

A decision support system based on neural network and genetic algorithm: Case study in breast cancer

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ABSTRACT

Introduction: Artificial intelligence has been changing the way healthcare has been provided in many high-risk environments or areas with poor healthcare facilities. The emergence of epidemics and new diseases, as well as the crucial role of early diagnosis in prevention and the adoption of more effective treatments have highlighted the need for accurate design and self-organization of Clinical Decision Support Systems (CDSSs).

Material and Methods: In this study, a CDSS based on a neural networks (NN) and genetic algorithm is proposed. Since, on the one hand, the performance of the neural network (NN) is highly dependent on its parameters, and on the other hand, there is a constant need for optimization experts to fine-tune the parameters in the use of new data, a new chromosomal structure is proposed to automatically extract the optimal NN architecture, the number of layers and neurons. The goal is to increase the reusability of the model and ease of use by health experts.

Results: To evaluate the performance of the model, two standard breast cancer (BC) datasets, WBC and WDBC, were used. The model uses 70% of the data set for training and the remaining equally used for evaluation and testing. The test accuracy of the proposed model on WBC and WDBC datasets was 98.51 and 97.55%, respectively. The optimal NN architecture on WBC consisted a three-hidden layers with 18, 15 and 19 neurons in each layers, and on WDBC consisted one hidden layer with a single neuron.

Conclusion: The proposed chromosomal structure is able to derive optimal NN architecture. In according to the high classification accuracy of the model in the diagnosis of BC and providing the different architectures in accordance with the hardware implementation considerations, the proposed model can be used effectively in the diagnosis of other diseases.

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INTRODUCTION

Continuous changes in medical processes, the emergence of new diseases and the importance of the early diagnosis have revealed the necessity of diagnostic decision support systems [1-3]. Simultaneous advances in information technology and new developments in artificial intelligence (AI) promise that artificial intelligence can help tackle challenges in global health, accelerate the achievement of health-related goals, and reduce the workload of health workers as well as the time and cost of providing services [4-7]. In recent decades, AI and machine learning have played a major role in medical applications, including diagnosis [8, 9],

assessing the risk of mortality and patient survival [10], predicting and monitoring disease outbreaks [11], and health policy and planning [5].

Since early diagnosis increases the chances of successful treatments, one of the important applications of AI-based methods in the health field is designing the medical diagnostic systems [12-14]. Considering that the possibility of treating breast cancer will be high if it is detected in the early stages, [15, 16], in this study, the application of machine learning in breast cancer diagnosis is investigated. According to the statistics published by the World Health Organization [17], breast cancer is the most common cancer (11.7% of all new cancer cases) in

the world; It was the fifth leading cause of death in women with 685,000 deaths in 2020

Uncontrolled cell growth in breast tissue is the most important cause of breast cancer, which can be benign or malignant. Malignant tumors are cancerous and the migration of their cells to distant organs is the main cause of death caused by breast cancer during metastasis [18, 19]. In contrast, benign tumors do not spread to other parts of the body and are therefore not cancerous [20]. Only a small percentage of breast tumors are cancerous and most of them are benign [21].

In the field of machine learning, breast cancer detection can be formulated as a two-class classification problem. Due to the success of neural networks as a machine learning algorithm in increasing classification accuracy and facilitating timely disease diagnosis, this method has been used in many researches to diagnose breast cancer and has shown high classification accuracy [4, 22]. Zarbakhsh and colleague [6] introduced a breast cancer tumor detection method that includes three feature selection modules with graph-based method, classification using radial basis neural network (RBF) and honey bee colony optimization module (ABC). The original Wisconsin Breast Cancer (WBC) dataset [23] was used to evaluate the method. By dividing 30 into 70 training and testing network sets, and selecting the 8 features with the best classification accuracy, the authors reported 99.59% accuracy by averaging over 50 independent runs and using 91 radial basis networks.

