuracy of 94.95% for the 2 second ECG signal and 95.11% accuracy for the five-second

ECG signals. The disadvantage of the proposed that it requires a fixed-length ECG signal and a huge database for the training process. Shinde *et al.* [23] a Heart Disease Prediction System was proposed by using MLFFNNs and a back-propagation NNs in four stages which are “normal, stage1, stage2, stage3 “of heart disease. They used the forward pass to calculate the output and compare it with the desired value, and backward pass to alter the value of the weights, and repeat the forward and backward passes until the error is low enough, it provides better performance than the traditional diagnosis methods and achieves an accuracy of 92%.

Alizadehsani *et al.* [24] proposed a data-mining algorithm for feature creation and selection on the Z-Alizadeh Sani dataset to make a rule-based classifier. The method added three new features to the data set regarding the LAD, LCX, and RCA. They made a comparison between the Naïve Bayes classifier, Sequential Minimal Optimization, K-Nearest Neighbors (KNN), SVM, and C4.5 with and without using the created features. The result shows that the SMO algorithm got the highest accuracy of 91.43% using the selected features and 92.09% using the selected and created features. Cüvitoğlu *et al.* [25] proposed a machine learning algorithm for diagnosing CAD on the Z-Alizadeh Sani dataset and they extend the number of samples from 303 to 500 cases, three classifiers were used to predict the stenosis of coronary arteries LAD, LCX, and RCA. Also, they made comparisons between various types of machine learning methods which are ANNs, SVM, Random Forest (RF), Naïve Bayes (NB), KNN, and ensemble learner which is the combination of these five ML algorithms. The methods archive an average accuracy higher than 80% and the ANNs reached 93% AUC (area under ROC) which is the best performance out of six methods. Alizadehsani *et al.* [26] applied a machine learning approach using radial basis function (RBF) and SVM to handle the model uncertainty in diagnosing the stenosis of major coronary arteries in individual LAD, LCX, and RCA on the Z-Alizadeh Sani dataset. They enhanced the proposed performance by using the accuracy rate and the hyperplane distance from a sample during the training phase. The proposed achieved accuracy rates of 82.67%, 83.67%, and 86.43% for RCA, LCX, and LAD respectively.

Joloudari *et al.* [28] proposed a hybrid machine learning called Genetic Support Vector Machine and Analysis of Variance (GSVMA) on the Z-Alizadeh Sani dataset for CAD diagnosis. The proposed used the genetic optimization algorithm to select crucial features and used SVM with Anova, Linear SVM, and LibSVM with radial basis function methods to classify the dataset. It has achieved an accuracy of 89.45% through 10-fold cross-validation and 35 selected features. Dipto, I. C. *et al.* [29] proposed a prototype system that uses Logistic Regression, Support Vector Machine, and Artificial Neural Network for detection of CAD and using on Z-Alizadeh Sani dataset. The author used SMOTE Algorithm to balance the dataset and used different evaluation methods such as Accuracy, AUC, and ROC to evaluate the system. The result shows that the Artificial Neural Network has the highest accuracy which is  $93.35\% \pm 2.56\%$  Joloudari, J. H. *et al.* [30] proposed an integrated method using machine learning (random trees, decision tree of C5.0, support vector machine, decision tree of Chi-squared automatic interaction detection) to diagnose CAD on the Z-Alizadeh Sani dataset on IBM Spss Modeler. The integrated method selects significant predictive features in order of their ranking to increase the accuracy of diagnosing CAD. the authors used a 10-fold cross-validation method Comparison of models in

terms of Accuracy. The Random trees achieved the highest accuracy of 91.47% with the most significant features of 40.

In this research, GAsBBO-NNs, BBO-MLPNNs, and PSO-MLPNNs models are used to design hybrid intelligent medical diagnosis models to improve the accuracy of the heart disease diagnosis system. With the selection of 14 features in optimization experiments based on Weighted SVM [27].

### 3. THE PROPOSED METHOD

#### 3.1 Dataset

The Z-Alizadeh Sani dataset contains 303 random records of patients; each record has 54 features [14]. These features are used as indicators of CAD patients. According to these features, the patients are categorized as CAD or Normal. The patient is categorized as CAD if at least one of the left anterior descending (LAD), left circumflex (LCX), and right coronary arteries (RCA) has stenosis greater than 50%, and otherwise, a patient is considered as Normal. The features are divided into four categories: demographics, symptoms, ECG, and “laboratory and echo” features.

