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Local Crossover: A new genetic operator for Grammatical Evolution

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Abstract: In this work, a new genetic crossover operator is proposed, which can be applied to problems solved by the Grammatical Evolution technique. This new operator intensively applies the one - point crossover procedure to randomly selected chromosomes with the aim of drastically reducing their fitness value. To apply the one point crossover method, a set of randomly selected chromosomes is selected from the current population. This new operator was applied to two techniques from the recent literature that exploit Grammatical Evolution: artificial neural network construction and rule construction. In both case studies, an extensive set of classification problems and data fitting problems were used to measure the effectiveness of the proposed genetic operator. The proposed operator significantly improved the performance of the above two machine learning techniques and in many cases there was a drastic reduction in the error in the test set.

Keywords: Genetic algorithms; Genetic Programming ; Grammatical Evolution; Genetic operators

1. Introduction

Genetic algorithms are stochastic optimization algorithms originated in the work of Holland [1]. They belong to a wide area of optimization algorithms called evolutionary techniques [2]. Genetic algorithms initiate by formulating candidate solutions of the objective problem. These solutions are evolved through a series of processes that mimic natural evolution, such as selection, crossover and mutation [3–5]. The genetic algorithms have been applied with success in a variety of problems, such as networking problems [6], problems arise in robotics [7,8], energy problems [9,10], medicine problems [11,12], agriculture problems [13] etc.

Grammatical Evolution [15] is an integer based genetic algorithm, where each chromosome represents a series of production rules derived from a Backus–Naur form (BNF) grammar [16]. Grammatical Evolution can be utilized to produce programs in any programming language. This method has been applied in a variety of cases derived from real - world problems, such as data fitting [17,18], credit classification [19], detection of network attacks [20], solving differential equations [21], monitoring the quality of drinking water [22], construction of optimization methods [23], application in trigonometric problems [24], composition of music [25], constructing neural networks [26,27], production of numeric constants with a variable number of digits [28], video games [29,30], estimation and management of energy consumption [31], combinatorial optimization [32], security and cryptography [33], production of decision trees [34], circuit design [35], discovering taxonomies in Wikipedia [36], trading algorithms [37], bioinformatics [38] etc.

Grammatical Evolution has been extended by many researches in recent bibliography. Among these extensions there are works, such as the Weighted Hierarchical Grammatical Evolution [39], which proposed a novel technique to map genotypes to phenotypes. Also, the method of Structured Grammatical Evolution [40,41], where one - to - one mapping

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between the chromosomes and the non-terminal symbols of the grammar, was suggested as an alternative program creation method. Also, O'Neill et al. suggested the usage of shape grammars in the Grammatical Evolution for evolutionary design [42]. Also the πGrammatical Evolution method [43] was suggested as an extension of the Grammatical Evolution, where a position - independent mapping was proposed. Another interesting work was the incorporation of the Particle Swarm Optimization(PSO) [44] to create programs in Grammatical Evolution, denoted as Grammatical Swarm [45,46]. Moreover, the method of Probabilistic Grammatical Evolution [47] has been introduced recently, where a new stochastic mapping mechanism for the Grammatical Evolution method is proposed. Recently, the optimization method of Fireworks algorithm [48] was applied as a learning algorithm for the Grammatical Evolution procedure [49]. Contreras et al. suggested the combination of Grammatical Evolution and modal interval analysis to sole problems with uncertainty [50]. Grammatical evolution has also been extended using programming techniques [51,52] or Christiansen grammars [53].

Additionally, many researchers have developed and published open source software for Grammatical Evolution, such as the graphical user interface (GUI) application of Grammatical Evolution in Java (GEVA)[54], a Java implementation called jGE [55], an R implementation of Grammatical Evolution called gramEvol (Grammatical Evolution for R) [56], the GRAPE software that implemented Grammatical Evolution in Python [57], the GeLab [58] software that suggested a Matlab toolbox for Grammatical Evolution, a software which produced classification programs with Grammatical Evolution called GenClass [59], the QFc software [60] the produced artificial features from the original ones with the assistance of Grammatical Evolution etc.

In this work, a new genetic operator for Grammatical Evolution is introduced, which is based on the one crossover technique. The new genetic operator is stochastically applied to the genetic population, randomly selecting a set of chromosomes on which to apply it. For each randomly selected chromosome, a group of chromosomes is stochastically formed from the current genetic population. Afterwards, a one - point crossover operation is performed between the selected chromosome and each of the generated group to search for a lower value of the fitness function. The new genetic operator was applied in two distinct cases of Grammatical Evolution methods: in the rule construction technique introduced recently [61] and in the neural network construction technique [62]. These machine learning tools were applied on a wide series of classification and regression datasets from the relevant literature and the experimental results indicated a reduction in classification or regression error from the application of the new genetic operator.

The main components of the proposed technique are the following:

1. The method can be applied as a genetic operator to all problems solved by the Grammatical Evolution technique and the only information it exploits is the fitness function of the problem.
2. The method has no dependence on the grammar of the objective problem.
3. By using an application rate the user can require fewer or more applications of the new operator.
4. Although this operator requires significant computing time for its execution, its application between chromosomes can be done using parallel techniques, since there is no dependency between its successive applications.
5. Simple linear operations are required for its implementation, such as crossing a point between chromosomes.
6. The method could theoretically be applied to other forms of genetic algorithms beyond Grammatical Evolution.

The rest of this article is divided as follows: in section 2 the basic principles of Grammatical Evolution are discussed as well as the proposed modification. In section 3 the used datasets are described followed by the experimental results and finally in section 4 some conclusions and guidelines for future research are discussed.