Deep neural network model is presented to diagnose breast cancer malignancy [24]. The model presented on the Wisconsin breast cancer diagnostic dataset WDBC [25, 26] has an input layer with 30 neurons, three hidden layers with 15, 7 and 3 neurons, respectively, and an output layer with one neuron. The accuracy of the model is reported to be 99% on 25% of the data.

A neural network-based breast cancer detection method was presented and trained on the WBC dataset [14]. At first, four features of gland thickness, cell size uniformity, cell shape uniformity, and bare nuclei were selected from the features of the data set using the recursive feature elimination (RFE) method and given as input to the deep neural network (DNN) with three hidden layers. The number of neurons in each hidden layer was preset to fixed values of 10, 20 and 10 respectively. The best classification accuracy of the model on 20% of the data set is reported as 98.62% test. A classification model of breast cancer mammography images based on radial basis neural network (RBNN) is proposed [16]. The proposed model includes a hidden layer that uses the cuckoo search optimization algorithm to extract and reduce features. The result of evaluating the model on the dataset of MIAS mammography images has been

reported to be 98.32% accurate.

It was investigated the performance of Multilayer Perceptron (MLP), Learning Vector Quantization (LVQ) and Bayesian neural networks with different structures on the diagnosis of benign and malignant breast cancer. Different constructs were evaluated on the WBC dataset [27]. The authors used 80% of the dataset for training, 10% for testing, and 10% for evaluation. The average accuracy of 10 times of running MLP, LVQ and Bayesian neural network on the test set is reported as 97.5, 97.6 and 98.3%, respectively. The best structure of MLP neural network on this data set has been reported by trial and error with two hidden layers and 10 neurons in each layer. Also, the optimal structure of Bayesian network has been reported by trial and error method with three hidden layers with 20, 10 and 5 neurons respectively.

A hybrid model based on neural network, multi-objective genetic model and Association Rules Mining is presented [12]. The purpose of this algorithm is to improve the classification accuracy of the neural network and the mentioned classification rules. The model was run on the WBC dataset and the WDBC dataset as 10 cross-validation (CV) runs. The optimal neural network for classifying WDBC data including a hidden layer with 7 neurons and discretizing the value of features into 7 intervals was obtained, the average accuracy of its implementation on the test set was reported as 99.82%. Also, the best neural network structure for classifying WBC data includes a network with one hidden layer and 3 neurons by discretizing the values of each feature into 7 intervals with an average accuracy of 97.22%.

Among the important factors on the efficiency of neural networks, the setting of its parameters includes the number of hidden layers and the number of neurons in the hidden layers [28, 29]. In many researches, the optimal design of the neural network structure is done by a human expert, which is a difficult trial and error process [30]. In order to reduce computational time and cost, researches have been conducted in the field of optimization of neural network parameters in the field of medicine [28, 31]. Genetic Algorithm (GA) is a very popular method to automatically determine high-performance neural network architecture in this field [1, 12, 32, 33].

A single-layer neural network-based method for classifying images of skin lesions is presented. Genetic algorithm is used to select the feature in the input layer and the number of neurons in the hidden layer. The best average performance of 5-fold cross-validation on ISIC images is reported to be 85.90% and the optimal number of neurons in the hidden layer is 11 [29].

A medical data classification model using content-based probabilistic neural network (CPNN) is

proposed. The proposed neural network includes an input layer, a pattern layer, an aggregation layer, and an output layer. Genetic algorithm was used to select the features as network input, the number of content and the number of clusters in each content. The proposed model was trained on 60% of the WDBC dataset and tested on the remaining 40%. The average accuracy of 10 times of cross-validation was reported as $97.4 \pm 0.07\%$ [1].

