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Adapt the parameters of RBF networks using Grammatical Evolution

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Abstract: Radial Basis Function networks are used in a variety of real-world applications such as medical data or signal processing problems.The success of these machine learning models lies in efficiently finding values for the model parameters. In this work, a new method of finding these values is formulated which is divided into two phases. In the first phase, with the use of Grammatical Evolution, an attempt is made to find value intervals for the model parameters using partition rules. In the second phase of the proposed method, an intelligent optimization algorithm such as a genetic algorithm, locates the optimal values of the parameters within the best value interval which is the output of the first phase. The proposed technique has been applied to a wide range of classification or data fitting problems and there has been a significant reduction in error exceeding 40% on most datasets.

Keywords: Neural networks; Genetic algorithms; Genetic programming; Grammatical evolution

Citation: Tsoulos, I.G.; Tzallas A; Karvounis E Adapt the parameters of RBF networks using Grammatical Evolution. *Journal Not Specified* **2022**, *1*, 0. https://doi.org/

Received:
Accepted:
Published:

1. Introduction

Many practical problems of the modern world can be thought of either as data fitting problems, as for example, problem from physics [1,2], chemistry [3,4], economics [5,6], medicine [7,8], etc. A machine learning tool, commonly used to handle these problems, is the Radial Basis Function (RBF) artificial neural network [9,10]. Usually, an RBF network is expressed using the following equation:

$$y(\overrightarrow{x}) = \sum_{i=1}^{k} w_i \phi(\| \overrightarrow{x} - \overrightarrow{c_i} \|) \tag{1}$$

where the symbols in the equation are defined as follows:

1. The vector $\overrightarrow{x}$ is the input pattern from dataset describing the problem. For the rest of this paper the notation d will be used to represent the number of elements in $\overrightarrow{x}$.
2. The parameter k denotes the number of weights used to train the RBF network and the associated vector of weights is denotes as $\overrightarrow{w}$.
3. The vectors $\overrightarrow{c_i}$, $i = 1, .., k$ stand for the so - called centers.
4. The outcome of the equations $y(\overrightarrow{x})$ stands for the estimated value of the network for the input pattern $\overrightarrow{x}$.

The function $\phi(x)$ usually is a Gaussian function given by:

$$\phi(x) = \exp\left(-\frac{(x-c)^2}{\sigma^2} \right) \tag{2}$$

The RBF networks were used in many cases, such as problems from physics [11–14], solving differential equations [15–17], robotics [18,19], face recognition [20], digital

communications [21,22], chemistry problems [23,24], economic problems [25–27], network security problems [28,29] etc. Also, recently a variety of papers have appeared proposing novel initialization techniques for the network parameters [30–32]. Also, Benoudjit et al [33] discuss the effect of kernel widths on RBF networks. Moreover, Neruda et al [34] presents a comparison of some learning methods for RBF networks. Additionally, a variety of pruning techniques [35–37] have been proposed to reduce the number of required parameters of the RBF networks. Due to the widespread usage of RBF networks but also because considerable computing time is often required for their effective training, in recent years a series of techniques have been proposed [38,39] for the exploitation of parallel computing units to adjust the parameters of neural networks.

In the same direction of research, other researchers propose to handle problems of categorization or data fitting, techniques such as Support Vector Machines (SVM) [40,41], decision trees [42,43] etc. Also, Wang et al suggested an auto - encoder reduction method, applied on a series of large datasets[44].

The training error of an RBF network is given by:

$$E(y(x,g)) = \sum_{i=1}^{m} \left(y(\overrightarrow{x}_i, \overrightarrow{g}) - t_i\right)^2 \tag{3}$$

Where the parameter m denotes the number of input patterns, the t_i values represent the expected output for the input pattern $\overrightarrow{x}_i$. The vector $\overrightarrow{g}$ represents the parameter set of the RBF network.

A common method of calculating the parameters in these neural networks uses a technique to calculate the centers of the functions $\phi(x)$ and then the weight vector $\overrightarrow{w}$ is calculated as a solution of a linear system of equations. Typically, the method used to calculate the centers is the well - known k-means method [45]. In many cases this way of estimating the parameters of the neural network leads to over-fitting of the model so that it cannot generalize satisfactorily to unknown data. Furthermore, since there is no range of values for the parameters, there is the possibility that they will take extremely large or extremely small values, with the result that any generalizability of the model is lost. This work suggests a two phase method to minimize the error of equation (3). During the first phase, an attempt is made to bound the parameter values to intervals in which the training error is likely to be significantly reduced. The identification of the most promising intervals for the parameters is performed using a technique that utilizes Grammatical Evolution[46], that collects information from the training data. The first phase attempts to create a small interval of values for the neural network parameters by applying a series of of division rules, with the assistance of the Grammatical Evolution. The determination of the value interval is done in such a way that it is faster and more efficient to train the parameters of the neural network with some optimization method during the second phase of the method. In general, if the value intervals for the parameters from the first phase are small in range, the second phase of the technique is expected to be significantly accelerated as well. During the second phase, the parameters of the RBF network can be trained within the optimal range found in the first phase using some global optimization method [47,48]. In the proposed approach, the widely used method of genetic algorithm [49–51] was used for the second phase of the process.

