A rule based method to locate the bounds of neural networks

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Abstract

An advanced method of training artificial neural networks is presented here, which aims to identify the optimal interval for initialization and training of artificial neural networks. The location of the optimal interval is performed using rules evolving from a genetic algorithm. The method has two phases: in the first phase, an attempt is made to locate the optimal interval and in the second phase, the artificial neural network is initialized and trained in this interval using a method of global optimization, such as genetic algorithms. The method has been tested on a range of categorization and function learning data and the experimental results are extremely encouraging.

1 Introduction

Artificial Neural networks (ANNs) are programming tools [1, 2] based on a series of parameters that are commonly called weights or processing units. They have been used in a variety of problems from different scientific areas, such as physics [3, 4, 5], solving of differential equations [6, 7], agriculture [8, 9], chemistry [10, 11, 12], economics [13, 14, 15], medicine [16, 17] etc. A common way to express a neural network is a function $N(\overrightarrow{x}, \overrightarrow{w})$, with $\overrightarrow{x}$ the input vector (commonly called pattern) and $\overrightarrow{w}$ the weight vector. A method that trains a neural network should be used to estimate the vector $\overrightarrow{w}$ for a certain problem. The training procedure can also be formulated as an optimization problem, where the target is to minimize the so-called error function:

$$E\left(N\left(\overrightarrow{x}, \overrightarrow{w}\right)\right) = \sum_{i=1}^{M} \left(N\left(\overrightarrow{x}_i, \overrightarrow{w}\right) - y_i\right)^2 \tag{1}$$

In equation 1 the set $(\overrightarrow{x_i}, y_i)$, $i = 1, ..., M$ is the dataset used to train the neural network, with y_i being the actual output for the point $\overrightarrow{x_i}$. The neural network $N(\overrightarrow{x}, \overrightarrow{w})$ can be modeled as a summation of processing units as proposed in

[18]:

$$N\left(\overrightarrow{x},\overrightarrow{w}\right)=\sum_{i=1}^{H}w_{(d+2)i-(d+1)}\sigma\left(\sum_{j=1}^{d}x_{j}w_{(d+2)i-(d+1)+j}+w_{(d+2)i}\right) \quad (2)$$

with H is the number of processing units of the neural network and d is the dimension of vector $\overrightarrow{x}$. The function$\sigma(x)$ is the sigmoid function defined as:

$$\sigma(x)=\frac{1}{1+\exp(-x)} \quad (3)$$

From the equation 2 one can obtain that the dimension of the weight vector w is computed as: $n=(d+2)H$. The function of equation 1 has been minimized with a variety of optimization methods during the past years such as: the Back Propagation method [19, 20], the RPROP method [21, 22, 23], Quasi Newton methods [25, 26], Simulated Annealing [34, 35], Genetic Algorithms [27, 28], Particle Swarm Optimization [29, 30] etc.

The present work proposes an innovative interval generation technique for the initialization and training of artificial neural network parameters. This new method has its roots in interval methods [31, 32, 33]. In current work, using arithmetic intervals, a set of rules for dividing the initial interval for the parameters of the artificial neural network is constructed. The construction is carried out using a hybrid genetic algorithm, in which chromosomes are the set of division rules. After the termination of the genetic algorithm, the artificial neural network is initialized in the interval resulting from the application of the optimal partitioning rules and then trained using a genetic algorithm.

This method used has two objectives: the first objective is to detect a small interval of initialization of the parameters of the artificial neural network and the second objective is to accelerate the training of the network. In the first target, using information from the training data the algorithm will make an attempt to identify that interval that will ultimately give better results. In the second objective, once a small value interval has been detected, a global optimization method can be used more efficiently to detect the lowest value of the network error.

The rest of this article is as follows: in section 2 the proposed method is discussed in detail, in section 3 the experimental datasets as well as the results from the application of the proposed method are provided and finally in section 4 some conclusions and guidelines for future enhancements are presented.

2 Method description

The proposed method consists of two major steps: in the first step, the construction of the partition rules of the initial value interval for the parameters of the artificial neural network is made and in the second step, the artificial neural network is initialized in the optimal space resulting from the first step

and training takes place. The training is performed through a second genetic algorithm. In the first genetic algorithm, the chromosomes are sets of partition rules of the initial value interval of the artificial neural network, and in the second genetic algorithm, the chromosomes are the parameters of the artificial neural network. It is obvious that this is a time consuming process and modern parallel techniques such as the OpenMP [36] library must be used to accelerate it. The first genetic algorithm is analyzed in subsection 2.1 and the second in subsection 2.5.