Based on the review of the limited works done in the field of optimization of network parameters, most of the works have optimized the number of neurons assuming a maximum of two hidden layers. While the appropriate parameters depend on the considered system and cannot be determined in advance [28]. As a result, the design of a self-organizing diagnostic decision support tool that can be automatically adjusted and easily re-evaluated by physicians when training data changes increases the chances of acceptance among health systems. Hence, in this study, a diagnostic decision aid model in the field of medicine based on neural network and genetic algorithm is introduced, which is able to adjust the structure of the network including the number of hidden layers and the number of neurons in each hidden layer. To evaluate the proposed model, two breast cancer data sets, WDBC and WBC, which are commonly evaluated in researches in this field, have been used. Considering the hardware implementation considerations of the model, different network structures are presented for each data set.

MATERIAL AND METHODS

Machine learning algorithms are able to discover nonlinear and high-dimensional relationships between features [34]. One of the machine learning methods of interest in breast cancer diagnosis are neural networks [6]. The neural network can greatly increase the accuracy and facilitate the timely diagnosis of the disease [4]. This algorithm is able to classify noisy data without needing information about the statistical distribution of monitored data [6]. Among the neural network models, neural networks are leading, which have the power to learn from examples and adapt to environmental changes [30]. In this study, multilayer perceptron (MLP) forward neural network with one input layer, one output layer and a number of hidden layers and error back propagation training algorithm are used.

Considering the effect of network parameters on its classification power, generalization ability and learning capacity, one of the challenges of decision-making diagnostic systems based on neural network is to design its structure including determining the number of layers and the number of neurons in each layer [16, 28, 29, 31, 35]. Although in most of the researches, the setting of these parameters is done by

trial and error by experts in this field, but the automatic methods of optimizing the network parameters, while reducing the time and computational cost of manual settings, require optimization experts every time to change the training data of the network in order to They eliminate the choice of optimal parameters. Among the optimization methods, the genetic algorithm is the most popular optimization algorithm based on evolution, which provides a powerful search in classification applications and has been successfully used in structure and parameters optimization problems [36-38]. For this reason, in this study, a method based on genetic algorithm is proposed to determine the optimal structure of the neural network.

This algorithm consists of three key components: composition, Cross Over and mutation. As the first step of this algorithm, an initial population of candidate solutions or chromosomes is generated randomly or heuristically, each solution is called an individual. In the selection process, chromosomes with the highest fitness are selected to eliminate chromosomes with low fitness [39]. Cross Over is a process in which two selected chromosomes with high fitness exchange part of their genes with each other to produce a new pair of chromosomes. This operator directs the evolutionary process towards regions containing potential solutions. After selection, the mutation operator is applied. The mutation operator is critical to the exploratory ability of the optimization algorithm and by changing one or a number of chromosome genes, it causes new individuals to be added to the population [40]. The process of generating a new generation continues until the condition of the end of the search is not satisfied. This condition can be reaching a desired fitness value or a certain number of repetitions of the algorithm.

One of the important issues in evolutionary design using the genetic algorithm is the representation of the genotype, which determines what is coded in the chromosomes [37]. In this study, a new genotype display is presented to simultaneously determine the number of neural network layers and the number of neurons in each layer. Figure 1 shows the proposed chromosome structure.

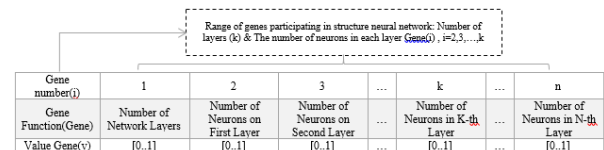


Fig 1: Proposed chromosome structure to simultaneously determine the number of layers and the number of nodes in each layer in the neural network structure.