The rest of this paper is divided in the following sections: in section 2 the proposed method is fully described, in section 3 the datasets used in the experiments are listed as well as the experimental results and finally in section 4 some conclusions are provided.

2. Method description

This section begins with a detailed description of the Grammatical Evolution technique and the grammar that will be used to generate partition rules for the parameter set of RBFs. Subsequently, the first phase of the proposed methodology will be extensively analyzed and then the second phase, where a Genetic Algorithm will be applied to the outcome of the first phase.

2.1. Grammatical Evolution

Grammatical evolution is a genetic algorithm where the chromosomes stand for the production rules of any given BNF (Backus–Naur form) grammar[52]. Grammatical Evolution has been used successfully in a variety of cases, such as function approximation[53,54], solution of trigonometric equations [55], automatic music composition of music [56], neural network construction [57,58], creating numeric constraints[59], video games [60,61], estimation of energy demand[62], combinatorial optimization [63], cryptography [64] etc. The BNF grammar can be used to describe the syntax of programming languages and usually it is defined as the set $G = (N, T, S, P)$ where

- N is the set of the so - called non-terminal symbols. Every non - terminal symbol is associated with a series of production rules used to produce terminal symbols.
- T is the set of terminal symbols.
- S is a the start symbol of the grammar and $S \in N$.
- P is a set of production rules, used to produce terminal symbols from non - terminal symbols. These rules are in the form $A \to a$ or $A \to aB,\ A, B \in N,\ a \in T$.

The algorithm starts from the symbol S and gradually creates terminal symbols by replacing non-terminal symbols with the right hand of the selected production rule. The rule is selected through the following procedure:

- Read the next element V from the current chromosome.
- The production rule is selected as: Rule = V mod R, where R is the total number of production rules for the current non – terminal symbol.

The BNF grammar used in this work is presented in Figure 1. The symbols enclosed in <> denote the non-terminal symbols of the grammar. The numbers in parentheses in the right part of the grammar indicate production rule sequence numbers. Every RBF network with k weights is constructed by the following series of parameters:

1. A series of vectors $c_i,\ i = 1, \ldots, k$ called centers.
2. For every Gaussian unit an additional parameter σ_i is required
3. The output weight vector $\overrightarrow{w}$.

The number n is the total number of parameters of the problem. In the case of this paper it is the total number of parameters of the RBF network. For the current work, the number n can be computed using the following formula:

$$n = (d + 2) \times k \tag{4}$$

The number n in the corresponding grammar is computed as follows:

1. For every center $\overrightarrow{c_i},\ i = 1, .., k$ there are d variables. Hence, the total number of parameters required by the centers are $d \times k$.
2. Every Gaussian unit required an additional parameter $\sigma_i,\ i = 1, .., k$, which means k more parameters.
3. The weight vector $\overrightarrow{w}$ used in the output has k parameters.

As an example of production considered the chromosome $x = [9, 8, 6, 4, 15, 9, 16, 23, 8]$ and $d = 2,\ k = 2,\ n = 8$. The steps to produce the final program $p_{\text{test}} = (x7, 0, 1), (x1, 1, 0)$ are outlined in Table 1. Every partition program consists of a series of partition rules. Each partition rule contains three elements:

1. The variable for which its original interval will be partitioned, for example x_7.
2. An integer number with values 0 and 1 at the left end of the value interval. If this value is 1, then the left end of the corresponding variable's value field will be divided by two, otherwise no change will be made.
3. An integer number with values 0 and 1 at the right end of the range of values of the variable. If this value is 1, then the right end of the corresponding variable's value field will be divided by two, otherwise no change will be made.

Hence, for the example program p_{test} the two partition rules will divide the right end of the variable x_7 and the left end of the variable x_1.

Figure 1. The BNF grammar used in the current work, to produce intervals for the RBF parameters.

```
S::=<expr>   (0)
<expr> ::=  (<xlist> , <digit>,<digit>)  (0)
           |<expr>,<expr>                (1)
<xlist>::=x1    (0)
           | x2 (1)
           .........
           | xn (n)
<digit>  ::= 0 (0)
           | 1 (1)
```

Table 1. Steps to produce a valid expression from the BNF grammar.

Expression	Chromosome	Operation
	9,8,6,4,15,9,16,23,8	9 mod 2=1
<expr>,<expr>	8,6,4,15,9,16,23,8	8 mod 2=0
(<xlist>,<digit>,<digit>),<expr>	6,4,15,9,16,23,8	6 mod 8=6
(x7,<digit>,<digit>),<expr>	4,15,9,16,23,8	4 % 2=0
(x7,0,<digit>),<expr>	15,9,16,23,8	15%2=1
(x7,0,1),<expr>	9,16,23,8	9 %2 =1
(x7,0,1),(<xlist>,<digit>,<digit>)	16,23,8	16%8=0
(x7,0,1),(x1,<digit>,<digit>)	23,8	23%2=1
(x7,0,1),(x1,1,<digit>)	8	8%2=0
(x7,0,1),(x1,1,0)		

2.2. The first phase of the proposed algorithm

The purpose of the first phase is to initalize the bounds of the RBF network and discover a promising interval for the corresponding values. For this initialization, the K-Means algorithm [45] technique is used, which is also used for the traditional RBF network training technique. A description of this algorithm in a series of steps is shown in Algorithm 1.