2. Materials and Methods

2.1. The Grammatical Evolution

The Grammatical Evolution considers chromosomes as set of production rules in the provided BNF grammar. BNF grammar is defined as a tuple $G = (N, T, S, P)$, where

- N defines the set of non-terminal symbols.
- T represents the set of terminal symbols.
- S corresponds to the that start symbol of the grammar.
- P is the set of production rules. These rules are in the form $A \to a$ or $A \to aB$, $A, B \in N$, $a \in T$. For Grammatical Evolution a sequence number is assigned to every production rule.

The grammar used for the rule machine learning method is outlined in Figure 1 and the grammar used for the neural network construction technique is displayed in figure 2.

Figure 1. The BNF grammar for the rule construction method.

```
<S>::= <ifexpr> value=<expr> else value=<expr>  (0)
<ifexpr>::= if(<boolexpr>) value=<expr> (0)
            |<ifexpr> else if(<boolexpr>) value=<expr> (1)
<boolexpr>::=<expr> <relop> <expr> (0)
            |<boolexpr> <boolop> <boolexpr> (1)
<relop>::= > (0)
           |>= (1)
           |<  (2)
           |<= (3)
           |=  (4)
           |!= (5)
<boolop>::=  & (0)
           | | (1)
<expr> ::=  (<expr> <op> <expr>)  (0)
           | <func> ( <expr> )    (1)
           |<terminal>            (2)
<op> ::=     +      (0)
           | -      (1)
           | *      (2)
           | /      (3)
<func> ::=   sin  (0)
           | cos  (1)
           |exp   (2)
           |log   (3)
<terminal>::=<xlist>                (0)
           |<digitlist>.<digitlist> (1)
<xlist>::=x1    (0)
           | x2 (1)
           .........
           | xD (D)
<digitlist>::=<digit>                  (0)
           | <digit><digit>            (1)
           | <digit><digit><digit>     (2)
<digit>  ::= 0 (0)| 1 (1)
           | 2 (2)| 3 (3)
           | 4 (4)| 5 (5)
           | 6 (6)| 7 (7)
           | 8 (8)| 9 (9)
```

Figure 2. The grammar for the neural network construction method.

```
S:=<sigexpr>                              (0)
<sigexpr>::=<Node>                        (0)
           | <Node> + <sigexpr>           (1)
<Node>::=<number>*sig(<sum>+<number>)     (0)
<sum>::= <number>*<xxlist>                (0)
           |    <sum>+<sum>               (1)
<xxlist>::= x1          (0)
             |    x2    (1)
             ..............
             |    xD    (D-1)
<number>::= (<digitlist>.<digitlist>)          (0)
             |    (-<digitlist>.<digitlist>)   (1)
<digitlist>::= <digit>              (0)
             | <digit><digitlist>   (1)
<digit>::= 0       (0)
             |  1   (1)
             ...........
             |  9   (9)
```

Non-terminal symbols are enclosed in <> in the used grammar. The numbers at the end of the production rules represent the sequence number of each rule. The parameter d represents the dimension of the used dataset (number of features). Grammatical Evolution produces valid expressions by starting from the starting symbol S and by following the production rules. The method selects the following production rules according to the scheme:

- **Get** the next element V from the current chromosome.
- **Select** the next rule as:

$$\text{Rule} = V \bmod \text{NR} \tag{1}$$

  where the value NR represents the total number of production rules for the under processing non – terminal symbol.

For a dataset with three features (x_1, x_2, x_3) an example of rule construction method could be the following:

$$\text{if}(x_1 > 2 + \sin(x_3))\text{value} = 10 + \exp(x_2) \text{ else value} = x_1$$

The terminal symbol value is used to denote the final outcome of the rule method. For the same dataset an example of neural network constructed by the Grammatical Evolution could be the following:

$$\text{NNC}(x) = 2.45\text{sig}(1.9x_1 + 3.11x_3 + 2.5) + 5.9\text{sig}(10.8x_2 + 6.25)$$

This grammar of Figure 2 is able to construct artificial neural networks in the form:

$$N(\vec{x}, \vec{w}) = \sum_{i=1}^{H} w_{(n+2)i-(n+1)} \sigma \left(\sum_{j=1}^{n} x_j w_{(n+2)i-(n+1)+j} + w_{(n+2)i} \right) \tag{2}$$

where the parameter H defines the number of processing units. These networks have one processing level, but the grammar could be easily extended to produce neural networks of additional levels. The function $\text{sig}(x)$ used in the previous example denotes the sigmoid function given by:

$$\text{sig}(x) = \frac{1}{1 + \exp(-x)} \tag{3}$$

used in the majority of cases of neural networks. Of course, the Grammatical Evolution procedure can construct neural networks with different activation functions or neural networks that use a mix of activation functions.

2.2. The genetic algorithm

The two machine learning techniques, in which the new genetic operator was applied, follow a series of similar execution steps, which are presented in detail below:

1. **Initialization step**.
   (a) **Set** $k = 0$ the generation counter.
   (b) **Set** N_g the maximum number of allowed generations.
   (c) **Set** as N_c the total number of chromosomes in the genetic population.
   (d) **Set** as p_s the selection rate, where $p_s \leq 1$.
   (e) **Set** as p_m the mutation rate, where $p_m \leq 1$
   (f) **Set** as p_{cr} the rate for the application of the new crossover operator, where $p_{cr} \leq 1$
   (g) **Set** as N_{cr} the number of chromosomes the will be selected for each chromosome where the new crossover operator will be applied.
2. **Fitness Calculation step**.
   (a) **For** $i = 1, \ldots, N_c$ **do**
      i. **Set** as f_i the fitness of chromosome i. For the case of rule creation model the grammar of Figure 1 is applied while for the case of neural network construction the grammar of Figure 2 is utilized.
   (b) **EndFor**
3. **Genetic operations step**.
   (a) **Apply** the selection procedure: In the first phase, the chromosomes are sorted according to their fitness. The $(1 - p_s) \times N_c$ best of these are transmitted unchanged to the next generation, while the rest will be replaced by chromosomes produced through crossover and mutation.
   (b) **Apply** the crossover procedure: During this procedure $p_s \times N_c$ offsprings are produced from the current population. For each pair $(\tilde{z}, \tilde{w})$ two distinct chromosomes (z, w) are selected from the population. These chromosomes are selected using tournament selection. The new offsprings are formulated using the one - point crossover procedure, graphically outlined in Figure 3.
   (c) **Perform** the mutation procedure. A random number $r \in [0, 1]$ is drawn for each element of every chromosome. The corresponding element is altered randomly if $r \leq p_m$.
   (d) **Apply** the new crossover operator: For every chromosome g_i, $i = 1, \ldots, N_c$ a random number $r \in [0, 1]$ is drawn. If $r \leq p_{cr}$ then apply the procedure described in subsection 2.3 on g_i.
4. **Termination check step**.
   (a) **Set** $k = k + 1$
   (b) **If** $k \leq N_g$ goto Fitness Calculation Step, **else** terminate.

