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World competitive contest-based artificial neural network: A new class-specific method for classification of clinical and biological datasets

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A R T I C L E   I N F O

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A B S T R A C T

Many data mining methods have been proposed to generate computer-aided diagnostic systems, which may determine diseases in their early stages by categorizing the data into some proper classes. Considering the importance of the existence of a suitable classifier, the present study aims to introduce an efficient approach based on the World Competitive Contests (WCC) algorithm as well as a multi-layer perceptron artificial neural network (ANN). Unlike the previously introduced methods, which each has developed a universal model for all different kinds of data classes, our proposed approach generates a single specific model for each individual class of data. The experimental results show that the proposed method (ANNWCC), which can be applied to both the balanced and unbalanced datasets, yields more than 76% (without applying feature selection methods) and 90% (with applying feature selection methods) of the average five-fold cross-validation accuracy on the 13 clinical and biological datasets. The findings also indicate that under different conditions, our proposed method can produce better results in comparison to some state-of-art meta-heuristic algorithms and methods in terms of various statistical and classification measurements. To classify the clinical and biological data, a multi-layer ANN and the WCC algorithm were combined. It was shown that developing a specific model for each individual class of data may yield better results compared with creating a universal model for all of the existing data classes. Besides, some efficient algorithms proved to be essential to generate acceptable biological results, and the methods’ performance was found to be enhanced by fuzzifying or normalizing the biological data.

1. Background

Classification is a process of placing samples in the related groups. The clinical data classification which is an important step in the clinical research, can be used to diagnose the seriously life-threatening diseases such as heart diseases or diabetes [1].

Based on the total number of samples, the clinical datasets are divided into two types [2]: balanced and unbalanced. Each class has an almost identical number of samples in the balanced datasets in contrast to the unbalanced datasets, in which the number of samples of every class is not alike. To deliver better results, a classifier inserts samples into the class with the largest number of samples. Since the produced model is unsuitable for classes with a small number of samples, learners will have problems with classes that have small numbers of samples. To deal with such limitations, our proposed algorithm, ANNWCC, can not only generate a specific model for every one of the existing classes but also apply to both the balanced and unbalanced data with several different class sizes.

There are many methods and algorithms which can be applied to solve the problem of classification. A learner such as an ANN, for example, can be applied to find the connection among samples in a specific class. Also, the researchers have proposed many new approaches to training artificial neural networks and have shown the usefulness of their approach in data classification. Leema et al. used the particle swarm optimization (PSO) algorithm to train the neural networks. For this purpose, first they applied their method to three datasets obtained from the University of California Irvine (UCI), then compared their acquired results with those delivered by the previously introduced methods. Although their proposed method seemingly had better performance compared to the other existing methods, there appears that the state-of-art meta-heuristic optimization algorithms had the ability to enhance its performance [3] Masoudi-Sobhanzade et al. introduced a...
new optimization algorithm and showed that their optimization algorithms can outperform other algorithms [4].

In the present study, the works related to the clinical data classification fall into several main categories, including:

i) The Supervised machine learning approaches: These methods aim to develop a model based on the machine learning methods such as ANNs [5], support vector machines [6], Bayesian networks [7] etc. To generate the model, first the data are divided into two training and testing sets, then the machine is trained and validated using the training and testing sets, respectively. Although the mentioned methods produce remarkable results, the state-of-art techniques can enhance their performance. Our proposed method, which is a combination of an ANN and the WCC algorithm, belongs in this class.

ii) The Unsupervised machine learning approaches: In this class of related works, unlike the first group, the existing data do not include any labels; and based on the relationship among data, they are classified into different categories. In this category, The K-nearest neighbour (KNN) is one of the most popular techniques used for clustering [8]. Our proposed method is also fall into this class.

iii) The Semi-supervised machine learning approaches: In the third group of machine learning techniques, some of the existing data include label whereas others not. A combination of supervised and unsupervised methods is usually employed for generating a model [9]. The ensemble techniques may also function properly in this category [10].

iv) The Heuristic-based approaches: This class of related works searches for some connections among the existing data and arranges data in groups using a heuristic algorithm. An efficient algorithm, proposed based on Gauss-Newton [11], a [12] combination of Expectation maximization (EM) and principal component analysis (PCA) [13], and an improved ReliefF algorithm [14], are several instances of works that belong to the fourth group. Although the mentioned methods have big advantages over the other ones and produce acceptable results, they have low performance compared with the meta-heuristic methods [15].