Algorithm 1 The K-Means algorithm.

1. **Repeat**
   (a) Set $S_j = \{\}$, $j = 1..k$
   (b) **For** every pattern x_i, $i = 1, ..., m$ **do**
      i. **Set** $j^* = \min_{i=1}^{k} \{D(x_i, c_j)\}$.
      ii. **Set** $S_{j^*} = S_{j^*} \cup \{x_i\}$.
   (c) **EndFor**
   (d) **For** every center c_j, $j = 1..k$ **do**
      i. **Set** as M_j the number of points in S_j
      ii. **Compute** c_j as
$$c_j = \frac{1}{M_j} \sum_{i=1}^{M_j} x_i$$
   (e) **EndFor**
2. **Calculate** the quantities s_j as
$$\sigma_j^2 = \frac{\sum_{i=1}^{M_j} (x_i - c_j)^2}{M_j}$$
3. **Stop** the algorithm, if there is no change in centers c_j.

Having calculated the centers c_i and the corresponding variances σ_i, the algorithm continues to compute the vectors $\overrightarrow{L}$, $\overrightarrow{R}$ with dimension n, that will be used as the initial bounds of the parameters. The above vectors are calculated through the procedure of the algorithm 2.

Algorithm 2 Algorithm to locate the vectors $\overrightarrow{L}$, $\overrightarrow{R}$

1. **Set** m=0
2. **Set** $F > 1$, the scaling factor.
3. **Set** $B > 0$, the initial upper bound for the weight vector $\overrightarrow{w}$.
4. **For** $i = 1..k$ **do**
   (a) **For** $j = 1..d$ **do**
      i. **Set** L_m=$-F \times c_{ij}$, R_m=$F \times c_{ij}$
      ii. **Set** $m = m + 1$
   (b) **EndFor**
   (c) **Set** $L_m = -F \times \sigma_i$, $R_m = F \times \sigma_i$
   (d) **Set** $m = m + 1$
5. **EndFor**
6. **For** $j = 1, ..., k$ **do**
   (a) **Set** $L_m = -B$, $R_m = B$
   (b) **Set** $m = m + 1$
7. **EndFor**

The bounds for the first $(d + 1) \times k$ variables of any given RBF network are considered as a multiple of the quantity F with the values calculated by the K-Means algorithm. The positive constant B is used to initialize the intervals for the weight $\overrightarrow{w}$. Afterwards, the following genetic algorithm is executed to locate the most promising vectors $\overrightarrow{L}$, $\overrightarrow{R}$ for the RBF parameters:

1. **Set** N_c as the number of chromosomes for the Grammatical Evolution.
2. **Set** as k the number of weights of the RBF network.
3. **Set** N_g the maximum number of allowed generations.
4. **Set** as p_s the selection rate of the algorithm, with $p_s \leq 1$.
5. **Set** as p_m the mutation rate, with $p_m \leq 1$.
6. **Set** $N_s$as the number of randomly created RBF networks, used in the fitness calculation.
7. **Initialize** randomly the N_c chromosomes as sets of random numbers.
8. **Set** $f^* = [\infty, \infty]$, the fitness of the best chromosome. The fitness function f_g of any given chromosome g is considered as an interval $f_g = \left[f_{g,\textbf{low}}, f_{g,\textbf{upper}}\right]$
9. **Set** iter=0.
10. **For** $i = 1, \ldots, N_c$ **do**
    (a) **Create** the partition program p_i using the grammar of Figure 1 for the chromosome cr_i.
    (b) **Produce** the bounds $\left[\vec{L_{p_i}}, \overrightarrow{R_{p_i}}\right]$ for the partition program p_i.
    (c) **Set** $E_{\min} = \infty$, $E_{\max} = -\infty$
    (d) **For** $j = 1, \ldots, N_S$ **do**
        i. **Create** randomly a set of parameters $g_j \in \left[\vec{L_{p_i}}, \overrightarrow{R_{p_i}}\right]$
        ii. **Calculate** the error $E_{g_j} = \sum_{j=1}^{M} \left(y(x_j, g_j) - t_j\right)^2$
        iii. **If** $E_{g_j} \leq E_{\min}$ **then** $E_{\min} = E_{g_j}$
        iv. **If** $E_{g_j} \geq E_{\max}$ **then** $E_{\max} = E_{g_j}$
    (e) **EndFor**
    (f) **Set** the fitness$f_i = [E_{\min}, E_{\max}]$
11. **EndFor**
12. **Apply** the selection procedure: Initially, the chromosomes of the population are sorted according to their fitness values. In order to compare two fitness values $f_a = [a_1, a_2]$ and $f_b = [b_1, b_2]$ the L^* operator is used:

$$L^*(f_a, f_b) = \begin{cases} \text{TRUE}, & a_1 < b_1, \text{OR } (a_1 = b_1 \text{ AND } a_2 < b_2) \\ \text{FALSE}, & \text{OTHERWISE} \end{cases} \quad (5)$$