The previous algorithm is also graphically illustrated in the flowchart of Figure 4.

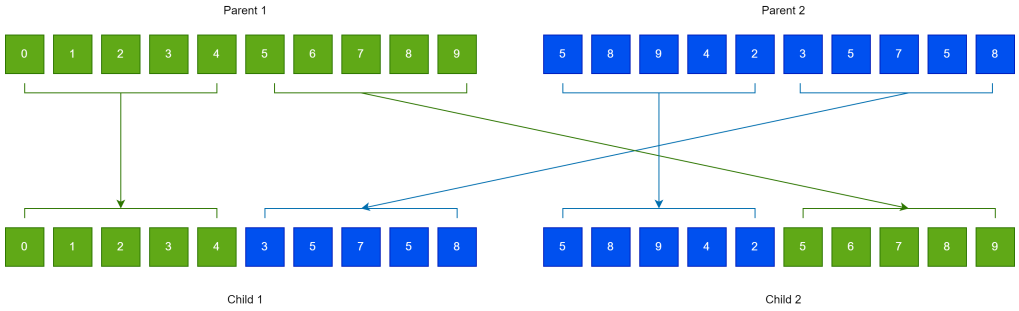

Figure 3. An example of the method of one - point crossover. This method is used as the crossover procedure in the Grammatical Evolution procedure.

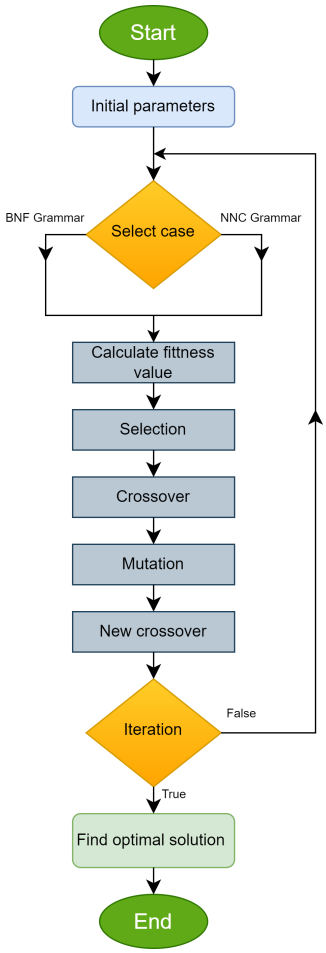

Figure 4. The main steps of the used genetic algorithm.

2.3. The new crossover operator

The new crossover operator performs the one - point crossover method on a selected chromosome using a set of randomly selected chromosomes from the current population. The steps of this procedure are listed below:

1. **Set** as g the chromosome where the operator will be applied and as f_g the corresponding fitness value.
2. **Create** the set $C = \{x_1, x_2, \ldots, x_{N_{cr}}\}$ of N_{cr} randomly selected chromosomes.
3. **For** $i = 1, \ldots, N_{cr}$ **do**
   (a) **Perform** one - point crossover between g and x_i. This procedure produces the offsprings g_1 and g_2 with associated fitness values f_{g_1} and f_{g_2}.

(b) **If** $f_{g_1} \leq f_g$ **then**

i. $g = g_1$

(c) **else if** $f_{g_2} \leq f_g$ **then**

i. $g = g_2$

(d) **Endif**

4. **EndFor**

3. Results

The suggested genetic operator was tested on a series of classification and regression datasets obtained from the recent bibliography and relevant websites. These datasets can be downloaded freely from the following series of websites:

1. The UCI dataset repository, https://archive.ics.uci.edu/ml/index.php(accessed on 12 August 2024)[63]
2. The Keel repository, https://sci2s.ugr.es/keel/datasets.php(accessed on 12 August 2024)[64].
3. The Statlib URL http://lib.stat.cmu.edu/datasets/(accessed on 12 August 2024).

3.1. Classification datasets

The following classification datasets were used in the conducted experiments:

1. **Appendictis** a medical dataset, proposed in [65].
2. **Australian** dataset [66], suggested for credit card transactions.
3. **Balance** dataset [67], used in a series of psychological experiments.
4. **Circular** dataset, that is an artificial dataset.
5. **Cleveland** dataset, a medical dataset found in a series of papers [68,69].
6. **Dermatology** dataset [70], a dataset related to dermatological deceases.
7. **Ecoli** dataset, a dataset related to protein problems[71].
8. **Fert** dataset. Fertility dataset related to relation of sperm concentration
9. **Haberman** dataset, which is related to breast cancer.
10. **Hayes roth** dataset, a datatet provided by [72].
11. **Heart** dataset [73], a medical dataset for the prediction of heart diseases.
12. **HeartAttack** dataset, a medical dataset related to heart diseases.
13. **HouseVotes** dataset [74], related to votes in the U.S. House of Representatives.
14. **Glass** dataset, which contains glass component analysis for glass pieces that belong to 6 classes.
15. **Liverdisorder** dataset [75], a medical dataset for the detection of liver disorders.
16. **Mammographic** dataset [77], a medical dataset about breast cancer.
17. **Parkinsons** dataset, a medical dataset related to the detection of Parkinson's disease (PD)[76].
18. **Pima** dataset [78], a medical dataset about the presence of diabetes.
19. **Popfailures** dataset [79], that to do with climate related measurements.
20. **Regions2** dataset, a medical dataset related to the detection of hepatitis C [80].
21. **Saheart** dataset [81], a medical dataset related to the detection of heart diseases.
22. **Segment** dataset [82], which is a dataset related to image processing.
23. **Spiral** dataset, which is an artificial dataset.
24. **Student** dataset [83], a dataset related to measurements in schools.
25. **Wdbc** dataset [84], a medical dataset related to cancer.
26. **Wine** dataset, which contains information about the quality of wines. [85,86].
27. **Eeg** datasets, a medical dataset contains EEG measurements [87]. From this dataset the following cased were selected in the conducted experiments: Z_F_S, Z_O_N_F_S, ZO_NF_S and ZONF_S.
28. **Zoo** dataset [88], used for animal classification in seven predefined categories.

3.2. Regression datasets

The following regression datasets were used in the conducted experiments:

1. **Abalone** dataset [89], a dataset used to predict the age of abalones.
2. **Airfoil** dataset, a dataset used in NASA [90].
3. **BK** dataset [91], related to the prediction of points in a basketball game.
4. **BL** dataset, it contains measurements from electricity experiments.
5. **Baseball** dataset, used to estimate the income of baseball players.
6. **Concrete** dataset [92], that is a civil engineering dataset.
7. **Dee** dataset, that contains measurements from the price of electricity.
8. **FY,** a dataset that contains measurements for the longevity of fruit flies.
9. **HO** dataset, provided from the the STALIB repository.
10. **Housing** dataset, presented in [93].
11. **Laser** dataset, that contains measurements from laser experiments
12. **LW** dataset, that contains measurements from low weight babies.
13. **MORTGAGE** dataset, that contains economic data from USA.
14. **MUNDIAL,** downloaded from the STALIB repository.
15. **PL** dataset, downloaded from the STALIB repository.
16. **QUAKE** dataset, that contains measurements from earthquakes.
17. **REALESTATE,** downloaded from the STALIB repository.
18. **SN** dataset, that contains measurements from an experiment related to trellising and pruning.
19. **Treasury** dataset, that contains economic data from USA.
20. **TZ** dataset, downloaded from the STALIB repository.
21. **VE** dataset, downloaded from the STALIB repository.

3.3. Experimental results

The code used in the experiments was coded in ANSI C++ using the Optimus optimization environment, available from https://github.com/itsoulos/OPTIMUS/(accessed on 12 August 2024). All the experiments were executed 30 times, using different initialization for the random generator each time and averages were recorded. For the case of classification problems, the average classification error as measured on the test set was recorded and, for the case of regression datasets, the average regression error as measured on the test set was recorded. The validation of the experiments was performed using ten - fold cross validation. The values of the experimental parameters are shown in Table 1.

Table 1. The values used in the experimental parameters.

PARAMETER	MEANING	VALUE
N_c	Number of chromosomes	500
N_g	Maximum number of generations	200
p_s	Crossover rate	0.10
p_m	Mutation rate	0.05
p_{cr}	New crossover rate	0.05
N_{cr}	New crossover items	100
H	Number of weights for neural network	10

The experimental results for the classification datasets are shown in Table 2 and the experimental results for the regression datasets are displayed in Table 3. The following applies to the tables of experimental results:

1. The column BFGS denotes the application of the BFGS optimization method [94] to train an artificial neural network with H hidden nodes.
2. The column GEN denotes the application of a genetic algorithm [95] to train an artificial neural network with H hidden nodes. The parameters of this genetic algorithm are the listed also in Table 1.

3. The column RULE refers to the simple rule construction method [14], without the application of the new crossover operator.
4. The column NNC refers to the method of neural network construction [62], without the application of the new crossover operator.
5. The column RULE_CROSS represents the application of the new crossover operator the rule construction machine learning model.
6. The column NNC_CROSS stands for the application of the new crossover operator to the neural network construction model.
7. The row AVERAGE denotes the average classification or regression row for all datasets.

Table 2. Experimental results for the classification datasets. The numbers in cells denote average classification error as calculated on the corresponding test set.