In order to present a suitable computer-aided diagnostic model, a 3-layer architecture based on artificial intelligence has been presented [16]. In this architecture the data received from the sensors, are classified in two categories of healthy and suspicious and if suspicious, finally the doctor will be informed for further examinations [16]. The suggested architecture, requires efficient methods for data classification, whose efficiency in suspicious case diagnosis could be enhanced with ANNWCC.

To ease the identification of disease-causing genes a tool named GPS has been introduced, whose main job is to prioritize and detect the patients genes [17]. To detect the most important disease-causing genes, this tool implements functional linkage networks. The procedure first uses HIPPIE datasets and various algorithms to examine different genes, then the candidate genes are prioritized. Finally, the classification of prioritized genes is done based on scoring schemes [17].

TRIZ article has also presented a method for choosing promising genes, which is able to detect the genes that have the most biological relevance with the disease [18]. For formulation, TRIZ makes use of optimization search operators along with modified BAT algorithm. In this method, mRMR is used as a filter approach, while SVM and MBA are used for classification approach. Hence, not only does it give a wide coverage in gene search space, it also finds the interaction between them [18].

To cure cancer patients, classified studies of cancer subgroups is required. In article [19], to classify the cancer molecular subtypes, in addition to SVM algorithms, optimization algorithms have also been used. The findings show efficient subsets obtained from miRNA and mRNA which are considered as diagnostic biomarkers and can classify molecular cancer groups [19].

In order to carefully study the protein structure, which is of most important biological macromolecules, a step-by-step classification algorithm has been presented [20]. Instead of classes related to the primary structure of proteins, this algorithm uses spatial configuration of proteins by predicting the structural classes of the secondary structure of proteins. Thus, extracting features from secondary structure series leads to a more accurate classification than previous methods [20].

Since the collected data are of the utmost importance in the field of biology, and so are the studies which should be conducted based on these data [21,22], some related works have made efforts to generate the clinical and biological datasets [23–26]. Despite the existence of many datasets in the field of biology, the data pre-processing and their missing values [27–29] remain a challenge [30]. In addition to the cited literature works, some other works have investigated different methods from various perspectives [31,32] and discussed their advantages and disadvantages as well as limitations [33,34]. Such studies give a few new directions for future reference.

The method suggested in this article is a method to classify the clinical and biological datasets. Employing the presented classification method in above-mentioned articles, could lead to detection of probable biomarkers, which is more reliable than other methods.

The biggest weakness of the methods introduced in the above-mentioned studies is their low performance based on the classification criteria. To address such a limitation, the current study proposes a method, named ANNWCC, which is a combination of a multi-layer perceptron artificial neural network (ANN) and the world competitive contests (WCC) algorithm. ANNWCC incorporates several steps, including: (i) the data pre-processing, in which the mentioned biological data are normalized or fuzzified and then passed to the learner, (ii) the data separating, in which the data are categorized and put in the corresponding groups according to the total number of distinct labels, (iii) the model generating, in which the proposed approach (ANNWCC), unlike the other methods that have developed a universal model for all of the data classes, generates a specific model for every individual group of data, and (iv) the data classifying, in which a sample is placed in the group with a minimum value of error between the sample and the group's model. If the values of error between a sample and three models are 0.01, 0.002, and 0.03, respectively, the sample will be placed in the second class.

The proposed method uses a multi-layer artificial neural network to generate a classifier model. ANNs, inspired by the biological neural network systems, are computational models that consist of several neurons connected to other neurons via synapses. The role of the synapses is to transmit signals from a neuron to another. An ANN is a framework or an algorithm, which can be applied to the machine learning practices such as the biological data classification [35]. Fig. 1 shows an example of ANN which includes two hidden layers, which are those between the input and output layers.