This structure contains $\max L + 1$ gene, where $\max L$ is the maximum number of acceptable layers for the

MLP network. The addition of the number one is due to the allocation of the first chromosome gene to determine the number of network layers designed by a chromosome. In this structure, the number of layers and neurons of each layer are coded by random numbers in the range (0, 1). To build a neural network, it is necessary to decode this structure. The concept of each gene, which is equivalent to its function, is determined based on formula 1:

$$gene(i) = \begin{cases} v(i) \times (maxL - 1) + 1 & \text{if } i = 1 \\ v(i) \times (maxN - 1) + 1 & \text{if } i \neq 1 \end{cases} \quad (1)$$

where maxN is the maximum number of neurons in each layer and maxL is the maximum number of neural network layers. Since the number of layers and neurons of each layer must be an integer greater than zero, according to equation 1, the value of each gene for the number of layers is always an integer in the range [1, maxL] and for the number of neurons in each layer in the range [1, maxN] will be. For example, if in the initialization of the genes of a chromosome, the value of the random number of gene number 1 is 0.2 and the user has selected the maximum number of layers to be 10, the network structure proposed by this chromosome will have three layers:

$$gene(1) = [0.2 \times (10 - 1) + 1] = [2.8] = 3$$

In this regard, the random number of the first gene is multiplied by maxL-1, then one unit is added and the upper limit of the number is chosen as the number of neural network layers. As a result, among the next 10 genes of the chromosome (the range of genes 2 to 11), only the values of genes 2 to 4 will participate in the construction of the proposed neural network, and genes 5 to 11 have no contribution in the structure of the neural network. Now, if the values of genes 2 to 4 are 0.25, 0.08 and 1, respectively, and the maximum number of neurons in each layer is selected by the user as 20, the number of neurons in layers 1 to 3 will be 6, 3 and 20 neurons, respectively. As a result, the neural network structure designed by each chromosome will never be more complicated than the default state set by the user. After decoding the chromosome and designing the structure of the neural network, the classification accuracy of the model is determined on the validation dataset as the

value of the chromosome fitness function. After the stopping condition of the genetic algorithm is fulfilled, the chromosomes with the highest degree of fitness are presented as the optimal structure of the neural network for the investigated problem. Figure 2 shows the flowchart of the proposed method.

In this research, the tournament structure is used for selection because in this method, justice is established and the chromosomes that have a low selection probability have a chance to be selected. Also, a uniform crossover is used for the crossover. In this type of crossover, the algorithm has more exploit and jumps towards optimal solutions. Complementary mutation is also used for mutation, which also increases the exploit.

In order to evaluate the efficiency of the proposed diagnostic model, two original and diagnostic breast cancer data set of Wisconsin, WBC and WDBC, from the UCI machine learning repository of the University of California have been used. The reason for using these two standard data sets is that they are common in the research conducted in the field of breast cancer diagnosis.

The WDBC diagnostic dataset contains information on 569 breast cancer tumors, including 357 (63%) benign tumor samples and 212 (37%) malignant tumor samples. 32 characteristics were calculated for each tumor, the first characteristic of the patients and the last characteristic of the tumor type (benign or malignant). The characteristics of the patients in this study have been omitted. Other features were calculated from the digital image using fine needle sampling, FNA, of the breast mass. These features describe the characteristics of the cell nucleus in the image, which are positioned by actiocontour models called snakes. By using snakes, 10 different features have been extracted to describe the size, shape and texture of the nucleus related to the tumor; Then, for each feature, the standard error, mean, and largest (or worst) value over the range of individual cells are calculated. All these features are numerical and larger values indicate a higher probability of tumor malignancy [25]. The features are listed in Table 1.