DATASET	BFGS	GEN	RULE	NNC	RULE_CROSS	NNC_CROSS
APPENDICITIS	18.00%	24.40%	14.70%	13.70%	14.80%	14.40%
AUSTRALIAN	38.13%	36.64%	14.27%	14.51%	14.46%	14.71%
BALANCE	8.64%	8.36%	28.79%	22.11%	17.47%	14.32%
CIRCULAR	6.08%	5.13%	13.25%	13.64%	9.12%	7.49%
CLEVELAND	77.55%	57.21%	48.24%	50.10%	47.52%	49.21%
DERMATOLOGY	52.92%	16.60%	43.77%	25.06%	38.00%	12.92%
ECOLI	69.52%	54.67%	55.18%	47.82%	53.48%	49.15%
FERT	23.20%	28.50%	17.40%	19.00%	17.50%	19.20%
HABERMAN	33.10%	27.80%	27.03%	28.03%	26.53%	28.37%
HAYES-ROTH	56.54%	35.85%	39.39%	35.93%	38.08%	24.08%
HEART	39.44%	26.41%	20.30%	15.78%	19.41%	15.33%
HEARTATTACK	46.67%	29.03%	23.63%	19.33%	23.70%	18.73%
HOUSEVOTES	7.13%	7.00%	3.48%	3.65%	4.51%	3.22%
GLASS	69.95%	55.09%	58.10%	57.10%	54.81%	53.82%
IONOSPHERE	13.37%	18.03%	15.06%	11.12%	14.14%	9.25%
LIVERDISORDER	42.59%	37.09%	37.09%	33.71%	35.68%	31.24%
MAMMOGRAPHIC	29.54%	16.33%	19.00%	17.78%	18.10%	17.12%
PARKINSONS	27.58%	16.58%	13.47%	12.21%	13.37%	11.47%
PIMA	35.59%	34.21%	27.85%	27.99%	27.30%	25.95%
POPFAILURES	5.24%	4.17%	5.44%	6.74%	5.02%	6.41%
REGIONS2	36.28%	33.53%	29.13%	25.52%	29.26%	24.46%
SAHEART	37.48%	34.85%	30.20%	30.52%	31.00%	28.64%
SEGMENT	68.97%	46.30%	71.51%	54.99%	61.99%	35.82%
SPIRAL	47.99%	47.67%	50.06%	48.39%	49.08%	48.04%
STUDENT	4.90%	6.75%	11.08%	5.78%	7.23%	5.06%
TRANSFUSION	25.59%	24.01%	25.19%	25.34%	24.46%	24.44%
WDBC	29.91%	7.87%	7.66%	6.95%	6.43%	6.48%
WINE	59.71%	22.88%	15.35%	14.35%	12.47%	9.88%
Z_F_S	39.37%	24.60%	16.40%	14.17%	8.77%	10.23%
Z_O_N_F_S	79.04%	64.26%	53.64%	49.18%	44.60%	42.30%
ZO_NF_S	43.04%	21.54%	14.10%	14.14%	8.39%	9.12%
ZONF_S	15.62%	4.36%	2.76%	3.14%	2.06%	2.70%
ZOO	12.10%	10.20%	14.80%	9.20%	11.10%	5.70%
AVERAGE	**36.39%**	**26.91%**	**26.28%**	**23.54%**	**23.93%**	**20.58%**

Table 3. Experimental results for the regression datasets. Numbers in cells represent average regression error as calculated on the corresponding test set.

DATASET	BFGS	GEN	RULE	NNC	RULE_CROSS	NNC_CROSS
ABALONE	6.38	7.17	7.36	5.05	5.32	4.63
AIRFOIL	0.003	0.001	0.003	0.003	0.002	0.002
BK	0.36	0.26	0.02	2.32	0.037	0.15
BL	1.09	2.23	2.53	0.021	0.023	0.40
BASEBALL	119.63	64.60	65.64	59.85	61.35	58.75
CONCRETE	0.023	0.001	0.013	0.008	0.009	0.005
DEE	2.36	0.47	0.43	0.26	0.32	0.23
FY	0.19	0.65	0.041	0.058	0.046	0.049
HO	0.62	0.37	0.019	0.017	0.019	0.014
HOUSING	97.38	35.97	47.99	26.35	26.74	19.10
LASER	0.03	0.084	0.055	0.024	0.032	0.019
LW	0.26	0.54	0.012	0.011	0.013	0.017
MORTGAGE	8.23	0.40	0.20	0.30	0.13	0.21
MUNDIAL	0.05	1.22	0.038	4.47	0.049	0.76
PL	0.11	0.03	0.056	0.045	0.035	0.036
QUAKE	0.09	0.12	1.13	0.045	0.73	0.046
REALESTATE	128.94	81.19	104.74	76.78	92.49	69.77
SN	0.16	0.20	0.025	0.026	0.026	0.024
TREASURY	9.91	0.44	0.15	0.47	0.12	0.30
TZ	0.21	0.097	0.036	5.04	0.035	0.061
VE	1.92	2.43	0.028	6.61	0.043	0.084
AVERAGE	**17.99**	**9.45**	**10.98**	**8.94**	**8.93**	**7.35**

The experimental results show a significant reduction in the mean error using the new genetic operator in both machine learning models. In a wide range of data sets, the proposed technique drastically reduces the error of data classification or fitting, as it is also represented in the graphs 5 and 6. These graphs show the number of datasets in which the application of the new genetic operator resulted in a drastic reduction in the corresponding error.

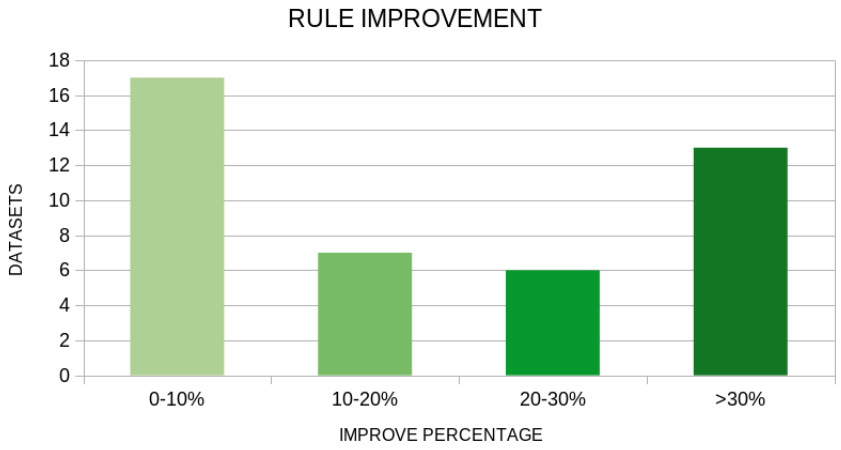

Figure 5. Number of datasets that improved in the RULE machine learning model using the proposed method. The vertical axis represents the number of data sets and the horizontal axis the percentage of reduction in error.