    Hence, the fitness value f_a is considered smaller than f_b if $L^*(f_a, f_b) = \text{TRUE}$. The first $(1 - p_s) \times N_c$ chromosomes with smaller fitness values are transferred intact to the next generation. The remaining chromosomes are replaced by offspring created in the crossover procedure. During the selection process for each offspring, two parents are selected from the population using the tournament selection.
13. **Apply** the crossover procedure. The crossover procedure will create new $p_s \times N_c$ chromosomes. For each new offspring two parents are selected from the population using the tournament selection. For each pair (z, w) of selected parents, two new chromosomes $\tilde{z}$ and $\tilde{w}$ are produced using the one - point crossover, shown in Figure 2.
14. **Apply** the mutation procedure. For each element of every chromosome, a random number $r \in [0, 1]$ is drawn. The corresponding element is altered randomly if $r \leq p_m$.
15. **Set** iter=iter+1
16. **If** iter$\leq N_g$ goto step 10.

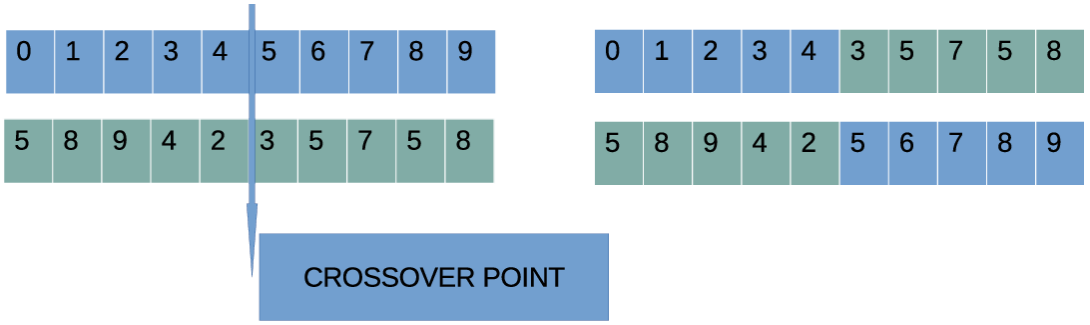

Figure 2. One point crossover, used in the Grammatical Evolution.

2.3. The second phase of the proposed algorithm

The second phase utilizes a genetic algorithm, to optimize the parameters of the RBF network within the best interval returned by the first phase of the method. The layout of each chromosome is shown in Figure 3.

Figure 3. The layout of chromosomes in the second phase of the proposed algorithm.

c_{11}	c_{12}	...	c_{1d}	σ_1	c_{21}	c_{22}	...	c_{2d}	σ_2	...	c_{k1}	c_{k2}	...	c_{kd}	σ_k	w_1	w_2	...	w_k

1. **Initialization Step**
   (a) **Set** N_c as the number of chromosomes.
   (b) **Set** N_g the maximum number of allowed generations.
   (c) **Set** k the weight number of the RBF network.
   (d) **Get** the best interval $S = [L_{\text{best}}, R_{\text{best}}]$ from the first step of subsection 2.2.
   (e) **Initialize** randomly the N_C chromosomes in in S.
   (f) **Set** as p_s the selection rate of the algorithm, with $p_s \leq 1$.
   (g) **Set** as p_m the mutation rate, with $p_m \leq 1$.
   (h) **Set** iter=0.
2. **Fitness calculation Step**
   (a) **For** $i = 1, \ldots, N_g$ **do**
      i. **Calculate** the fitness f_i of chromosome g_i as $f_i = \sum_{j=1}^{m} \left(y(x_j, g_i) - t_j\right)^2$
   (b) **EndFor**
3. **Genetic operations step**
   (a) **Selection procedure.** The chromosomes are sorted according to their fitness values. The $(1 - p_s) \times N_c$ chromosomes with the lowest fitness values are transferred intact to the next generation. The remaining chromosomes are substituted by offspings created in the crossover procedure. During the selection process for each offspring, two parents are selected from the population using the tournament selection.
   (b) **Crossover procedure**: For every pair (z, w) of selected parents two additional chromosomes $\tilde{z}$ and $\tilde{w}$ are produced using the following equations:

$$\begin{aligned} \tilde{z}_i &= a_i z_i + (1 - a_i) w_i \\ \tilde{w}_i &= a_i w_i + (1 - a_i) z_i \end{aligned} \tag{6}$$

   The value a_i is considered as a random number with the property $a_i \in [-0.5, 1.5]$ [65].
   (c) **Mutation procedure**: For each element of every chromosome, a random number $r \in [0, 1]$ is drawn. The corresponding element is altered randomly if $r \leq p_m$.

4. **Termination Check Step**
   (a) **Set** $iter = iter + 1$
   (b) **If** iter$\leq N_g$ goto step 2.

The steps of the proposed algorithm are also outlined graphically in Figure 4 using a flowchart.