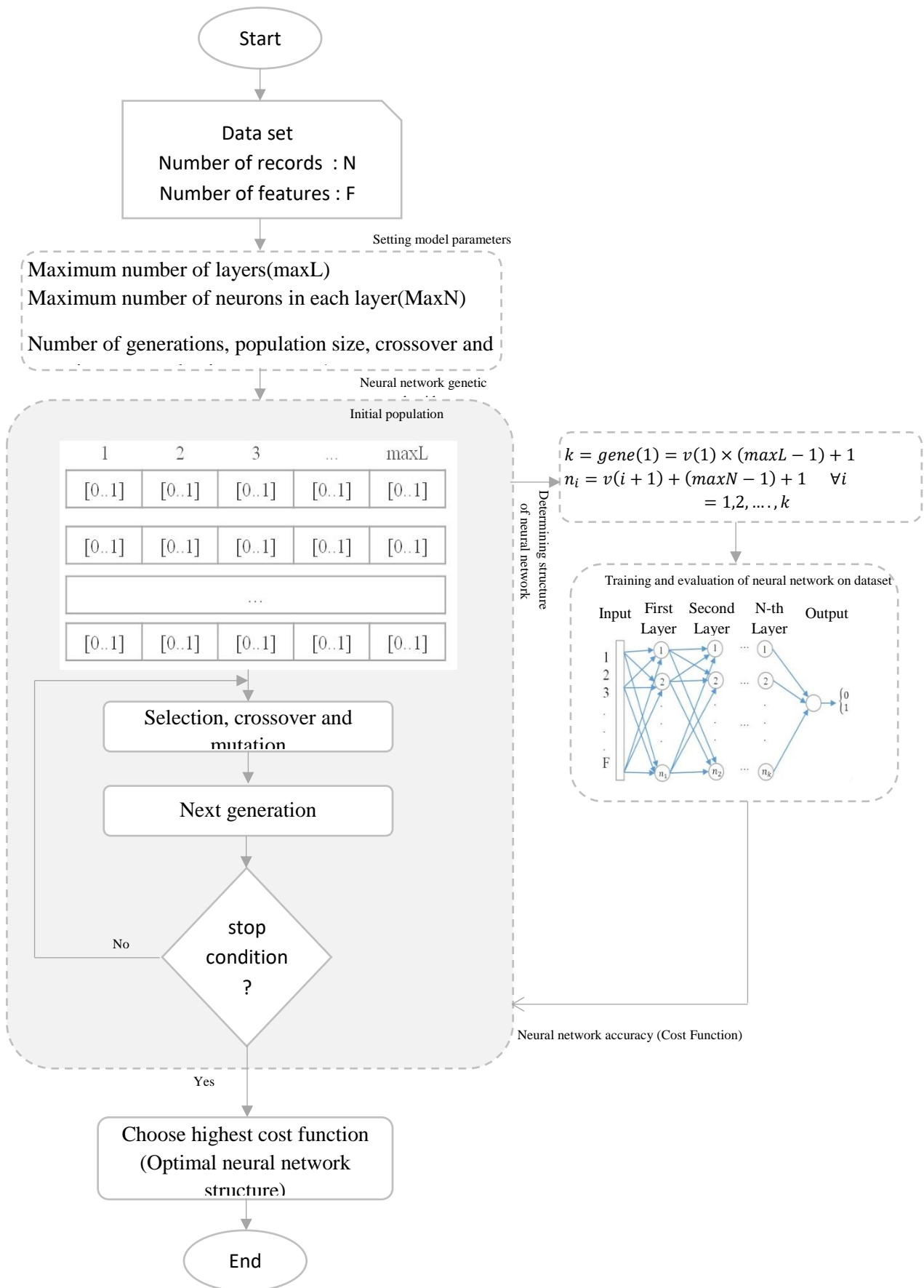


Fig 2: Flowchart of the proposed genetic algorithm-neural network model

Table 1: Characteristics of WDBC dataset

Feature	Description
Radius	Average distances from the center to points on the circumference.
Texture	Standard deviation of gray-level values
Environment	The total distance between consecutive points of the snake
Area	The number of pixels inside the snake is equal to and half of the pixels on its perimeter.
Compression	The degree of compression is equal to the power of two environments divided by one minus the area
Smoothness	Local variations along the radii
Concavity	The intensity of the concave parts of the contour
Concave points	Number of concave contour points
Symmetry	Symmetry of cell nucleus
Fractal dimension	The fractal dimension is equal to one minus the shoreline approximation

The original WBC dataset has 699 records and 11 attributes, including patient identification codes, which are excluded from this study. 458 samples are related to the benign class (66%) and 241 samples are related to the class of malignant tumors (34%). In this collection, 16 records are missing in the column related to the bare nuclear feature, which have been removed in this study. Table 2 shows the characteristic information of the dataset.