#### 3.2 Preprocessing Phase

Different preprocessing sub-step may be used depending on the nature of the dataset [31], Data-type portability, feature selection, and data cleaning were used in this research. This section will describe these steps in detail. For feature selection, the features selected in [21] are used which are represented in Table 1. We used the Highest 14 weight features as input of the proposed method, where these features were extracted from demographics, symptoms, ECG signal, and laboratory. The selection was done based on the Weighted SVM method. This method uses F-score to measure the weights of the features [27]. F-score is a technique that measures the discrimination of two sets of real numbers. For a training instance  $x_k$ ,  $k = 1, 2, \dots, m$ , and  $n_+$  is the number of positive instances, and  $n_-$  is the number of the negative instances then the F-score of  $i$ th feature is calculated using Eq. (1). The feature is likely to be more discriminative if it has a high F-score [27].

$$F(i) = \frac{(\bar{x}_i^{(+)} - \bar{x}_i)^2 + (\bar{x}_i^{(-)} - \bar{x}_i)^2}{\frac{1}{n_+ - 1} \sum_{k=1}^{n_+} (x_{k,i}^{(+)} - \bar{x}_i^{(+)})^2 + \frac{1}{n_- - 1} \sum_{k=1}^{n_-} (x_{k,i}^{(-)} - \bar{x}_i^{(-)})^2} \quad (1)$$

Where the  $i$ th feature average of the whole, positive and negative instances are represented with  $\bar{x}_i$ ,  $\bar{x}_i^{(+)}$ ,  $\bar{x}_i^{(-)}$ , Respectively;  $x_{k,i}^{(+)}$  is the  $i$ th feature of the  $k$ th positive instance, and  $x_{k,i}^{(-)}$  is the  $i$ th feature of the  $k$ th negative instance.

For the data normalization, in this work the range between  $[-1,1]$  is used, Min-Max normalization is calculated using the following equation:

$$y = 2 \frac{x - x_{\min}}{x_{\max} - x_{\min}} - 1. \quad (2)$$

Where  $y$  is the normalized value,  $x$  is the original value of the feature,  $x_{\min}$  is the minimum value of the feature and  $x_{\max}$  is the maximum value of the feature.

**Table 1. The selected feature and its weights.**

Feature	Weight	Feature category	Selected Feature
Typical chest pain	1.0	Symptoms	✓
Atypical	0.88	Symptoms	✓
Age	0.88	Demographic	✓
Nonanginal	0.58	Symptoms	✓
DM (Diabetes Mellitus)	0.44	Demographic	✓
T inversion	0.44	ECG	✓
FH (Family History)	0.42	Demographic	✓
Region RWMA	0.40	Laboratory and echo	✓
HTN (Hypertension)	0.40	Demographic	✓
TG (Triglyceride mg/dL)	0.35	Laboratory and echo	✓
PR (Pulse Rate ppm)	0.33	Symptoms	✓
Diastolic murmur	0.32	Symptoms	✓
Current smoker	0.31	Demographic	✓
Dyspnea	0.31	Symptoms	✓
ESR (Erythrocyte Sedimentation Rate mm/h)	0.29	Laboratory and echo	
BP (Blood Pressure mm Hg)	0.27	Symptoms	
Function class	0.25	Symptoms	
Sex	0.24	Demographic	
FBS (Fasting Blood Sugar mg/dL)	0.24	Laboratory and echo	
St depression	0.23	ECG	
St elevation	0.21	ECG	
Q wave	0.20	ECG	

### 3.3 Building Models Phase

MLPNNs and EAs are used to design a heart disease classification model to classify the Z-Alizadeh Sani dataset. GAs, PSO, and BBO are effective optimization techniques that are used to optimize a set of optimal weights for MLPNNs. The next sub-sections will describe the proposed approach in detail.

#### 3.3.1 Multi-layer perceptron neural networks

Neural networks are learning systems inspired by simulating the biological system of the human brain [32]. It can learn and represent information and map it to the corresponding output that needs to predict. The most used type of NNs is the multilayer perceptron (MLP) [33], it is a feed-forward neural network that consists of three or more layers: an input layer, hidden layers, and output layer, where each layer has a number of neurons  $n$ ,  $h$ , and  $m$ . MLPNNs are fully connected; each neuron in one layer is connected to every neuron in the next layer with a certain weight, each connection has a different weight value which is determined using the learning process. The structure of MLPNNs is depicted in Fig. 1.

MLPNNs have two phases: forward and backward propagation. In the forward phase, the output is predicted and the error is calculated and sent back to the backward propagation phase. During the backward propagation, the calculated error is propagated back through the network to adjust the weights and reduce the error in the output layer.

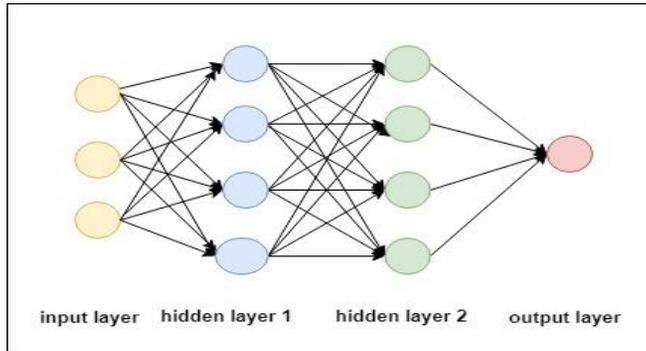


Fig. 1. General structure of MLPNNs.