As can be seen from Fig. 1 (where B represents bias) there are two neurons in each hidden layer. The output of a neuron can be calculated using Eq. (1):

\[
O_{i,j} = \sum_{k=1}^{n} W_{k,j} + B_{j}
\]

where \( O_{i,j} \) is the output of the \( j \)-th neuron in the \( i \)-th hidden layer, \( B \) and \( W \) are the bias and edge weights respectively, and \( W_{k,j} \) is the weight of the edge (synapse) between the \( k \)-th neuron in the (\( i-1 \))-th hidden layer and the \( j \)-th neuron in the \( i \)-th hidden layer.

Training of an ANN, in which the values of synapses or edges are determined, is a non-deterministic polynomial (NP) problem. In the case of these problems, it is not possible to find an optimal solution in a polynomial-time order and for this reason, the heuristic and meta-heuristic methods such as the optimization algorithms are applied to the train of ANN training [3]. WCC, which has been inspired by the
rules of human sports, is an optimization algorithm with a meta-heuristic search strategy and shows a high level of performance compared to other optimization algorithms. The current study formulates the WCC algorithm to the training of the ANN problem and investigates and its contribution to classify of clinical and biological data. The introduced method of ANNWCC can be applied in the third layer of the above-mentioned architecture.

2. Methods

ANNWCC, whose framework has been depicted in Fig. 2, is being applied at several stages. In the first step, the data pre-processing is carried out on a biological dataset. Normalization, in which the data of the groups are changed in the same range using Eq. (2), and fuzzification, which determines the degree to which each datum belongs to a group (Eq. (2)), are used at the data pre-processing stage.

\[
nrv_i = a + \frac{(v_i - vmin) \times (b - a)}{vmax - vmin}
\]

where \(a\) and \(b\) are the upper and lower bounds of \([a, b]\), in which the groups’ data should be converted, and \(v_{min}\), \(v_{max}\), and \(v_{rv_i}\) are the current values that should be normalized, the minimum value of the related group, the maximum value of the related group, and the normalized value, respectively.

In Eq. (3), which is a fuzzification equation, AVG, \(v_{min}\), \(v_{max}\), and \(f_{min}\) are the average value of a group, the minimum value of a group, the current value which should be converted into a fuzzy value, and the fuzzified value, respectively. A group’s data change in the range of \([0,1]\) using Eq. (3).

\[
f_{min} = \frac{|(v_i - AVG)|}{(AVG - vmin)}
\]

In the next step, ANNWCC divides a clinical or biological dataset into several groups based on the total number of class labels and puts every sample in its relevant group. After dividing the datasets of each class into training and testing sets, ANNWCC generates a model for each class of data using an ANN.

The number of the hidden layers in an ANN and their neurons pose a design challenge because the computation time will increase as the number of the hidden layers goes up. Thus, there should be a trade-off between these factors. Eqs. (4) and (5) show the way the number of the hidden layers and their neurons are determined in ANNWCC:

\[
nh = \log (N)
\]

\[
n_{h_i} = \log (n_{h_{i-1}}), 1 < i \leq nh, n_{h_i} = N
\]

Where \(N\), \(nh\), and \(n_{h_i}\) are the number of neurons in the input layer, the number of the hidden layers, and the number of neurons in the \(i\)th hidden layer, respectively.

2.1. The WCC-based ANN method

The ANNWCC training which is the final step toward generating the desired model, is an NP problem that cannot be solved within a reasonable period of time. Studies have shown that using optimization algorithms to train ANNs yields comparatively more acceptable results. We use WCC for ANN training due to its remarkable performance in the NP problems. By the approach employed in the present study, each team is considered a potential model for the clinical data classification. The number of players are computed using Eq. (6):

\[
np = \sum_{i=1}^{nh} (n_{h_i} \times n_{h_{i-1}} - 1) + n_{h_i}
\]

Where \(np\) is the number of players on a team.