2.1 Locating the best rules

Firstly, we introduce the rule set I_n where:

$$I_n = \{(l_1, r_1), (l_2, r_2), \ldots, (l_n, r_n)\} \tag{4}$$

where $l_i \in \{0,1\}$, $r_i \in \{0,1\}$, $i = 1, \ldots, n$. The set I_n defines the set of partition rules for a function defined as

$$f : S \to R, S \subset R^n \tag{5}$$

with S:

$$S = [a_1, b_1] \otimes [a_2, b_2] \otimes \ldots [a_n, b_n] \tag{6}$$

If $l_i = 1$ then $a_i = \frac{a_i}{2}$ and if $r_i = 1$ then $b_i = \frac{b_i}{2}$. For example consider the Rastrigin function:

$$f(x) = x_1^2 + x_2^2 - \cos(18x_1) - \cos(18x_2), \ x \in [-1, 1]^2 \tag{7}$$

Also consider the set $I_2 = \{(1,0), (0,1)\}$ The produced bounding box for the Rastrigin function is now $S' = [-0.5, 1] \times [-1, 0.5]$.

Subsequently, we introduce the extended set C_{Kn} as a set of production rules defined as:

$$R_{Kn} = \left\{ I_n^{(1)}, I_n^{(2)}, \ldots, I_n^{(K)} \right\} \tag{8}$$

where $I_n^{(i)}$, $i = 1, .., K$ are rule sets of equation 4. For example let $K = 2$ for the Rastrigin function and $R_{22} = \{\{(0,1), (1,0)\}, \{(1,0), (1,1)\}\}$. The final bounding box is considered after applying the sets $\{(0,1), (1,0)\}$ and $\{(1,0), (1,1)\}$ in the original box S. The computation steps are:

1. **Apply** $\{(0,1), (1,0)\}$to S yielding $S' = [-0.5, 1] \times [-1, 0.5]$
2. **Apply** $\{(1,0), (1,1)\}$ to S' yielding $S'' = [-0.25, 1] \times [-0.5, 0.25]$

We consider chromosomes in the form of equation 8 for the first phase of the proposed method. The value n is the total number of parameters of the neural network. The fitness of every chromosome g is an interval $f_g = \left[f_{g,\min}, f_{g,\max} \right]$.

Hence, in order to compare two different intervals $a = [a_1, a_2]$ and $b = [b_1, b_2]$ we incorporate the following function:

$$L^*(a,b) = \begin{cases} \text{TRUE}, & a_1 < b_1, \text{OR } (a_1 = b_1 \text{ AND } a_2 < b_2) \\ \text{FALSE}, & \text{OTHERWISE} \end{cases} \quad (9)$$

Hence, the steps of the genetic algorithm of the first phase are the following:

Initialization step

1. **Set** K as the number of rules.
2. **Set** $S = [-F, F]^n$, as the initial bounding box for the parameters of the neural network. F is considered as a positive number with $F > 1$.
3. **Set** N_C as the total number of chromosomes.
4. **Set** N_S the number of samples in fitness evaluation.
5. **Set** P_s as the selection rate, where $P_s \leq 1$.
6. **Set** P_m as the mutation rate, where $P_m \leq 1$.
7. **Set** $t = 0$ the current generation number.
8. **Set** N_t the maximum number of generations allowed.
9. **Initialize** randomly the chromosomes $C_i,\ i = 1, .., N_C$ as sets of the equation 8.

Termination check step

1. **Set** t=t+1
2. **If** $t \geq N_t$ **terminate**.

Genetic operations step

1. **For** every chromosome $C_i,\ i = 1, .., N_C$ calculate the corresponding fitness value f_i using the algorithm of subsection 2.2.
2. **Apply** the selection operator. Initially, the chromosomes are sorted according to their fitness value. The sorting utilizes the function $L^*(a,b)$ of equation 9 to compare fitness values. The best $(1 - P_s) \times N_c$ are copied to the next generation while the rest of them are substituted by offsprings created through the crossover procedure. The mating parents for the crossover procedure are selected using the well - known technique of tournament selection.

3. **Apply** the crossover operator: For every pair of selected parents (z, w), two children (cz, cw) are produced using the uniform crossover procedure described in subsection 2.3.