The training process of the MLPNNs is mapping the input to the corresponding output. It begins with providing input and initial weights to the MLPNNs then adjusting the weights to minimize the error between the desired and actual output of the network. The output of the MLPNNs is the weighted sums of the inputs which are calculated using the following equation:

$$Y_{ij} = f \left( \sum_i^n w_{ij} \cdot x_i \right). \tag{3}$$

Where  $w_{ij}$ : is the connection weight between the  $i$ th node in the input layer and the  $j$ th node in the hidden layer, and  $x_i$ : is the  $i$ th input, where  $f$  is the activation function. To stop the training process, there is a certain threshold  $\theta$  is set depending on the error of the MLPNNs which represents the difference between the desired and actual output. The fitness function used is the Mean Square Error (MSE) illustrated as in the following equation:

$$MSE = \frac{1}{2} \sum_i^n (y_d - y_i)^2. \tag{4}$$

Where  $y_d$  is the target output data and  $y_i$  is the actual output of the neural networks. The training process continues to tune the weights and minimize the error to be small enough regarding  $\theta$ . The weights were updated using the following equation:

$$\Delta w_{i+1} = \alpha \cdot y_i \cdot \delta_j. \tag{5}$$

Where  $\alpha$  is the learning rate,  $y_i$  is the actual output of the  $i$ th layer, and  $\delta_j$  can be calculated as:

$$\delta_j = [1 - y_i] \cdot (y_d - y_i). \tag{6}$$

MLPNNs that contains two hidden layers will use Eqs. (5) and (6) with new  $\delta_k$  that depends on the previous value of  $\delta_j$ .

### 3.3.2 Genetic algorithm–biogeography-based optimization based neural networks

Many EAs have been employed to optimize ANNs parameters and find the optimal weights to achieve a better performance of the networks [10]. GAs [34], PSO [35], and BBO are some of the optimization algorithms that are applied to optimize the NNs Parameter's [36, 37]. The proposed model (GAsBBO-MLPNNs) combined two optimization algorithms which are GAs [12] and BBO [11] with MLPNNs to Improve the Diagnosis of Heart disease. The GAsBBO-MLPNNs take advantage of both GAs and BBO to optimize the MLPNNs weights. GAs recombines different individuals in the population and explicitly use a selection operation to create the solutions. While the BBO algorithm does not recombine the individual, and its solution is improved and maintained from one iteration to the next by migration habitants [38]. For that, GAs were used to generate a set of solutions to use as the initial population for the model, then the BBO algorithm was used to maintain and improve the solution to find the optimal weight and basis for the NNs. A stopping criterion is set for GAs which is a maximum number of generations. After that, the best population of GAs generations is set as an initial population (Habitats) for BBO which will again search for the best solution (weights and biases). The BBO stopped after a certain MSE or a maximum number of generations. Fig. 2 illustrates the steps of the GAsBBO-MLPNNs approach.

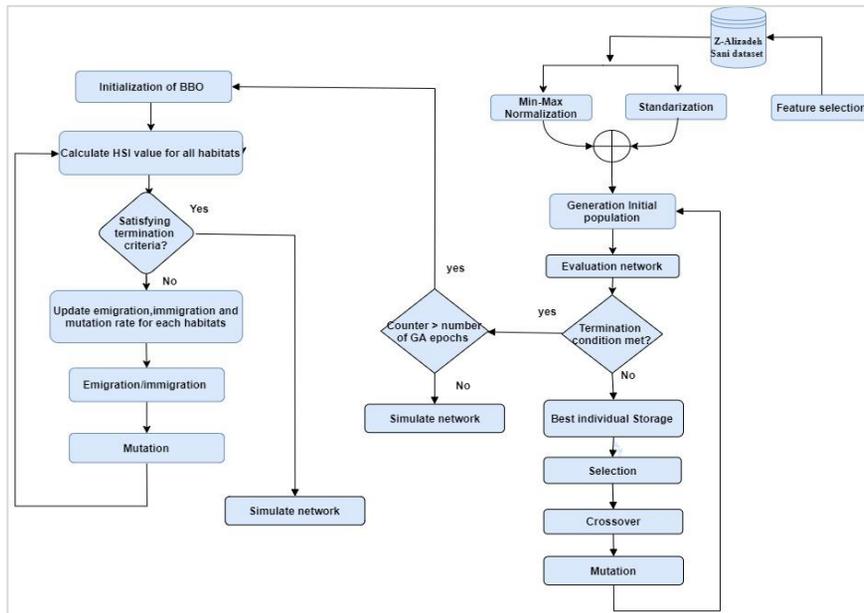


Fig. 2. Genetic algorithm-bio geographical based optimization neural networks.