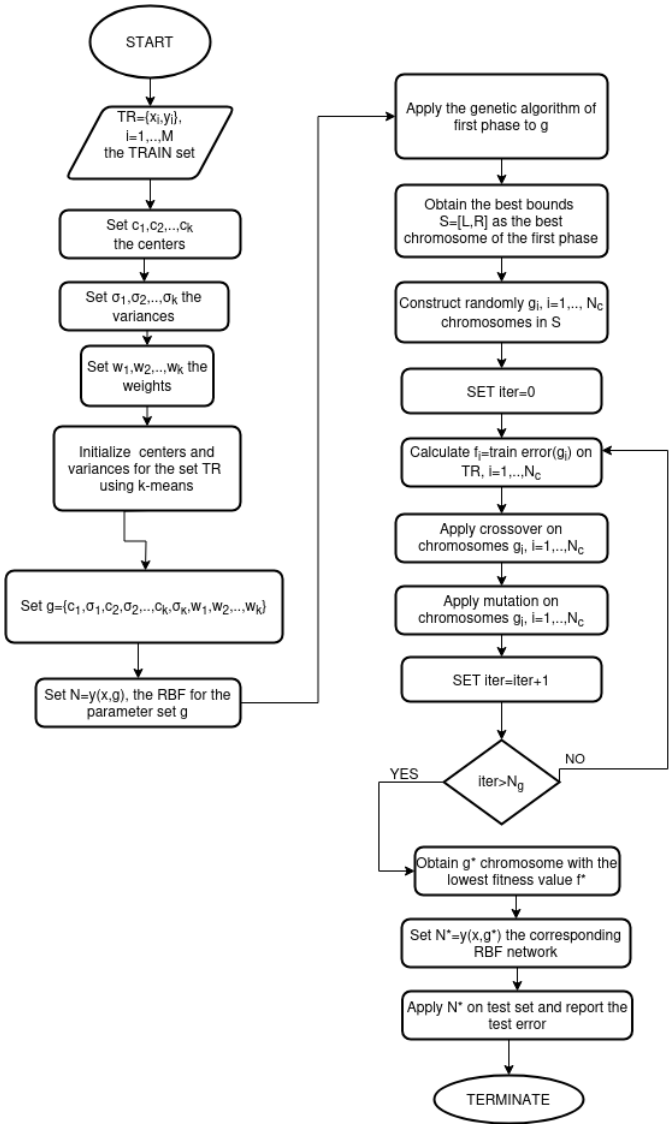

Figure 4. The flowchart of the proposed algorithm.

3. Experiments

The suggested method was tested on a series of classification and regression problems from the relevant literature and was compared against some other well -known machine learning models. The following databases were used to obtain the datasets:

1. The UCI dataset repository, https://archive.ics.uci.edu/ml/index.php(accessed on 9 September 2023)
2. The Keel repository, https://sci2s.ugr.es/keel/datasets.php(accessed on 9 September 2023)[66].
3. The Statlib URL ftp://lib.stat.cmu.edu/datasets/index.html(accessed on 9 September 2023).

3.1. Experimental datasets

The classification datasets have as follows:

1. **Appendictis** dataset, a medical dataset proposed in [67].
2. **Australian** dataset [68], an dataset related to economic data.
3. **Balance** dataset [69], which used to predict psychological states.
4. **Cleveland** dataset, which is a medical dataset related to heart diseases [70,71].
5. **Dermatology** dataset [72], a medical dataset.
6. **Hayes roth** dataset[73].
7. **Heart** dataset [74], a medical dataset related to heart diseases.
8. **HouseVotes** dataset [75], related to Congressional voting records.
9. **Ionosphere** dataset, used for classification of radar returns from the ionosphere [76,77].
10. **Liverdisorder** dataset [78], a medical dataset.
11. **Mammographic** dataset [79], used to identify breast tumors.
12. **Parkinsons** dataset, a medical dataset related to the Parkinson's Disease[80].
13. **Pima** dataset, a medical dataset[81].
14. **Popfailures** dataset [82], a dataset related to climate measurements.
15. **Spiral** dataset, an artificial dataset with 2 features and two classes. The patterns for the first class are produced according to the equation: $x_1 = 0.5t\cos(0.08t)$, $x_2 = 0.5t\cos\left(0.08t + \frac{\pi}{2}\right)$ and the second class data using**:** $x_1 = 0.5t\cos(0.08t + \pi)$, $x_2 = 0.5t\cos\left(0.08t + \frac{3\pi}{2}\right)$
16. **Regions2** dataset [83].
17. **Saheart** dataset [84], a medical dataset about heart diseases.
18. **Segment** dataset [85], an image processing dataset.
19. **Wdbc** dataset [86], used to identify breast tumors.
20. **Wine** dataset, used to classify wines [87,88].
21. **Eeg** dataset, a medical dataset about EEG measurements[89] . The datasets used are denoted as Z_F_S, ZONF_S and ZO_NF_S.
22. **Zoo** dataset [90], used to classify animals.

The following regression datasets were used in the experiments:

1. **Abalone** dataset [91].
2. **Airfoil** dataset, a dataset derived from NASA [92].
3. **Baseball** dataset, a dataset used in baseball games.
4. **BK** dataset [93], used to predict the points in a basketball game.
5. **BL** dataset, an electrical engineering dataset.
6. **Concrete** dataset, related to civil engineering[94].
7. **Dee** dataset, used to predict the energy consumption.
8. **Diabetes** dataset, a medical dataset.
9. **FA** dataset, related to fat measurements.
10. **Housing** dataset, provided in [95].
11. **MB** dataset [96].
12. **MORTGAGE** dataset, which contains economic data.
13. **NT** dataset[97].
14. **PY** dataset[98].
15. **Quake** dataset, used to predict earthquakes [99].
16. **Treasure** dataset, which contains data about the economy.
17. **Wankara** dataset, a dataset used for climate measurements.