4. **Apply** the mutation operator using the algorithm of subsection 2.4.

5. **Goto** Termination Check Step.

2.2 Fitness evaluation for the rule genetic algorithm

The fitness value for each chromosome g is considered as an interval $f = [f_{\min}, f_{\max}]$ where $f_{\min}$is an estimation of the lower value obtained using the rules of the chromosome g and $f_{\max}$is an estimation of the maximum value. In order to calculate the fitness of every set of rules C the following steps are performed:

1. **Set** $f_{\min} = \infty$
2. **Set** $f_{\max} = -\infty$
3. **Apply** the rule set g to the original bounding box S. The outcome of this application is the new bounding box S_g.
4. **For** $i = 1, .., N_S$ **do**
   (a) **Produce** a random sample $w \in S_g$
   (b) **Calculate** the training error $E_g = E\left(N\left(\overrightarrow{x}, \overrightarrow{w}\right)\right)$ using equation 1.
   (c) **If** $E_g \leq f_{\min}$ then $f_{\min} = E_g$.
   (d) **If** $E_g \geq f_{max}$ then $f_{\max} = E_g$.
5. **EndFor**
6. **Return** the interval $f = [f_{\min}, f_{\max}]$ as the fitness of chromosome g.

2.3 Crossover for the rule genetic algorithm

The crossover for the genetic algorithm of the first phase is performed using uniform crossover. For every couple (z, w) of selected parents two children (cz, cw) are produced through the following procedure:

1. **For** $i = 1..K$ **do**
   (a) **Let** $z^{(i)} = \left\{l_z^{(i)}, r_z^{(i)}\right\}$ the i item of the chromosome z.
   (b) **Let** $w^{(i)} = \left\{l_w^{(i)}, r_w^{(i)}\right\}$ the i item of the chromosome w.
   (c) **Produce** a random number $r \leq 1$
   (d) **If** $r \leq 0.5$ **then**
      i. **Set** $\mathrm{cz}^{(i)} = \left\{l_z^{(i)}, r_w^{(i)}\right\}$

ii. **Set** $\mathrm{cw}^{(i)} = \left\{ l_w^{(i)}, r_z^{(i)} \right\}$

(e) **Else**

i. **Set** $\mathrm{cz}^{(i)} = \left\{ l_w^{(i)}, r_z^{(i)} \right\}$

ii. **Set** $\mathrm{cw}^{(i)} = \left\{ l_z^{(i)}, r_w^{(i)} \right\}$

(f) **Endif**

2. **EndFor**

2.4 Mutation for the rule genetic algorithm

The steps for the mutation procedure for the genetic algorithm of the first phase have as following:

1. **For** $i = 1, .., N_C$ **do**

(a) **Let** $C_i = \left\{ C_i^{(1)}, C_i^{(2)}, \ldots, C_i^{(K)} \right\}$ the i chromosome of the population.

(b) **For** $j = 1, .., K$ **do**

i. **Let** $C_i^{(j)} = \left\{ l_i^{(j)}, r_i^{(j)} \right\}$

ii. **Take** $r \leq 1$ a random number.

iii. **If** $r \leq P_m$ **then** alter randomly with probability 50% the $l_i^{(j)}$ or the $r_i^{(j)}$ part of $C_i^{(j)}$.

(c) **EndFor**

2. **EndFor**

2.5 Second phase

In the second phase the best chromosome g_b defined as

$$g_{\mathrm{b}} = \left\{ \{l_{b,1}, r_{b,1}\}, \{l_{b,2}, r_{b,2}\}, \ldots, \{l_{b,K}, r_{b,K}\} \right\} \tag{10}$$

is used to transform the original bounding box $S = [-F, F]^{(n)}$ to a new box S_b. The new hyperbox is defined as

$$S_b = [a_{g,1}, b_{g,1}] \times [a_{g,2}, b_{g,2}] \times \ldots \times [a_{g,n}, b_{g,n}] \tag{11}$$

This hyperbox will be used to bound the parameters of the neural network. The parameters of the network are trained using a genetic algorithm with the following steps:

Initialization step

1. **Set** N_C as the total number of chromosomes.
2. **Set** P_s as the selection rate, where $P_s \leq 1$.
3. **Set** P_m as the mutation rate, where $P_m \leq 1$.
4. **Set** $t = 0$ the current generation number.
5. **Set** N_t the maximum number of generations allowed.
6. **Initialize** randomly the chromosomes $C_i,\ i = 1, .., N_C$ inside the bounding box S_b.