Table 2: Characteristics of the WBC dataset (23, 27)

Feature	Range of values
Clump Thickness	1-10
Uniformity of Cell Size	1-10
Uniformity of Cell Shape	1-10
Marginal Adhesion	1-10
Single Epithelial Cell Size	1-10
Bare Nucleoli	1-10
Bland Chromatin	1-10
Normal Nucleoli	1-10
Mitoses	1-10

The implementation of the proposed model and its evaluation have been carried out in MATLAB software and on a system with the processing specifications of Intel ® Core™ i7-8550U CPU @ 1.80GHz 1.99 GHz and 12.0 GB of RAM memory and 64-bit operating system. In order to compare the performance of the proposed methods with the existing methods, due to the effect of the way of dividing the data as well as the random property in the different operations of the optimization methods, it was not possible to implement other methods. Although different methods have reported accuracy on different amounts of data, and some of them do not know the accuracy on the reported evaluation or test set, but in this study, the best report provided in researches related to the accuracy of the proposed

model is compared on the test set.

RESULTS

To evaluate the proposed model, two well-known breast cancer data sets, WBC and WDBC, were used. Each data set was divided into three data sets, training, evaluation and testing, respectively, in the proportion of 70%, 15% and 15%. In order to remove the influence of the distribution of training, evaluation and testing samples on the performance of the network in the examination of different structures in order to achieve a correct comparison of the accuracy of different structures, at first, with the help of the divide Block function from the set of neural network functions of the MATLAB software, the data set was divided into three groups: training, evaluation and testing and until the end of the implementation of the program, these sets were used to train and evaluate the neural networks created by the genetic algorithm.

The parameters of the maximum number of layers and the number of neurons in each layer were selected as 10 and 20, respectively. The initial population number was 10, the number of generations was 10, the crossover rate was 0.8 and the mutation rate was 0.3. Selection, covariance and mutation operators were used, respectively, tournament, uniform and complementary operators. After decoding the coded neural network structure in the chromosome structure, the designed neural network was executed 100 times to calculate the chromosome fitness value and its average accuracy on the evaluation set was calculated as the chromosome fitness. The number of APKs per run is 1000 and the maximum failure is 20. In order to reduce the effect of random assignment of chromosomes in the genetic algorithm, the proposed algorithm was executed three times. Table 3 shows the results of running the proposed algorithm on the WDBC dataset. These results are the 20% of chromosomes with the highest fitness. All parameters are calculated by trial and error.

Table 3: Optimal neural network structures proposed for breast cancer diagnosis of WDBC dataset

Network structure	Accuracy of the model		
	Test	Assessment	Train
[The number of neurons in the first layer- ...- the number of neurons in the kth layer]			
[1]	97.55	98.07	98.78
[9-20]	97.07	98.76	99.07
[20-13-14]	97.07	98.89	99.09
[19-13-17]	96.88	98.95	99.18
[9-18-7-10-8]	96.65	98.58	98.78
[18-3-15]	96.65	98.71	99.14

The condition of accepting a solution is that the

accuracy of the training set is not lower than the accuracy of the evaluation set. Among the different solutions of the second row with a two-layer structure and with 9 and 20 neurons in the hidden layers respectively, it performs well in terms of the simplicity of the structure and efficiency in all three modes of training, testing and evaluation.

Table 4 shows the result of implementing the proposed method on the WBC set. These solutions are 20% of the solutions with the highest degree of chromosome fit from running the model on this data set. For all modes, the accuracy of the test is over 98%.