The score function which determines the suitability of a potential answer, is defined using Eq. (7). As shown in this equation, if a particular model in a relative class assigns the input samples to the closer output values, it will perform better than others. Eq. (7) is known as the root mean squared error (RMSE).

\[
RMSE = \sqrt{\frac{1}{n} \sum_{i=1}^{n} (y_i - p_i)^2}
\]

where \(n\), \(y_i\), and \(p_i\) are the number of samples in a class, the value assigned to a group’s samples, and the predicted value of a sample, respectively.

ANNWCC generates an individual model for each existing class. After samples of a dataset are evaluated by every one of the created models, a test sample is labelled with a class number that reflects the closeness of its model’s output to the mean of its class. Eq. (8) shows the way a test sample is assigned to a class.

\[
L_i = \{k \mid (o_{k} - avg_{k})\} \text{ is a minimum for all } 1 \leq k \leq m
\]

where \(o_{k}\), \(avg_{k}\), \(L_i\), and \(m\) are the \(k\)th model’s output for the \(i\)th test sample, the average value of the training samples obtained from the \(k\)th model in the \(i\)th class, the label determined for the \(i\)th test sample, and the number of classes, respectively.

In the proposed method, parameters, including the total number of teams, groups, and attempts that improve and fulfill the scoring function, should be defined at the beginning of the algorithm. Like other optimization algorithms, WCC begins with the first population of the potential answers named Teams. Every team, which is generated randomly, is considered a candidate solution that determines the weights of the ANN’s edges. Then, the generated teams are randomly placed in some groups which have equal numbers of teams. Teams compete with each other and improve their scores (RMSE) through four operations. The WCC algorithm consists of four operations, including shooting, attacking, passing, and crossing which change the candidate solution or the weights of an ANN and introduce some new potential answers. In this study, shooting, attacking, passing, and crossing operations have been formulated using Eqs. (9), (10), (11) and (12), respectively.

\[
\sum_{i=1}^{k} (Team_{i}(v1) = Team_{i}(v2))
\]

Where \(k\) and Team are a random integer value between 1 and \(n\) (the total number of the ANN’s edges) and a candidate solution that determines the weights of an ANN. \(v1\) and \(v2\) are two integer values between 1 and \(n\).

\[
\sum_{i=1}^{k} (Team_{i}(rand(n)) = rand(RNG))
\]

Where RNG determines the range of values assigned to variables or
edges of ANN.

\[
\sum_{i=1}^{k} (\text{Team}(v_1) = \text{Team}(v_2) \&\& \text{Team}(v_2) = \text{Team}(v_1))
\]

(11)

\[
\sum_{i=m}^{k} (\text{Team}(m) = \text{Team}(m + 1))
\]

(12)

Where \(k\) and \(m\) are two integer values between 1 and \(n\).

In the proposed algorithm, there is a referee who evaluates the effect of an action on a team and keeps scores. If an operation enhances the team’s score, the new changes will be accepted by that team; otherwise, they will be ignored. Matches are held at two stages: 1) group matches; and 2) elimination matches. At the end of the elimination stage, a champion is selected as an answer to the problem. This scenario, in which individual iterations are called seasons, will be repeated until an acceptable response is produced. The above-mentioned operations which change a team’s values have been illustrated in Fig. 3.

After holding the group competitions, teams with a higher score ascend to the elimination stage and continue their competition. Like the grouping stage, the elimination stage is held based on the mentioned operations. At the end of the elimination phase, the remaining team is considered to be the answer to the problem [36].