Termination check step

1. **Set** t=t+1
2. **If** $t \geq N_t$ **goto** Local Search Step.

Genetic operations step

1. **Calculate** the fitness value of every chromosome
   (a) **For** $i = 1..N_C$ **Do**
      i. **Set** $f_i = E\left(N\left(\overrightarrow{x}, C_i\right)\right)$ using the equation 1.
   (b) **EndFor**
2. **Apply** the crossover operator. In this phase the best $(1 - P_s) \times N_c$ chromosomes are transferred intact to the next generation. The rest of the chromosomes are substituted by offsprings created through crossover. The selection of two parents $x = (x_1, x_2, ..., x_n),\ \ y = (y_1, y_2, ..., y_n)$ for crossover is performed using tournament selection. Having selected the parents, the offsprings $\tilde{x}$ and $\tilde{y}$ are formed using the following:

$$\begin{aligned} \tilde{x_i} &= r_i x_i + (1 - r_i)\, y_i \\ \tilde{y_i} &= r_i y_i + (1 - r_i)\, x_i \end{aligned} \tag{12}$$

   where r_i are random numbers in $[-0.5, 1.5]$ [37].
3. **Apply** the mutation operator. The mutation scheme is the same as in the work of Kaelo and Ali[38]:
   (a) **For** $i = 1..N_C$ **do**
      i. **For** $j = 1..n$ **do**
         A. **Let** $r \in [0, 1]$ a random number

B. **If** $r \leq P_m$ alter the element C_{ij} using the following

$$C_{ij} = \begin{cases} C_{ij} + \Delta\left(\mathrm{t}, b_{g,i} - C_{ij}\right) & t = 0 \\ C_{ij} - \Delta\left(\mathrm{t}, C_{ij} - a_{g,i}\right) & t = 1 \end{cases} \tag{13}$$

where t is a random number that takes either the values 0 or 1 and $\Delta(\mathrm{t}, y)$ is calculated as:

$$\Delta(t, y) = y\left(1 - r^{\left(1 - \frac{t}{N_t}\right)z}\right) \tag{14}$$

where $r \in [0, 1]$ is a random number and z is a user defined parameter.

ii. **EndFor**

(b) **EndFor**

4. **Goto** Termination check step.

Local Search step

1. **Set** C^* the best chromosome of the population.
2. **Apply** a local search procedure $C^* = \mathcal{L}\left(C^*\right)$. The local search procedure used was a BFGS method of Powell [39].

3 Experiments

The proposed method is evaluated on a series of classification and regression problems from the relevant literature. The classification problems used for the experiments were found in most cases in two internet databases:

1. UCI dataset repository, `https://archive.ics.uci.edu/ml/index.php`
2. Keel repository, `https://sci2s.ugr.es/keel/datasets.php`[40].

The regression datasets are in most cases available from the Statlib URL `ftp://lib.stat.cmu.edu/datasets/index.html`. The proposed method is compared against a neural network trained by a genetic algorithm and the results are reported.

3.1 Experimental datasets

The following classification datasets were used:

1. **Appendictis** a medical dataset, proposed in [41].
2. **Australian** dataset [42], the dataset is related to credit card applications.
3. **Balance** dataset [43], which is used to predict psychological states.

4. **Cleveland** dataset, a dataset used to detect heart disease used in various papers[44, 45].

5. **Bands** dataset, a printing problem used to identify cylinder bands.

6. **Dermatology** dataset [46], which is used for differential diagnosis of erythemato-squamous diseases.

7. **Hayes roth** dataset. This dataset[48] contains **5** numeric-valued attributes and 132 patterns.

8. **Heart** dataset [47], used to detect heart disease.

9. **HouseVotes** dataset [49], which is about votes in the U.S. House of Representatives Congressmen.

10. **Ionosphere** dataset. The ionosphere dataset contains data from the Johns Hopkins Ionosphere database and it has been studied in a bunch of papers [50, 51].

11. **Liverdisorder** dataset [52], used for detect liver disorders in peoples using blood analysis.

12. **Mammographic** dataset [53]. This dataset be used to identify the severity (benign or malignant) of a mammographic mass lesion from BI-RADS attributes and the patient's age. It contains 830 patterns of 5 features each.

13. **Page Blocks** dataset [54], used to detect the page layout of a document.