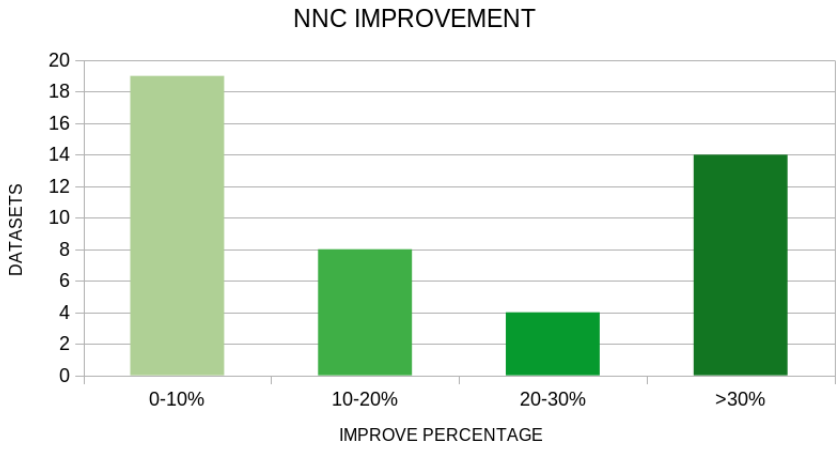

Figure 6. Number of datasets that improved in the NNC machine learning model using the proposed method. The vertical axis represents the number of data sets and the horizontal axis the percentage of reduction in error.

Furthermore, the box plots for the classification cases are shown in Figures 7 and 8 for the rule construction model and the network construction model respectively.

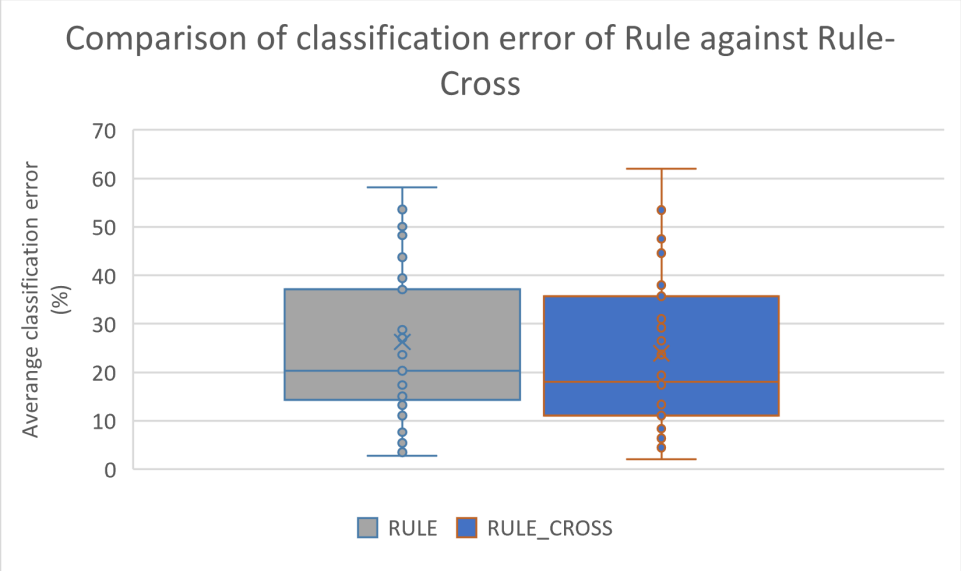

Figure 7. Box plot for the comparison between the original rule construction model and the improved one that utilizes the new crossover operator.

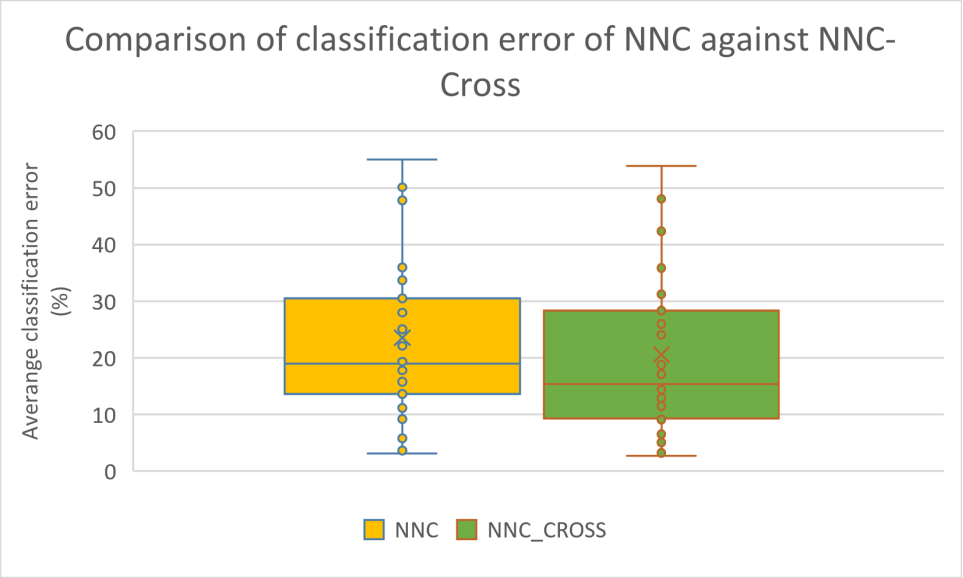

Figure 8. Box plot for the comparison between the original rule construction model and the improved one that utilizes the new crossover operator.

Box plots for the same comparisons as deduced from the results on the regression datasets are shown in Figures 9 and 10 respectively.