Table 4: Optimal neural network structures proposed for breast cancer diagnosis of WBC data set.

Network structure [The number of neurons in the first layer- ...- the number of neurons in the kth layer]	Accuracy of the model		
	Test	Assessment	Train
[18-15-19]	98.51	98.58	98.08
[17-18-11]	98.5	98.54	98.01
[18-18-20]	98.47	98.6	98.08
[18-17-20-8]	98.46	98.54	97.99
[18-17-19]	98.22	98.66	98.18
[18-18-11]	98.39	98.64	98.07

Table 5 presents the comparison of the performance of the proposed model with similar works on WBC and WDBC datasets. Based on the effectiveness of the methods on the WDBC dataset, the proposed method has the smallest structure, i.e. it has only one single neuron hidden layer; However, its accuracy on the test set, which contains 15% of the total samples of the data set, is quite adequate.

Table 5: Comparison of the efficiency of the proposed model with some existing methods

Method	WDBC Dataset		WBC Dataset	
	Accuracy	Structure of the NN	Accuracy	Structure of the NN
ABC+RBF (6)	-	-	99.59	[91]
(24) Deep neural network	99	[15-7-13]	-	-
RFE+DNN (14)	-	-	98.62	[10-20-10]
Bayesian neural network (27)	-	-	98.3	[20-10-5]
MLP (27)	-	-	97.5	[10-10]
MLP+NSGA +Assosiation rule mining (12)	97.22	[7]	99.82	[3]
(1) CPNN	97.4	-	-	-
Suggested method	97.55	[1]	98.51	[18-15-19]

DISCUSSION

Machine learning is used in different applications in the fields of engineering [41, 42] and medicine [5, 34] and tries to automatically extract and exploit the information in the data set [12]. Learning methods are particularly effective in disease diagnosis, where AI-based interventions can be used in countries with few health care providers, and machine learning-based tools in risk assessment can supplement clinical knowledge and support. Help health care workers in clinical decisions [5, 9]. Considering the increasing prevalence and the high death rate caused by breast cancer on the one hand and the dependence of the survival rate of breast cancer on the stage of its diagnosis on the other hand, the design of computer diagnostic systems to facilitate early detection in the early stages and achieve the results A more favorable clinical outcome is necessary [15, 22, 43].

One of the effective methods in the field of breast cancer diagnosis is neural networks, which has been widely used in the medical industry. However, the use of these clinical decision support tools and their experimental design still have limitations [31, 32]. One of them is setting network parameters. Adjusting the parameters increases efficiency, but this work is done by knowledge engineers and not by doctors [3]. As a result, the design of a self-organizing diagnostic decision support tool based on neural network, which, while exploiting its generalization and classification power, has the ability to re-execute on new data without the need of system specialists, can reduce the time and cost of services among health systems. Therefore, in this study, a diagnostic decision aid model in the field of medicine based on neural network and genetic algorithm has been introduced, which is able to adjust the structure of the network including the number of hidden layers and the number of neurons in each hidden layer.

CONCLUSION

The results of the implementation of the proposed model on both standard datasets of Wisconsin breast cancer, WBC and WDBC, with a classification accuracy of 97%, show the appropriate performance of the method and the potential of exploitation in diagnostic applications of other diseases.

Also, the variety of structures extracted by the proposed model makes it suitable for hardware design. Considering the success of the algorithm in the diagnosis of benign and malignant tumors, it is suggested that in future work, using multi-objective optimization algorithms, in addition to focusing on the accuracy of the classification, try to design a model with high diagnostic reliability of positive and negative samples (i.e. PPV and NPV indexes).

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AUTHOR'S CONTRIBUTION

All authors contributed to the literature review, design, data collection and analysis, drafting the manuscript, read and approved the final manuscript.

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CONFLICTS OF INTEREST

The authors declare no conflicts of interest regarding the publication of this study.

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