The general steps of the GAsBBO-MLPNNs algorithm are described in the following steps:

1. Initialization of the GAsBBO-MLPNNs parameter. This includes a) Determination of Crossover probability, Mutation probability, Number, and the size of the population; b) creating a random initial population with determining the weights and biases of the

- network; c) determining the maximum number of generations for GAs; d) Number of the initial population of BBO algorithm.
2. Calculating the fitness for each chromosome using the feed-forward networks (MSE) in Eq. (3).
  3. Creating a new generation of the population through selection, crossover, and mutation operations.
  4. Saving the best chromosome of the population in the buffer.
  5. Going to 2, repeat until reach stopping criteria which is the maximum number of generations.
  6. Initializing the BBO habitats with the GAs best chromosomes from the saved buffer.
  7. Calculating the Habitat Suitability Index (HSI) for each habitat.
  8. Updating the emigration, immigration, and mutation rate for each habitat
  9. Modifying (Emigrate and immigrate) the habitats according to emigration, immigration rate.
  10. Select the number of habitats and mutate some of their weights according to the mutation rate.
  11. Selecting the elite to prevent the emigration, immigration, and mutation operation from corrupting them in the next generation.
  12. Going to Step 7, and repeat the process until satisfying the termination criteria.

The general procedure that was used in performing GAsBBO-MLPNNs on the Z-Alizadeh Sani data set is illustrated in Fig. 2.

The GAs algorithm consists of  $n$ ,  $n = [1, 2, \dots, n]$  individuals which represent the candidate solutions of the problem. Each solution has a set of properties that can be altered and mutated based on a predefined probability. The BBO algorithm consists of  $n$ ,  $n = [1, 2, \dots, n]$  habitats which represent the candidate solutions of the problem.

The main idea of the BBO algorithm was inspired by the study of the distribution of biological organisms over time and space. Different ecosystems represented in habitats (islands) are investigated to find the relationship between habitants in terms of emigration, immigration, and mutation [11]. BBO employs the number of habitats that represent the candidate solutions, these habitats are analogous to the GAs chromosomes. Each habitat in the BBO algorithm has a number of (Habitants) species that are similar to GAs genes, which is used to present the problem variables. Also, the Habitat Suitability Index (HSI) indicates the goodness of the solution which is similar to fitness function in GAs, habitats with high HSI have a good solution while habitats with low HSI have a poor one. The algorithm determines the number of Elites (best habitats) for the next generation depending on the HSI value. The habitats evolve based on the following three rules:

- Habitats with a high HSI have a large number of species (Habitants) and are more likely to emigrate to Habitats with low HSI.
- Habitats with low HSI have a small number of species (Habitants) and are more likely to immigrate species (Habitants) from Habitats with high HSI.
- Habitats may have changes that occur in their species (Habitants) suddenly due to random events regardless of HSI value.

These concepts lead to achieving a balance between different geographical regions; the BBO algorithm uses this concept to improve the HIS of different habitats. Which results in improving the initial random habitats of the problem. BBO starts with random initial habitats that consist of number habitants that represent the problem variables, each habitat represents a candidate solution of the problem, and each one has a different immigration, emigration, and mutation rate. The habitats emigrate, immigrate, and mutate their habitants using the following equations:

$$\mu_k = \left( \frac{E \times k}{N} \right). \quad (7)$$

Where  $\mu_k$  is the emigration rate,  $E$  is the maximum emigration rate,  $k$  is the number of habitants in the current habitat, and  $N$  is the maximum number of habitants allowed to be in the habitat and it's determined by HSI.

$$\lambda_k = I \left( \frac{1-k}{N} \right) \quad (8)$$

Where  $\lambda_k$  is the immigration rate,  $I$  is the maximum immigration rate,  $k$  is the number of habitants in the current habitat, and  $N$  is the maximum number of habitants allowed to be in the habitat and it's determined by HSI.

$$m(k) = m_{\max} \left( \frac{1-P_k}{P_{\max}} \right) \quad (9)$$

Where  $m(k)$  is the mutation rate,  $m_{\max}$  is the maximum mutation probability defined by the user,  $P_k$  is the mutation probability for the current habitat, and  $P_{\max} = \operatorname{argmax}(P_k)$ ,  $k = 1, 2, 3, \dots, N$ . Elitism is used to prevent immigration from corrupting the best solution when done by saving a predefined number of best solutions at each iteration.

Each solution has a set of properties that can be migrated, immigrated, and mutated. The output of the neurons in the MLPNNs is calculated using Eq. (3). The hidden and output layers have to apply an activation function to calculate and pass the output of neurons [39], some of the activation functions used for training the neural networks. The activation functions are chosen according to the problem to be solved and the neural network model. The step activation function is the most wield activation function applied in pattern recognition and classification problems [39]. For the GASBBO-MLPNNs model, the sigmoidal activation function in Eq. (10) is used to calculate the hidden layer of the NNs, and the step activation function in Eq. (11) to classify the final output.