14. **Parkinsons** dataset. This dataset is composed of a range of biomedical voice measurements from 31 people, 23 with Parkinson's disease (PD)[55].

15. **Pima** dataset [56], used to detect the presence of diabetes.

16. **Popfailures** dataset [57], that is related to climate model simulation crashes of simulation crashes.

17. **Regions2** dataset. It is created from liver biopsy images of patients with hepatitis C [58]. From each region in the acquired images, 18 shape-based and color-based features were extracted, while it was also annotated form medical experts. The resulting dataset includes 600 samples belonging into 6 classes.

18. **Saheart** dataset [59], used to detect heart disease.

19. **Segment** dataset [60]. This database contains patterns from a database of 7 outdoor images (classes).

20. **Wdbc** dataset [61], which contains data for breast tumors.

21. **Wine** dataset, used to detect through chemical analysis determine the origin of wines and is been used in various research papers [62, 63].

22. **Eeg** datasets. As an real word example, consider an EEG dataset described in [9] is used here. The dataset consists of five sets (denoted as Z, O, N, F and S) each containing 100 single-channel EEG segments each having 23.6 sec duration. With different combinations of these sets the produced datasets are Z_F_S, ZO_NF_S, ZONF_S.

23. **Zoo** dataset [64], where the task is classify animals in seven predefined classes.

Also, the following regression datasets were used:

1. **Abalone** dataset [66]. This data set can be used to obtain a model to predict the age of abalone from physical measurements.

2. **Airfoil** dataset, which is used by the NASA for a series of aerodynamic and acoustic tests [67].

3. **Baseball** dataset, a dataset to predict the salary of baseball players.

4. **BK** dataset. This dataset comes from Smoothing Methods in Statistics [68] and is used to estimate the points scored per minute in a basketball game.

5. **BL** dataset: This dataset can be downloaded from StatLib. It contains data from an experiment on the affects of machine adjustments on the time to count bolts.

6. **Concrete** dataset. This dataset is taken from civil engineering[69].

7. **Dee** dataset, used to predict the daily average price of the electricity energy in Spain.

8. **Diabetes** dataset, a medical dataset.

9. **Housing** dataset. This dataset was taken from the StatLib library which is maintained at Carnegie Mellon University and it is described in [70].

10. **FA** dataset, which contains percentage of body fat and ten body circumference measurements. The goal is to fit body fat to the other measurements.

11. **MB** dataset. This dataset is available from Smoothing Methods in Statistics [71] and it includes 61 patterns.

12. **MORTGAGE** dataset, which contains the Economic data information of USA.

13. **PY** dataset, (Pyrimidines problem). The source of this dataset is the URL: `https://www.dcc.fc.up.pt/~ltorgo/Regression/DataSets.html` and it is a problem of 27 attributes and 74 number of patterns. The task consists of Learning Quantitative Structure Activity Relationships (QSARs) and provided by [72].

14. **Quake** dataset. The objective here is to approximate the strength of a earthquake.

15. **Treasure** dataset, which contains Economic data information of USA from 01/04/1980 to 02/04/2000 on a weekly basis.

16. **Wankara** dataset, which contains weather information.

3.2 Experimental results

The method is compared against a genetic algorithm with the same parameters that are shown in Table 1. All the experiments were conducted 30 times with different seeds for the random number generator each time and averages were taken. To perform the experiments, the software *IntervalGenetic* which is freely available from `https://github.com/itsoulos/IntervalGenetic` was utilized. The experimental results for classification datasets are shown in Table 2 and the results for the regression datasets are outlined in Table 3. For classification problems, the average classification error on the test set is shown and for regression datasets the average mean squared error on the test set is displayed. In all cases, 10 fold cross validation was used. The column DATASET stands for the name of the Dataset incorporated, the column GENETIC denotes the application of a neural network of H hidden nodes trained by a genetic algorithm, the column $F = 50$ represents the application of the proposed method with $F = 50$ as the initial value, the column $F = 100$ stands for the results of the proposed method with $F = 100$ and finally the column $F = 200$ represents the results of the proposed method with $F = 200$. In both tables, an additional row was added at the end showing the average classification or regression error for all datasets and it is denoted by the name AVERAGE.

As can be seen from the experimental results, the proposed method is significantly superior to the genetic algorithm, especially in the case of regression data. For the case of classification datasets, the proposed method reduces the average classification error by 27%, while in the case of regression datasets, the reduction in average test error is raised to 75%. Also, the change of the parameter f does not seem to have a significant effect on the performance of the algorithm and the proposed algorithm achieves high performance even for small values of this parameter.