3. Results

We implemented a multi-layer perceptron ANN in the MATLAB programming language on a system with 12 GB of RAM, corei7 CPU, and Windows 10.1 operating system. To train an ANN, we used the WCC algorithm, a discrete symbiotic optimization search (DSOS) [37], and the PSO algorithms [38]. To carry out this experiment, we used 13 clinical and biological datasets obtained from the UCI Machine Learning Repository [39]. Table 1 presents the following information about these datasets: the number of references to each dataset (REF), the name of the datasets, the number of instances (NOI), the number of features (NOF) without considering the class labels, the number of classes (NOC), the data types (DT), and the missing values (MV). The Cleveland Heart Disease (CHD) dataset was prepared in two ways: as the CHD with two classes (CHD2) and the CHD with five categories (CHD5). The CHD2 was generated by merging the risk level of heart disease and heart disease class labels. The Statlog Heart Disease (SHD) dataset consists of two classes, indicating the presence and absence of heart disease. The Pima Indian Diabetes (PID) dataset has been made up of two groups of people those with diabetes and those without diabetes. Hepatitis (HEP), Liver Disorders (LIV), Lung Cancer (LUNG), Parkinson’s Disease (PAR), and the Wisconsin Diagnostic Breast Cancer (WDBC) datasets are the other ones whose features have been also

Fig. 2. The framework of the proposed method.
In the first experiment, we investigated the effect of the input data type on the ANN training stage, and then compared the three algorithms’ performance on the CHD2, the normalized CHD2 (NCHD2), and the fuzzified CHD2 (FCHD2) datasets. It was found that an optimization algorithm with a faster convergence speed and similar results obtained from its different executions is the most suitable algorithm. Convergence means that an optimization algorithm can yield an optimal answer as the dedicated time or the number of iterations increases. Since optimization algorithms usually have operators that change the candidate solutions randomly, the produced answers may vary to some extent. However, different executions may yield similar answers. To address such a problem, it is recommended that optimization algorithms should be executed at least 30 individual times [52]. The variable behaviour of an optimization algorithm in its different executions should be measured from the stability perspective. An optimization algorithm with similar output values in its different executions functions better compared to others. For the purpose of classification, the convergence and stability were examined in terms of accuracy (ACC), a correlation (COR) between actual and predicted labels, and RMSE [53]. Based on the mentioned criteria, an evaluation of the WCC, DSOS, and PSO algorithms was made in Figs. 4 & 5 and Table 2, respectively.

Every algorithm was executed 30 times, with 50 seasons per execution. The best-obtained results have been illustrated in Fig. 4, which shows the convergence of the algorithms on the PID dataset and

![Fig. 3. An example of ANN training. The changes are accepted if they reduce RMSE.](image)

(a) An ANN with one hidden layer and 8 edges is considered.
(b) The first population consists of two teams whose players are equal to the number of ANN's edges. Every player determines a weight for the specified edge.
(c) The status of the teams before the attacking operators are shown. Team #2 is the attacker team and selects two players randomly.
(d) The attacker team adds random values to its selected values and sends them toward to randomly selected players in Team #1.
(e) Team #2 is the shooter and selects two players randomly.
(f) The shooter team sends its selected values toward Team #1.
(g) The status of a team before crossing. In this operator, the permutation of values in a specified range is changed.
(h) The status of Team #1 is presented after crossing.
(i) the status of a team before passing. In this operator, two players who are chosen randomly change their values.
(j) The status of Team #1 after passing.

presented in Table 1.

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Table 1
Datasets used.

| REF | Name      | NOI | NOF | NOC | DT       | MV   |
|-----|-----------|-----|-----|-----|----------|------|
| [40] | CHD2      | 303 | 13  | 2   | Numerical and binary | NO   |
| [40] | CHD5      | 303 | 13  | 5   | Numerical and binary | NO   |
| [41] | SHD       | 270 | 13  | 2   | Numerical and binary | NO   |
| [42] | PID       | 768 | 8   | 2   | Numerical | NO   |
| [43] | HEP       | 150 | 19  | 2   | Numerical and binary | YES  |
| [44] | LIV       | 345 | 6   | 2   | Numerical and binary | NO   |
| [45] | LUNG      | 32  | 56  | 3   | Numerical and binary | YES  |
| [46] | PAR       | 197 | 22  | 2   | Real     | YES  |
| [47] | WDBC      | 569 | 31  | 2   | Real     | NO   |
| [48] | ARGENE    | 900 | 10,000 | 2 | Numerical | NO   |
| [49] | ARRYTH    | 452 | 279 | 16  | Double   | YES  |
| [50] | PARKINSON | 756 | 754 | 2   | Numerical and binary | NO   |
| [51] | GENEEXPR  | 801 | 20,531 | 5 | Double   | NO   |