3.2. Experimental results

The used RBF network was coded in ANSI C++ using the freely available Armadillo library [100]. The optimization methods used were also freely available from the OPTIMUS computing environment, downloaded from https://github.com/itsoulos/OPTIMUS/(accessed on 9 September 2023). To validate the results, the 10 - fold validation technique was used in

all datasets. The experiments were conducted 30 times for every dataset using a different seed for the random generator each time. In the conducted experiments, the drand48() random function of the C - programming language was employed. The average classification error is reported for the case of classification datasets and the average mean test error for the regression datasets. The machine used in the experiments was an AMD Ryzen 5950X with 128GB of RAM, running the Debian Linux operating system. All the values for the parameters of the used algorithms are shown in Table 2. The results obtained for the classification datasets are shown in Table 3 and for the regression datasets are listed in Table 4.

The following applies to the results tables:

1. The column PROP represents an artificial neural network [101,102] with 10 hidden nodes trained with the Rprop method [103].
2. The column ADAM denotes the incorporation of the Adam optimizer [104,105] to train an artificial neural network with 10 hidden nodes.
3. The column NEAT (NeuroEvolution of Augmenting Topologies) [106] denotes the application of the NEAT method for neural network training.
4. The column RBF-KMEANS represents the original two -phase training method for RBF networks, where in the first phase the centers and variances are estimated through the K-Means algorithm and in the second phase the output weights are calculated by solving a linear system of equations.
5. The column GENRBF stands for the RBF training method introduced in [107].
6. The column PROPOSED represents the results obtained by the proposed method.
7. An extra line was also added to the experimental tables under the title AVERAGE. This line represents the average classification or regression error for all datasets.

Table 2. The values used for the experimental parameters.

PARAMETER	VALUE
N_c	200
N_g	100
N_s	50
F	10.0
B	100.0
k	10
p_s	0.90
p_m	0.05

Table 3. Experimental results for the classification datasets. The first column is the name of the used dataset. Every number in cells denotes average classification error as measured on the test set.

DATASET	RPROP	ADAM	NEAT	RBF-KMEANS	GENRBF	PROPOSED
Appendicitis	16.30%	16.50%	17.20%	12.23%	16.83%	15.77%
Australian	36.12%	35.65%	31.98%	34.89%	41.79%	22.40%
Balance	8.81%	7.87%	23.14$	33.42%	38.02%	15.62%
Cleveland	61.41%	67.55%	53.44%	67.10%	67.47%	50.37%
Dermatology	15.12%	26.14%	32.43%	62.34%	61.46%	35.73%
Hayes Roth	37.46%	59.70%	50.15%	64.36%	63.46%	35.33%
Heart	30.51%	38.53%	39.27%	31.20%	28.44%	15.91%
HouseVotes	6.04%	7.48%	10.89%	6.13%	11.99%	3.33%
Ionosphere	13.65%	16.64%	19.67%	16.22%	19.83%	9.30%
Liverdisorder	40.26%	41.53%	30.67%	30.84%	36.97%	28.44%
Mammographic	18.46%	46.25%	22.85%	21.38%	30.41%	17.72%
Parkinsons	22.28%	24.06%	18.56%	17.41%	33.81%	14.53%
Pima	34.27%	34.85%	34.51%	25.78%	27.83%	23.33%
Popfailures	4.81%	5.18%	7.05%	7.04%	7.08%	4.68%
Regions2	27.53%	29.85%	33.23%	38.29%	39.98%	25.18%
Saheart	34.90%	34.04%	34.51%	32.19%	33.90%	29.46%
Segment	52.14%	49.75%	66.72%	59.68%	54.25%	49.22%
Spiral	46.59%	48.90%	50.22%	44.87%	50.02%	23.58%
Wdbc	21.57%	35.35%	12.88%	7.27%	8.82%	5.20%
Wine	30.73%	29.40%	25.43%	31.41%	31.47%	5.63%
Z_F_S	29.28%	47.81%	38.41%	13.16%	23.37%	3.90%
ZO_NF_S	6.43%	47.43%	43.75%	9.02%	22.18%	3.99%
ZONF_S	27.27%	11.99%	5.44%	4.03%	17.41%	1.67%
ZOO	15.47%	14.13%	20.27%	21.93%	33.50%	9.33%
AVERAGE	**26.56%**	**32.36%**	**30.11%**	**28.84%**	**33.35%**	**18.73%**

Table 4. Experimental results for the regression datasets. The first column is the name of the used regression dataset. Also, the numbers in cells denote average regression error on the test set.