Step activation function:

$$Y = \frac{1}{1 + e^{-x}}. \quad (10)$$

Sigmoidal activation function:

$$Y = \begin{cases} 0 & \text{for } x < 0 \\ 1 & \text{for } x \geq 0 \end{cases}. \quad (11)$$

### 3.4 Metrics Selection

There are several metrics associated with class “pattern recognition and classification” and statistically measure its performance [40]. This research will focus on the following metrics: Confusion matrix, True positive (TP), False positive (FP), False negative (FN), True negative (TN), Accuracy, Sensitivity (Recall), and Specificity. In the following paragraphs, the definitions of these terms according to heart disease diagnosis the problem are illustrated in Eqs. (12)-(17):

**Table 2. Confusion matrix description for heart disease diagnosis problem.**

		Predicted Classes		
		CAD	Normal	Total
Actual Classes	CAD	TP	FP	TP+FP
	Normal	FN	TN	FN+TN
	Total	TP+FN	FP+TN	TP+FP+FN+TN

**TP:** The number of samples correctly categorized as CAD.

**FP:** The number of samples incorrectly categorized as CAD.

**TN:** The number of samples correctly categorized as Normal.

**FN:** The number of samples incorrectly categorized as Normal.

**Accuracy:** The main metric that used to measure the performance in class pattern recognition and classification which represented by the following formula:

$$Accuracy = \frac{TP+TN}{TP+FP+FN+TN}. \tag{12}$$

**Sensitivity or Recall:** The percentage of records that classified correctly as CAD to all records that classified as CAD, and can be calculated using the following equation:

$$Recall = \frac{TP}{TP+FN}. \tag{13}$$

**Specificity:** The percentage of records correctly predicted as normal to all records predicted in the Normal class.

$$Specificity = \frac{TN}{TN+FP}. \tag{14}$$

**Precision:** The percentage of records correctly predicted as CAD to all records predicted in CAD class.

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

**G-mean:** is the cost function constructed based on g-mean of specificity for normal class and the sensitivity of the hostile class, it used to measure the balance between classifications. The G-mean calculated using the following formula:

$$G - mean = \sqrt{Sensitivity * specificity}. \tag{16}$$

F-measuring: it measures the balance between precision and sensitivity (recall). The F-measure was calculated using the following formula:

$$F - \text{measuring} = \frac{2 * \text{recall} * \text{precision}}{\text{recall} + \text{precision}}. \quad (17)$$

#### 4. EXPERIMENTS AND RESULTS

The proposed was evaluated by applying it to the Z-Alizadeh Sani data set that contains 303 records. We used the Highest 14 weight features as input of the experiments using the try and error way, where increasing the number of features didn't improve the prediction accuracy. The GAsBBO-MLPNNs, BBO-MLPNNs, and PSO-MLPNNs algorithms were used to create class classification on the dataset. Before stating in describing the algorithms, it is determined the best data normalization methods to use later in the experiments. A hybrid system that combines GAs-BBO, BBO, and PSO with neural networks was used to build a pattern recognition and classification model as a Heart Disease Diagnosis system. The performance of GAsBBO-MLPNNs, BBO-MLPNNs, and PSO-MLPNNs depends on a number of iteration (N), a number of the neurons in the hidden layers (L) where the hidden layers have the same number of neurons, the population size (P), the activation function of the hidden layers where sigmoidal activation function was used, and the parameters of each optimization algorithm that have an important role in improving the performance of the algorithm which depends on the dataset used. The cross-validation method called K-Fold Cross-Validation [41] was used to build and evaluate the models. Based on the K-Fold Cross-Validation method the data is partitioned into  $k$  equally sized folds. For each fold  $i$ , the data divided into  $k$  partition, the  $i$ th the fold is used for testing while the remaining folds are used for training the model. In this research, Tenfold cross-validation is used to evaluate the models where 90 percent of the dataset is used for training the model and the remaining 10 percent of the dataset used to perform the testing phase. The overall accuracy was used in the parameter optimization phase, while the performance of the proposed models was measured using the overall accuracy, F-score, confusion matrix, overall accuracy, Sensitivity (Recall), and Specificity.

##### 4.1 PSO-MLPNNs Experiments on Z-Alizadeh Sani Dataset

The goal of the experiments performed using the PSO-MLPNNs model was to find the best L, and N, and P that will be used to build a PSO-MLPNNs Heart disease detection and prediction solution. Table 3 includes the result of these models. It shows that the best model was achieved using L = 10, N=200, and P = 60 where we try different values for P to find the optimal one for learning, and increasing the population size to more than 60 didn't enhance the learning process. The model achieved the best performance with N = 200 and L = 10, where the performance parameters of the average folds represented as 92.64%, 88.8%, 86.43%, 80.79% for training accuracy, test accuracy, G-mean, F-measure respectively. While the testing accuracy for the best fold is 93.5%, and for the worst fold is 82.8%.