Table 1 demonstrates that all the three algorithms converge successfully on the non-preprocessed, fuzzified, and normalized PID datasets. The lower is the value of RMSE, the more effective is the algorithm. Although the model generated by each algorithm is different from the ones produced by the other two algorithms, every algorithm’s performance is remarkable on the PID datasets their RMSE value is almost zero. As indicated in Fig. 4, when data pre-processing is not carried out, the performance of the algorithms will be low in terms of accuracy and correlation. The WCC algorithm achieves 100% of accuracy and correlation on both the fuzzified and normalized datasets, whereas the DSOS and PSO algorithms reach 100% of classification accuracy and correlation only on the normalized datasets. Fig. 5 shows the stability of the algorithms in 30 individual executions.

Fig. 5 illustrates the performance of the algorithms from the stability perspective in terms of error, accuracy, and correlation on the non-preprocessed, fuzzified, and normalized PID datasets. Although WCC, PSO, and DSOS all show acceptable as well as similar results, WCC outperforms others. Figs. 4 and 5 show that the pre-processing stage is essential in the ANNWCC’s training and improves the performance of the algorithms. The normalized datasets yield better results on the PID datasets compared with the other dataset types.

To investigate the performance of the algorithms on all the three types of PID datasets in detail, an evaluation of the algorithms’ performance on the training and testing datasets with different sizes was made. To this end, the data were divided into various parts, and the methods were applied to them. The results have been shown in Table 2. As observed earlier, once again algorithms produced acceptable results even with a minimum size of the training datasets. In comparison to PSO and DSOS, the WCC algorithm yielded better results. It was revealed that DSOS and PSO function approximately in a similar way. The results reported in the current investigation, show that the proposed method can be a suitable option for a dataset with a small size of samples. However, the performance of the obtained models can be enhanced by applying various feature selection approaches.

In the third experiment, we evaluated the algorithms’ performance on all the datasets. For this purpose, the datasets were divided into five folds. In the 5 iterations, one of the folds was used as the testing set and the other ones as the training sets. The algorithms were ran in 30 individual executions on the three types of data: non-pre-processed, fuzzified, and normalized. The results have been shown in Table 3. This table presents the name of the algorithms (AN), the type of datasets on which the algorithms have maximum performance, the elapsed time (ET) of the algorithms which is presented in seconds, accuracy (ACC), the confidence interval (CI) which determines the accuracy range with a specific probability, and the p-value. Since the order of the input has been changed to calculate the p-value and CI, the cross-validation results were reported in different runs. Accuracy, specificity (SPC), sensitivity (SEN), and the false-positive rate (FPR) were calculated using Eqs. (13) through (16), where n is the number of classes, m is the number of samples, and TPi, TNi, FPi, and FNi, are the true positive, true negative, false positive, and false-negative rates of the ith class, respectively.

\[
ACC = \frac{\sum_{i=1}^{n} (TP_i + TN_i)}{m} 
\]  
\[
SPC = \frac{\sum_{i=1}^{n} (TN_i)}{n} 
\]  
\[
SEN = \frac{\sum_{i=1}^{n} (TP_i)}{n} 
\]  
\[
FPR = 1 - SPC 
\]

As indicated in Table 3, the performance of WCC, which is approximately the same for both the normalized and fuzzified datasets, is better than the other two algorithms. Besides, PSO and DSOS deliver better results only on the normalized data sets. Also, as evidenced by Table 3, algorithms demonstrate distinct performance on different data types; while DSOS produces the best results on the CDHS and HEP datasets, PSO yields the most desirable effects on the PAR dataset. Also, WCC delivers the most appropriate results on the CHD2, LUND, and WDBC datasets. In the case of the SHD, PID, and LIV datasets, each algorithm performs in much the same way as the other two algorithms do. In general, although all of the algorithms function properly, compared to DSOS and PSO, WCC seems to produce the most desired results in terms of CI, P-value, and the elapsed time.