DATASET	RPROP	ADAM	NEAT	RBF-KMEANS	GENRBF	PROPOSED
ABALONE	4.55	4.30	9.88	7.37	9.98	5.16
AIRFOIL	0.002	0.005	0.067	0.27	0.121	0.004
BASEBALL	92.05	77.90	100.39	93.02	98.91	81.26
BK	1.60	0.03	0.15	0.02	0.023	0.025
BL	4.38	0.28	0.05	0.013	0.005	0.0004
CONCRETE	0.009	0.078	0.081	0.011	0.015	0.006
DEE	0.608	0.630	1.512	0.17	0.25	0.16
DIABETES	1.11	3.03	4.25	0.49	2.92	1.74
HOUSING	74.38	80.20	56.49	57.68	95.69	21.11
FA	0.14	0.11	0.19	0.015	0.15	0.033
MB	0.55	0.06	0.061	2.16	0.41	0.19
MORTGAGE	9.19	9.24	14.11	1.45	1.92	0.014
NT	0.04	0.12	0.33	8.14	0.02	0.007
PY	0.039	0.09	0.075	0.012	0.029	0.019
QUAKE	0.041	0.06	0.298	0.07	0.79	0.034
TREASURY	10.88	11.16	15.52	2.02	1.89	0.098
WANKARA	0.0003	0.02	0.005	0.001	0.002	0.003
AVERAGE	**11.71**	**11.02**	**11.97**	**10.17**	**12.54**	**6.46**

On average, the proposed technique appears to be 30-40% more accurate than the immediate best. In many cases, this percentage exceeds 70%. Moreover, in the vast majority

of problems, the proposed technique significantly outperforms the next best available method in terms of test error. However, the proposed technique consists of two stages and in each of them a genetic algorithm should be executed. This means that it is significantly slower in computing time compared to the rest of the techniques and, of course, it needs more computing resources. Of course, since we are talking about Genetic Algorithms, the training time required could be significantly reduced by using parallel techniques that take advantage of modern parallel computing structures such as the MPI interface [108] or the OpenMP library [109]. The superiority of the proposed technique is also reinforced by the statistical tests carried out on the experimental results and presented in figure 5.

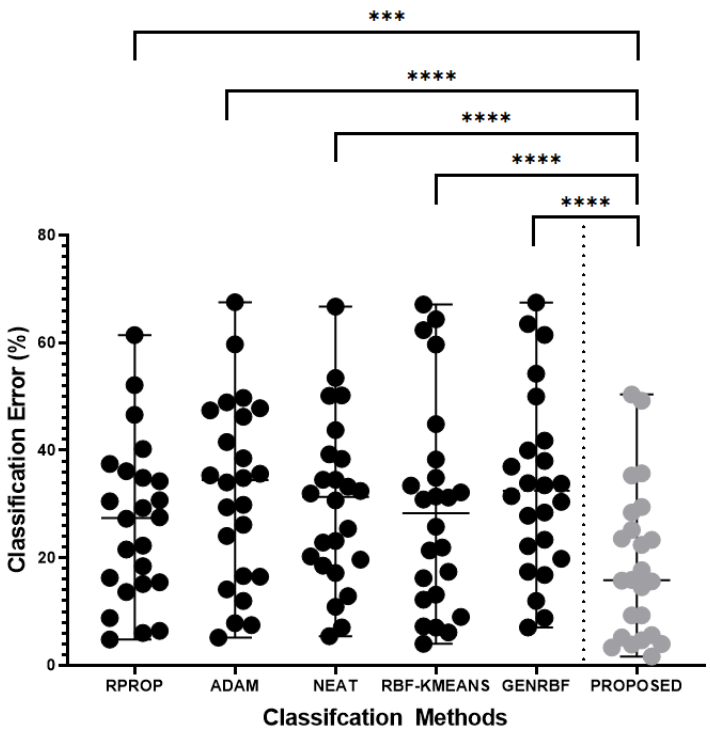

Figure 5. Scatter plot representation and the two-sample paired (Wilcoxon) signed-rank test results of the comparison for each of the five (5) classification methods (RPROP, ADAM, NEAT, RBF-KMEANS, and GENRBF) with the PROPOSED method regarding the classification error in twenty-four (24) different public available classification datasets. The stars only intend to flag significance levels for the two most used groups. A p-value of less than 0.001 is flagged with three stars (**). A p-value of less than 0.0001 is flagged with four stars (***).

In addition, an additional set of experiments was performed on the classification data in which the critical parameter F took the values 3, 5 and 10. The aim of this set of experiments was to establish the sensitivity of the proposed technique to changes in its parameters. The experimental results are presented in the table 5 and a statistical test on the results is presented in figure 6. The results and the statistics test indicate that there is no significant difference in the efficiency of the method for different values of the critical parameter F.

Table 5. Experimental results with the proposed method and using different values for the parameter F on the classification datasets.