4 Conclusions

An innovative method of training artificial neural networks was presented in this paper. The method consists of two important phases: in the first phase through

Table 1: Experimental parameters.

PARAMETER	VALUE
K	20
H	10
N_C	200
N_S	50
N_t	200
P_s	0.10
P_m	0.01

Table 2: Experiments for classification datasets

DATASET	GENETIC	$F = 50$	$F = 100$	$F = 200$
Appendicitis	18.10%	15.00%	14.00%	16.07%
Australian	32.21%	24.85%	30.20%	28.52%
Balance	8.97%	7.42%	7.42%	7.67%
Bands	35.75%	32.00%	32.25%	33.06%
Cleveland	51.60%	41.64%	44.66%	44.39%
Dermatology	30.58%	15.49%	11.00%	10.80%
Hayes Roth	56.18%	28.72%	28.84%	32.05%
Heart	28.34%	15.58%	17.07%	16.22%
HouseVotes	6.62%	3.92%	3.78%	3.26%
Ionosphere	15.14%	12.25%	9.71%	7.12%
Liverdisorder	31.11%	30.90%	29.54%	30.70%
Lymography	23.26%	18.98%	17.52%	17.67%
Mammographic	19.88%	17.01%	17.60%	15.97%
PageBlocks	8.06%	7.73%	7.01%	6.71%
Parkinsons	18.05%	14.81%	13.86%	12.53%
Pima	32.19%	23.51%	25.31%	27.49%
Popfailures	5.94%	6.13%	5.93%	5.30%
Regions2	29.39%	24.01%	23.14%	23.62%
Saheart	34.86%	28.94%	29.04%	29.93%
Segment	57.72%	47.38%	49.49%	40.61%
Wdbc	8.56%	6.23%	5.28%	5.49%
Wine	19.20%	5.51%	6.55%	6.22%
Z_F_S	10.73%	4.70%	5.61%	6.01%
ZO_NF_S	8.41%	5.39%	4.67%	5.81%
ZONF_S	2.60%	1.85%	2.07%	2.24%
ZOO	16.67%	14.83%	11.40%	8.50%
AVERAGE	**23.47%**	**17.49%**	**17.42%**	**17.08%**

Table 3: Experiments for regression datasets.

DATASET	GENETIC	$F = 50$	$F = 100$	$F = 200$
ABALONE	7.17	4.22	4.18	3.89
AIRFOIL	0.003	0.003	0.003	0.003
BASEBALL	103.60	49.47	51.07	53.57
BK	0.027	0.017	0.017	0.019
BL	5.74	0.0019	0.0016	0.0016
CONCRETE	0.0099	0.0053	0.0044	0.0042
DEE	1.013	0.187	0.205	0.203
DIABETES	19.86	0.31	0.31	0.29
HOUSING	43.26	19.28	18.50	17.75
FA	1.95	0.011	0.012	0.012
MB	3.39	0.048	0.047	0.047
MORTGAGE	2.41	0.57	0.70	0.53
PY	105.41	0.016	0.014	0.014
QUAKE	0.040	0.036	0.036	0.036
TREASURY	2.929	0.473	0.677	0.622
WANKARA	0.012	0.0003	0.0002	0.0002
AVERAGE	**18.55**	**4.67**	**4.74**	**4.81**

a hybrid genetic algorithm, an attempt is made to identify the optimal interval of initialization and training of the network parameters and at the second phase the training of the parameters in the optimal intervals of the first phase is done using a genetic algorithm. The optimization of the optimal interval in the first phase is done by using partition rules of the initial interval that are applied in order. This technique aims to reduce the parameter search space and then significantly speed up network configuration training.

The proposed method was tested on a series of classification and regression datasets from the relevant literature and the experimental results seem to be very promising compared to the genetic algorithm procedure. However, since the method consists of two computational phases, it is much slower than other training techniques of artificial neural networks and therefore, the use of parallel processing techniques is considered necessary.

Future improvements to the proposed method may include the incorporation of additional global optimization techniques instead of genetic algorithms, the usage of more advanced stopping rules and the application of the method to other types of neural networks such as Radial Basis Function networks (RBF).

Compliance with Ethical Standards

All authors declare that they have no has no conflict of interest.

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