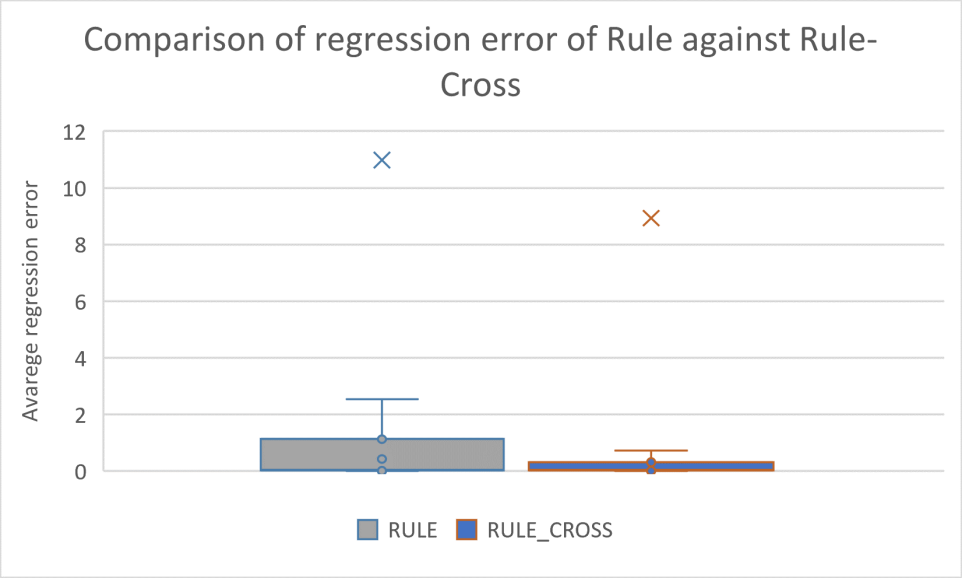

Figure 9. Box plot for the comparison between the original rule construction model and the improved one that utilizes the new crossover operator for the regression datasets.

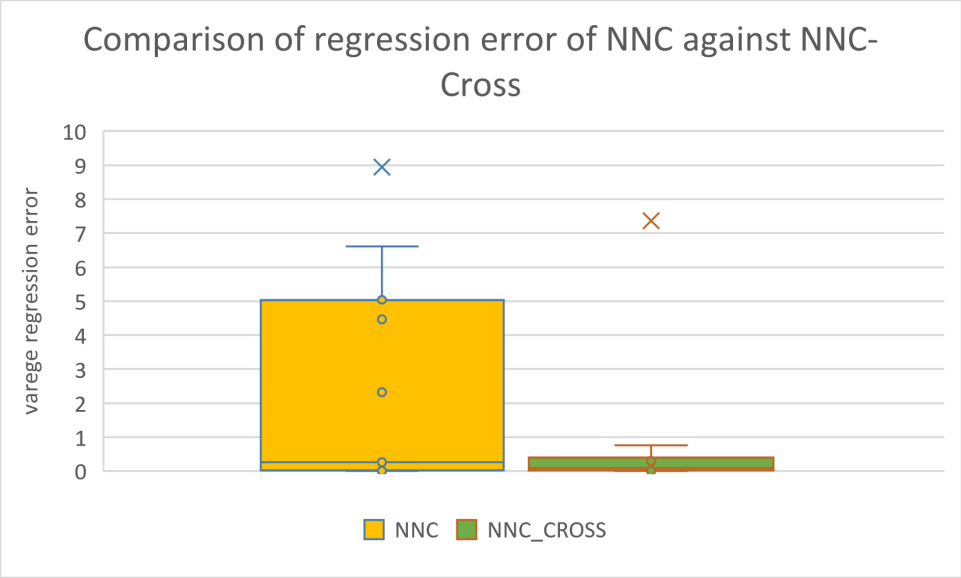

Figure 10. Box plot for the comparison between the original rule construction model and the improved one that utilizes the new crossover operator for the regression datasets.

These figures confirm the significant improvement brought about by the use of the new operator in the effectiveness of the two techniques that utilize Grammatical Evolution. This improvement appears to be greater in the datasets used in data fitting.

Also, a statistical comparison was performed between the two machine learning methods and the enhanced ones that use the new crossover operator. This comparison was performed for the classification datasets, and it is graphically outlined in Figure 11.

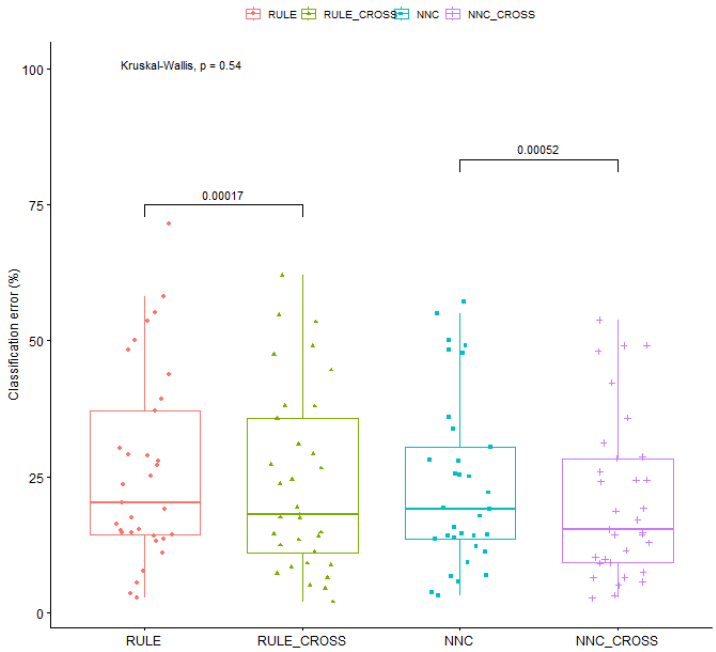

Figure 11. Statistical comparison between the improved machine learning methods and the original methods for the classification datasets.

Moreover, an additional test was executed in order to measure the effectiveness of the new crossover rate parameter denoted as p_{cr}. In this experiment the rule construction

machine learning model was applied on the classification datasets using different values for the critical parameter p_{cr} and the results are shown in Table 4.

Table 4. The effect of different values of p_{cr} to the RULE machine learning model. The model is applied to the classification datasets.