DATASET	$F = 3$	$F = 5$	$F = 10$
Appendicitis	15.57%	16.60%	15.77%
Australian	24.29%	23.94%	22.40%
Balance	17.22%	15.39%	15.62%
Cleveland	52.09%	51.65%	50.37%
Dermatology	37.23%	36.81%	35.73%
Hayes Roth	35.72%	32.31%	35.33%
Heart	16.32%	15.54%	15.91%
HouseVotes	4.35%	3.90%	3.33%
Ionosphere	12.50%	11.44%	9.30%
Liverdisorder	28.08%	28.19%	28.44%
Mammographic	17.49%	17.15%	17.72%
Parkinsons	16.25%	15.17%	14.53%
Pima	23.29%	23.97%	23.33%
Popfailures	5.31%	5.86%	4.68%
Regions2	25.97%	26.29%	25.18%
Saheart	28.52%	28.59%	29.46%
Segment	44.95%	48.77%	49.22%
Spiral	15.49%	18.19%	23.58%
Wdbc	5.43%	5.01%	5.20%
Wine	7.59%	8.39%	5.63%
Z_F_S	4.37%	4.26%	3.90%
ZO_NF_S	3.79%	4.21%	3.99%
ZONF_S	2.34%	2.26%	1.67%
ZOO	11.90%	10.50%	9.33%
AVERAGE	**19.03%**	**18.93%**	**18.73%**

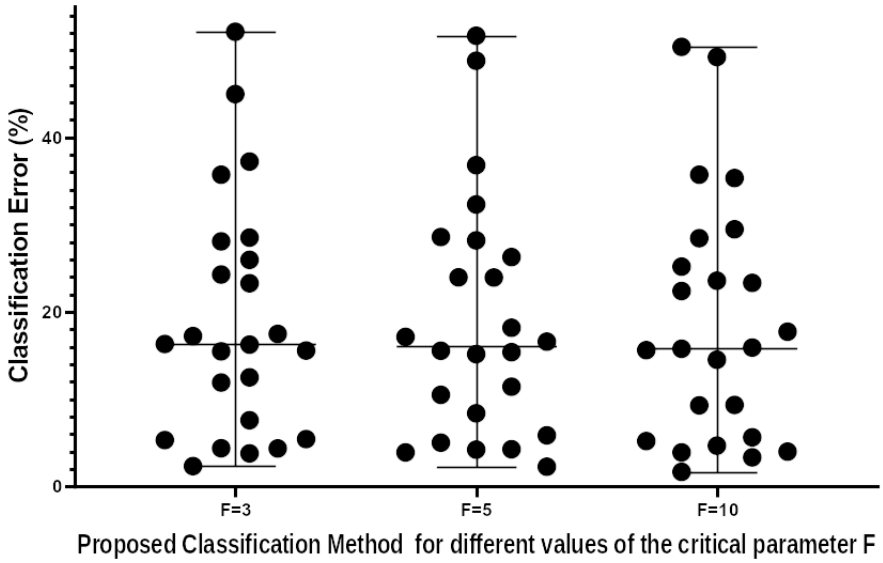

Figure 6. A Friedman test was conducted to determine whether different values of the critical parameter F had a difference or not in the classification error of the proposed method in twenty-four (24) other publicly available classification datasets. The analysis results for three different values of the critical parameter F (F=3, F=5, F=10) indicated no significant difference.

4. Conclusions

In the present work, an innovative two-stage technique was proposed for efficient training of RBF artificial neural networks. In the first stage of the application, using Grammatical Evolution, the interval of values of the neural network parameters is partitioned, so as to find a promising range that may contain low values of the training error. In the second stage, the neural network parameters are trained within the best range of values found in the first stage. The training of the parameters of the second phase is carried out using a Genetic Algorithm. The proposed method was applied on a wide series of well -known datasets from the relevant literature and was tested against a series of machine learning models. The new training technique was compared with the traditional method of training RBF networks but also with other training techniques of machine learning models and from the experimental results its superiority is evident in percentages that exceed 40%. However, since the proposed technique consists of two genetic algorithms executed sequentially, the execution time required is longer compared to other techniques especially for datasets with many patterns. An immediate solution to reduce the execution time of the method would be the use of parallel computing techniques, since genetic algorithms can by nature be directly parallelized.

Future improvements to the proposed method may include:

1. Application of the proposed method to other types of artificial neural networks.
2. Use of intelligent learning techniques in place of the K-Means technique to initialize the neural network parameters.
3. Using techniques to dynamically determine the number of necessary parameters of the neural network. For the time being, the number of parameters is considered constant, but this has the consequence of observing over-training phenomena in various data sets.
4. Implementation of crossover and mutation techniques that focus more on the existing interval construction technique for the model parameters.
5. Use of efficient termination techniques for Genetic Algorithms, for the most efficient termination of techniques without wasting computing time on unnecessary iterations.
6. Incorporation of parallel programming techniques to speed up the method.

Author Contributions: I.G.T., A.T. and E.K. conceived the idea and methodology and supervised the technical part regarding the software. I.G.T. conducted the experiments, employing several datasets, and provided the comparative experiments. A.T. performed the statistical analysis. E.K. and all other authors prepared the manuscript. E.K. and I.G.T. organized the research team and A.T. supervised the project. All authors have read and agreed to the published version of the manuscript.

Funding: This research received no external funding.

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Institutional Review Board Statement: Not applicable.

Acknowledgments: The experiments of this research work were performed at the high performance computing system established at Knowledge and Intelligent Computing Laboratory, Department of Informatics and Telecommunications, University of Ioannina, acquired with the project "Educational Laboratory equipment of TEI of Epirus" with MIS 5007094 funded by the Operational Programme "Epirus" 2014–2020, by ERDF and national funds.

Conflicts of Interest: The authors declare no conflict of interest.

Not applicable.

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