**Table 3. PSO-MLPNNs models results.**

PSO-MLPNNs Models Results									
						Average-fold PSO-MLPNNs			
Training Accuracy			Test Accuracy			G-mean		F-Measure	
92.64%%			88.80%			86.43%		80.79%	
N	L	Training Accuracy	Testing Accuracy	Sensitivity	Specificity	Precession	Negative Prediction	F-Measure	G-mean
100	10	90.80%	85.10%	75.90%	89.20%	72.80%	90.23%	74.32%	82.28%
150		91.75%	86.40%	75.55%	91.51%	79.32%	89.34%	77.39%	83.15%
200		92.64%	88.80%	81.01%	92.21%	80.57%	92.09%	80.79%	86.43%
100	20	92.45%	82.80%	69.47%	89.46%	73.76%	86.60%	71.55%	78.83%
150		92.58%	85.80%	75.34%	90.17%	75.01%	90.25%	75.17%	82.42%
200		92.75%	88.40%	78.63%	92.49%	81.68%	90.74%	80.13%	85.28%
100	35	91.86%	85.50%	75.38%	91.56%	79.60%	88.39%	77.43%	83.08%
150		92.24%	87.40%	81.67%	91.01%	77.24%	92.51%	79.39%	86.21%
200		93.09%	88.70%	80.89%	92.73%	81.82%	91.59%	81.35%	86.61%

Fig. 3 shows the accuracy of the PSO-MLPNNs model related to the number of iteration (N) [100,150,200] and number of neurons in hidden layers (L) [10,20,35], where the best accuracy was achieved with L=10 and N=200.

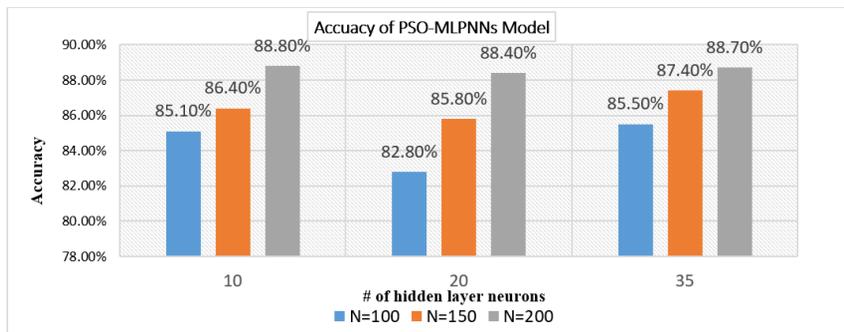


Fig. 3. The accuracy of the PSO-MLPNNs model.

#### 4.2 BBO-MLPNNs Experiments on Z-Alizadeh Sani Dataset

The goal of the experiments performed using the BBO-MLPNNs model was to find the best L, and N, and P that will be used to build a BBO-MLPNNs Heart disease detection and prediction solution. Table 4 includes the result of these models. It shows that the best model was achieved using L = 10, N = 150, and P = 60, where we try different values for P to find the optimal one for learning and increased the population size more than 60 didn't enhance the learning process, and the optimal values of the Mutation probability were 0.4 and the fitness function was MSE (Eq. 4) in this paper. The performance parameters of the average folds represented as 94.5%, 93.1%, 92.19%, 87.79% for training accuracy, test accuracy, G-mean, F-measure respectively. While the testing accuracy for the best fold is 96.7% and the worst fold is 86.2%.

**Table 4. The BBO-MLPNNs models results.**

BBO-MLPNNs result with $L = 10, N = 150, P = 60$ .									
						Average result BBO-MLPNNs			
Training Accuracy			Test Accuracy			G-mean		F-Measure	
94.50%			93.10%			92.19%		87.97%	
N	L	Training Accuracy	Testing Accuracy	Sensitivity	Specificity	Precession	Negative Prediction	F-Measure	G-mean
100	10	92.89%	90.03%	81.24%	93.51%	84.73%	91.59%	82.95%	87.16%
150		94.46%	93.01%	89.74%	94.70%	86.26%	95.81%	87.97%	92.19%
200		94.24%	92.64%	88.95%	95.12%	87.23%	95.34%	88.08%	91.98%
100	20	92.64%	88.34%	79.01%	93.07%	82.65%	90.71%	80.79%	85.75%
150		93.81%	91.35%	87.48%	93.29%	83.48%	94.86%	85.43%	90.34%
200		93.75%	91.65%	82.72%	96.23%	80.84%	92.13%	86.59%	89.22%
100	35	92.72%	89.05%	80.08%	93.19%	82.79%	91.67%	81.41%	86.39%
150		93.78%	90.64%	83.23%	94.85%	87.09%	92.57%	85.12%	88.85%
200		93.93%	91.62%	87.30%	94.17%	85.01%	94.39%	86.14%	90.67%