Table 4 summarizes and compares the three algorithms based on the above-mentioned criteria which have been computed using the “ANOVA 1” function (MATLAB) with the default parameters. As shown in Table 4, although the results produced by the other two algorithms are suitable, once again WCC delivers the most favourable results on all the datasets. In the case of DSOS and PSO, although they produce similar results, DSOS’ performance is slightly better than PSO’s. Since feature selection (FS) is one of the primary data pre-processing steps which may help produce better results, the effects of FS on the performance of the proposed method was also investigated. For this purpose, after the desired features were selected using the FeatureSelect software application [15], they were applied to the methods and the final models were generated using the selected features. The obtained datasets, called the FS-based datasets, together with their average results, have been shown in Table 4.

The receiving operation characteristic (ROC) curve is a graphical method for determining the separation ability of the models in the samples of classes [54]. An algorithm with a curve close to the top left-hand side of the graph has a high ability to separate the data. Based on the average of the best 30 individual executions of algorithms on all the datasets, Fig. 6 is represented. As it is shown in Fig. 6, although the ROC curves of all the three algorithms show their remarkable separation ability, WCC outperforms DSOS and PSO in its ability to separate the data. Moreover, the separation ability of DSOS is better than that of PSO.

The vertical axis of the ROC curves marks the sensitivity of the algorithms, which is computed using Eq. (16), and the horizontal axis presents the false positive rate (FPR) which is equal to \(1 - SPC\) and is calculated by Eq. (16). The Purple, blue, red, and yellow curves show the ROC curves of the random guess, WCC, DSOS, and PSO algorithms, respectively. Although all the three algorithms’ ROC curves are approximately in harmony/agreement, the area under the WCC’s curve (AUC) is larger than the ones under the other two algorithms’ curves.

The PID, CHD, and SHD datasets, whose attributes and properties such as the total number of samples were presented in Table 1, have been frequently used in various studies. In the final experiment, we made a comparison between the results of some previously done studies in the literature works and those of the three algorithms described in this paper. The research references, publication dates, authors’ names, methods’ names, and the best value for the accuracy obtained by each
Fig. 4. An evaluation of the algorithms' performance based on the RMSE, accuracy, and correlation. The WCC, PSO and DSOS algorithms are shown by the blue, red and green curves, respectively. The first, second and third columns show the results obtained for the non-preprocessed PID, fuzzified PID and normalized PID datasets, respectively. (a) Comparison of convergence based on the RMSE criterion. (b) Comparison of convergence based on the accuracy criterion. (c) Comparison of convergence based on the correlation criterion. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)
Fig. 5. Evaluation of the algorithms based on the RMSE, accuracy and correlation criteria. WCC, PSO, and DSOS are shown by the blue, red and green curves, respectively. The first, second and third columns show the results obtained for the non-preprocessed, fuzzified and normalized PID datasets, respectively. (a) Comparison of stability based on the RMSE criterion, (b) Comparison of stability based on the accuracy criterion. (c) Comparison of stability based on the correlation criterion. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)
were identical. In most cases, based on the findings, WCC, PSO, and algorithms. WCC produced the best results on the CHD2 dataset. And finally, the results delivered by WCC, PSO, and DSOS on the SHD dataset were identical. In most cases, based on the findings, WCC, PSO, and DSOS outperformed the other previously proposed approaches.

4. Discussion

In this part, first, we make a comparison between ANNWCC and the other clinical data classification approaches, then discuss its capabilities from different perspectives:

1. The Applied method aspect: The proposed method, employed for classification, is different from the other introduced methods. Unlike ANNWCC, which is a combination of the designed ANN and the WCC algorithm, a majority of classification methods are based on either an ANN, which uses classical or modified training methods [71–77] or an optimization algorithm which determines a weighting method for the classification of data [78–81]. In contrast to the other approaches which introduce a universal model for all the different kinds of data [82–84], ANNWCC generates a specific model for each class of data.