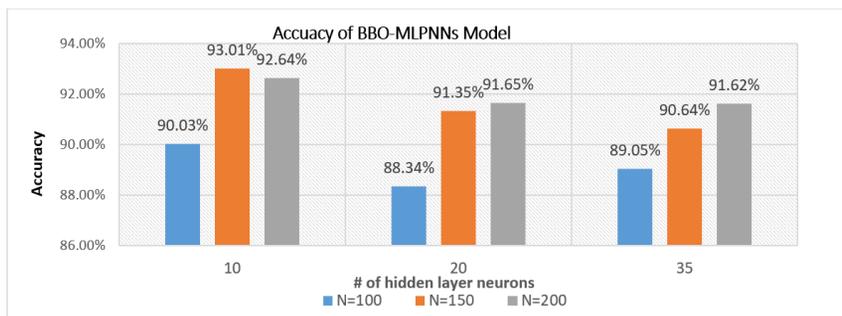


Fig. 4. The accuracy of the BBO-MLPNNs model.

Fig. 4 shows the accuracy of the BBO-MLPNNs model related to a number of iteration (N) [100,150,200] and a number of neurons in hidden layers (L) [10,20,35], where the best accuracy was achieved with  $L = 10$  and  $N = 150$ .

#### 4.3 GASBBO-MLPNNs Experiments on Z-Alizadeh Sani Dataset

The goal of the experiments performed using the GASBBO-MLPNNs model was to find the best number of neurons in the hidden layers (L), and N, and P that will be used to build a GASBBO-MLPNNs Heart disease detection and prediction solution. Table 5 includes the result of these models. It shows that the best model was achieved using  $L = 10, N = 100$ , and  $P = 60$ , where we try different values for P to find the optimal one for learning and increased the population size more than 60 didn't enhance the learning process, and the optimal values of BBO Mutation probability was 0.4, GA Mutation probability was 0.5, GA Crossover probability was 0.2 and the fitness function was MSE (eq 4) in this paper. The performance parameters of the average folds represented as 95.5%, 94.5%, 95.60%, 89.96% for training accuracy, test accuracy, G-mean, F-measure respectively. While the testing accuracy for the best fold is 96.8% and the worst fold is 90.3%.

**Table 5. GAsBBO-MLPNNs models results.**

GAsBBO-MLPNNs result with $L = 10, N = 100, P = 60$ .									
Training Accuracy						Average result GAs-BBO-MLPNNs			
Training Accuracy			Test Accuracy			G-mean		F-Measure	
95.50%			94.50%			95.60%		89.94%	
N	L	Training Accuracy	Testing Accuracy	N	L	Training Accuracy	Testing Accuracy	N	L
50	10	95.00%	93.80%	50	10	95.00%	93.80%	50	10
100		95.50%	94.50%	100		95.50%	94.50%	100	
150		94.70%	93.10%	150		94.70%	93.10%	150	
50	20	94.40%	92.80%	50	20	94.40%	92.80%	50	20
100		94.80%	92.80%	100		94.80%	92.80%	100	
150		94.40%	92.50%	150		94.40%	92.50%	150	
50	35	91.90%	89.50%	50	35	91.90%	89.50%	50	35
100		92.60%	90.50%	100		92.60%	90.50%	100	
150		93.50%	91.50%	150		93.50%	91.50%	150	

Fig. 5 shows the accuracy of the GAsBBO-MLPNNs model related to a number of iteration (N) [50,100,150] and a number of neurons in hidden layers (L) [10,20,35], where the best accuracy was achieved with L=10 and N=100.

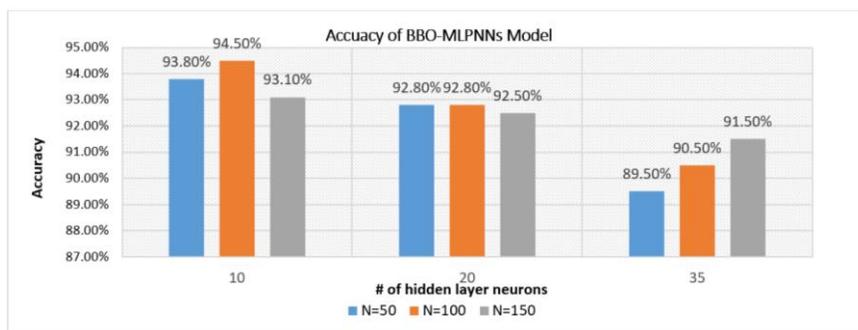


Fig. 5. The accuracy of the GAsBBO-MLPNNs model.

### 5. DISCUSSION OF THE RESULTS

In this section, we will show the superiority of the proposed approach in comparison to other hybrid models and with of the previous works. GAsBBO-MLPNNs, BBO-MLPNNs, and PSO-MLPNNs model was applied on the Z-Alizadeh Sani data set, where different parameters related to these algorithms were optimized. Tables 3-5 show the list of experiments that were performed on the Z-Alizadeh Sani dataset with the optimized parameters. The experiments show that the GAsBBO-MLPNNs model has a better performance than BBO-MLPNNs and PSO-MLPNNs concerning the overall accuracy, G-mean, and F-measure. Several works are published on the Z-Alizadeh Sani dataset, the two closest to this work are used to evaluate this work which is referred to [15, 21].

As mentioned in the related works section, the proposed referred by [15] data mining method for diagnosis of coronary artery disease (using SMO algorithm), they create three

features to improve the diagnosis accuracy, the proposed referred by [21] hybrid system using GAs and NNs to predict the cardiovascular disease. Figure 7 and Table 6 show the result of our work compared with both works in [15, 21, 28-30].

Table 6 shows that the proposed GAsBBO-MLPNNs produce a result of 94.5%, 96.4%, 94.8% in Accuracy, Sensitivity, and Specificity respectively. GAsBBO-MLPNNs Outperform the SMO classifiers, GAs-NNs, GSVMA, ANN, and Random trees in terms of accuracy. Where the accuracy of our ten-fold GAsBBO-MLPNNs was 94.50% vs. 93.85% for GAs-NNs, 92.09% for SMO classifier, 89.45% for GSVMA, 93.35% for ANN, and 91.47% for Random tree models. Even the GSVMA got a better result in specificity and ANN got a better result in Sensitivity; our model got a bitter result in terms of accuracy 94.50%.

**Table 6. Comparison between our model and the previous work in [15, 21, 28-30].**

Model	Accuracy	Sensitivity	Specificity
SMO classifiers	92.09%	97.22%	79.31%
GAs-NNs	93.85%	97%	92%
GSVMA	89.45%	81.22%	<b>100%</b>
ANN	93.35%	<b>97.67%</b>	77.7%
Random Trees	91.47%	—	—
The proposed GAsBBO-MLPNNs	<b>94.50%</b>	96.40%	94.80%

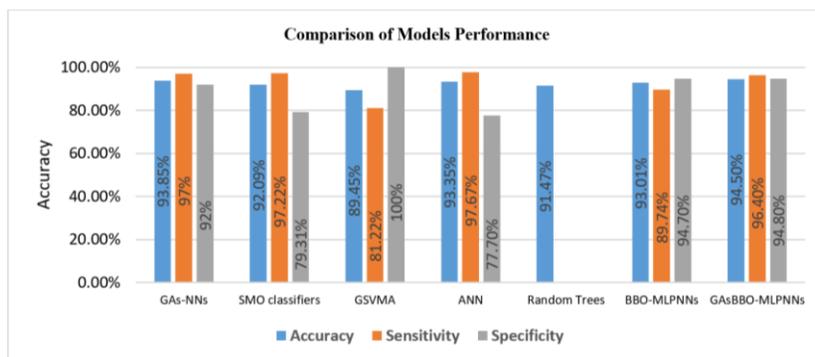


Fig. 6. Comparison of the performance of the proposed approach and the previous work.

## 6. CONCLUSIONS

The term “heart disease” is often used to refer to cardiovascular disease. Cardiovascular disease is caused by Blocking or narrowing of the vessels that can lead to chest pain or heart attack. Heart disease is the leading cause of death globally. However, saving lives can be achieved by the early and accurate diagnosis of the various types of heart diseases and providing the appropriate treatment. In this research, the performance of the classification of CAD was improved by optimizing the MLPNNs parameter using Evolutionary Algorithms. A hybrid system that combines Genetic Algorithm (GAs) and Biogeography-Based Optimization (BBO) were used to optimize the MLPNNs parameters [GAsBBO-MLPNNs]. The proposed approach produces better performance than another hybrid

approach that combined PSO-MLPNNs, and BBO-MLPNNs, and previous works in terms of accuracy and Specificity, where the detecting of CAD and Normal class was improved. The GAsBBO-MLPNNs approach produces the best result on the Z-Alizadeh Sani dataset with  $L = 10$ ,  $N = 100$ ,  $P = 60$ , and it achieved 93.85%, 95.6%, 89.94%, 96.4%, 94.8% in accuracy, G-mean, F-measure, Sensitivity, Specificity respectively. In future work, datasets from other sources will be used to test the performance of the proposed approach and expand the scope of the proposed from heart diseases to other diseases such as Lung Cancer and Alzheimer's disease. Different features will be applied such as extraction and reduction methods to improve the performance of the system.

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