2. The Dataset types: In contrast to the previously introduced works, which have focused on just a specific dataset and based their evaluation on a single data type [85–87], ANNWCC’s performance / effect has been investigated on 13 different medical and biological datasets. ANNWCC is also operable on both the balanced and unbalanced datasets, while a majority of the other approaches have focused on just the balanced data [88–90]. In addition to the above-mentioned findings, it was revealed that there is a connection between the number of hidden layers and the computational time enhancing.

3. The Scalability aspect: Unlike the other approaches which have only one specific application, ANNWCC’s results indicate that it can be enhanced.

5. Conclusion

In this paper, we proposed a new method based on a combination of ANN and the WCC algorithm to classify the clinical datasets. For the purpose of this classification, we employed several real datasets obtained from the UCI Machine Learning Repository and different literature.

### Table 2
An evaluation of the algorithms’ performance on the training and testing datasets with different sizes.

| Dataset | AL_name | ACC | % CI | P_value |
|---------|---------|-----|------|---------|
| CHD2    | WCC     | 80.01 | [91 92] | 1.6E-15 |
| PSO     | 93.25   | 94   |
| DSOS    | 100     | 94   |
| Fuzzified PID | WCC | 62.96 | [71 72] | 0.052 |
| PSO     | 80.56   | 100  |
| DSOS    | 76.39   | 93   |
| Normalized PID | WCC | 80.56 | [71 72] | 0.052 |
| PSO     | 93.06   | 100  |
| DSOS    | 100     | 100  |

### Table 3
Comparison of algorithms’ performance on all of the datasets.

| Type          | ET | ACC % CI | P_value |
|---------------|----|----------|---------|
| NA            |    |          |         |
| CHD2          | WCC | 80.01 | [91 92] | 1.6E-15 |
| PSO           | 93.25 | 94   |
| DSOS          | 100     | 94   |
| Fuzzified PID | WCC | 62.96 | [71 72] | 0.052 |
| PSO           | 80.56   | 100  |
| DSOS          | 76.39   | 93   |
| Normalized PID | WCC | 80.56 | [71 72] | 0.052 |
| PSO           | 93.06   | 100  |
| DSOS          | 100     | 100  |

### Table 4
Overall comparison of algorithms’ performance.

| AN          | ET   | ACC % CI | P_value |
|-------------|------|----------|---------|
| All datasets | WCC | 6367.518 | [75.69 75.46] | 5.42E-5 |
| PSO         | 2823.065 | 75.735 | [71.23 71.84] | 3.67E-4 |
| DSOS        | 8539.04 | 75.764 | [73.23 71.61] | 3.07E-3 |
| Fuzzified datasets | WCC | 4005.55 | 75.093 | 6.66E-11 |
| PSO         | 1899.62 | 86.243 | [83.03 85.85] | 3.05E-11 |
| DSOS        | 5883.741 | 86.243 | [83.96 84.43] | 3.71E-11 |
works. We separated each group’s data and generated a model for each one. Then we evaluated the performance of the algorithms on various experiments and described their functionality. Convergence, stability, error, the correlation between predicted and actual labels, accuracy, sensitivity, and specificity were the main criteria used for the comparison of the algorithms. Based on the above-mentioned criteria, the results produced by the WCC algorithm seemed to be better than those delivered by the other ones. We also compared the current studies’ reported results on the PID, CHD, and SHD datasets with the results reported by the previously done studies on these datasets, and found out that the proposed method can achieve remarkable results in terms of the average value of accuracy for the PID and SHD datasets.

Author contribution statements

Zohre Arabi designed the project, prepared the manuscript, and performed the analysis. Ali Rezaee and Ahmad Habibizad Navin reviewed the manuscript and supervised the project. Mehdi Hosseinzadeh designed the project, prepared data for the analysis, reviewed the manuscript and supervised the project. All authors read and approved the final version of the manuscript.

Declaration of Competing Interest

None.

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