DATASET	RULE	$p_{cr} = 0.025$	$p_{cr} = 0.05$	$p_{cr} = 0.075$
APPENDICITIS	14.70%	15.80%	14.80%	15.10%
AUSTRALIAN	14.27%	13.96%	14.46%	14.03%
BALANCE	28.79%	20.18%	17.47%	18.07%
CIRCULAR	13.25%	11.00%	9.12%	9.78%
CLEVELAND	48.24%	48.24%	47.52%	46.07%
DERMATOLOGY	43.77%	38.60%	38.00%	36.00%
ECOLI	55.18%	52.49%	53.48%	48.83%
FERT	17.40%	16.70%	17.50%	18.50%
HABERMAN	27.03%	27.57%	26.53%	26.87%
HAYES-ROTH	39.39%	35.69%	38.08%	36.77%
HEART	20.30%	20.48%	19.41%	20.37%
HEARTATTACK	23.63%	22.83%	23.70%	22.53%
HOUSEVOTES	3.48%	3.48%	4.51%	3.13%
GLASS	58.10%	55.62%	54.81%	52.76%
IONOSPHERE	15.06%	15.14%	14.14%	14.14%
LIVERDISORDER	37.09%	34.79%	35.68%	33.50%
MAMMOGRAPHIC	19.00%	18.34%	18.10%	17.90%
PARKINSONS	13.47%	13.95%	13.37%	13.21%
PIMA	27.85%	27.80%	27.30%	27.84%
POPFAILURES	5.44%	5.33%	5.02%	5.32%
REGIONS2	29.13%	28.82%	29.26%	28.00%
SAHEART	30.20%	30.00%	31.00%	30.18%
SEGMENT	71.51%	67.36%	61.99%	63.91%
SPIRAL	50.06%	50.42%	49.08%	49.60%
STUDENT	11.08%	7.50%	7.23%	6.07%
TRANSFUSION	25.19%	24.20%	24.46%	24.68%
WDBC	7.66%	5.79%	6.43%	6.41%
WINE	15.35%	15.47%	12.47%	13.59%
Z_F_S	16.40%	11.63%	8.77%	9.10%
Z_O_N_F_S	53.64%	47.14%	44.60%	44.04%
ZO_NF_S	14.10%	10.50%	8.39%	8.42%
ZONF_S	2.76%	2.64%	2.06%	2.14%
ZOO	14.80%	11.30%	11.10%	8.70%
AVERAGE	**26.28%**	**24.57%**	**23.93%**	**23.50%**

Looking at the table of results, one can see a significant decrease in the average classification error when the application rate of the genetic operator increases from 2.5% to 5%. However, the rate of reduction of the average error decreases significantly when the application rate increases to 7.5%. This finding reinforces the idea of implementing the new genetic operator at a rate of 5%.

Another experiment was conducted in order to measure the importance of the parameter N_{cr}, which controls the number of chromosomes participating in the new crossover operator. In this experiment the neural network construction method was applied on the classification datasets using different values for the parameter N_{cr} while the parameter p_{cr} was fixed to 2.5%. The results from this experiment are shown in Table 5.

Table 5. The effects of the parameter N_{cr} to the NNC machine learning model. The experiments were conducted on the classification datasets. In all experiments the value p_{cr} was set to 0.025.

DATASET	**NNC**	$N_{cr} = 25$	$N_{cr} = 50$	$N_{cr} = 100$
APPENDICITIS	13.70%	14.00%	14.50%	14.70%
AUSTRALIAN	14.51%	14.46%	14.13%	13.97%
BALANCE	22.11%	22.29%	17.76%	18.05%
CIRCULAR	13.64%	11.90%	9.38%	8.46%
CLEVELAND	50.10%	49.69%	48.90%	49.17%
DERMATOLOGY	25.06%	20.51%	18.20%	16.29%
ECOLI	47.82%	47.79%	47.39%	47.52%
FERT	19.00%	18.70%	19.20%	18.70%
HABERMAN	28.03%	28.27%	28.43%	26.70%
HAYES-ROTH	35.93%	31.54%	27.77%	27.69%
HEART	15.78%	15.07%	16.00%	14.67%
HEARTATTACK	19.33%	20.13%	19.73%	18.50%
HOUSEVOTES	3.65%	3.30%	3.26%	3.13%
GLASS	57.10%	55.38%	54.62%	54.29%
IONOSPHERE	11.12%	10.63%	10.71%	9.89%
LIVERDISORDER	33.71%	32.03%	32.53%	31.12%
MAMMOGRAPHIC	17.78%	17.72%	17.64%	17.12%
PARKINSONS	12.21%	12.53%	12.79%	11.58%
PIMA	27.99%	27.26%	27.68%	26.09%
POPFAILURES	6.74%	6.33%	6.91%	6.35%
REGIONS2	25.52%	26.20%	25.47%	24.82%
SAHEART	30.52%	30.61%	29.81%	29.58%
SEGMENT	54.99%	53.07%	49.24%	42.90%
SPIRAL	48.39%	48.08%	48.20%	48.34%
STUDENT	5.78%	5.40%	5.20%	4.10%
TRANSFUSION	25.34%	25.26%	24.80%	24.47%
WDBC	6.95%	6.82%	7.39%	6.59%
WINE	14.35%	11.82%	11.77%	9.88%
Z_F_S	14.17%	12.60%	13.50%	9.98%
Z_O_N_F_S	49.18%	48.20%	46.24%	44.73%
ZO_NF_S	14.14%	12.72%	12.18%	10.42%
ZONF_S	3.14%	3.18%	2.82%	2.58%
ZOO	9.20%	8.20%	8.10%	7.50%
AVERAGE	**23.54%**	**22.78%**	**22.19%**	**21.21%**

The lowest average classification error is observed for $N_{cr} = 100$, however, no major changes are observed in the classification errors as the parameter increases. Furthermore, is expected the average execution time to increase as the value N_{cr} increases and this is demonstrated in Figure 12, where the average execution time for the neural network construction method is plotted with respect to the N_{cr} .

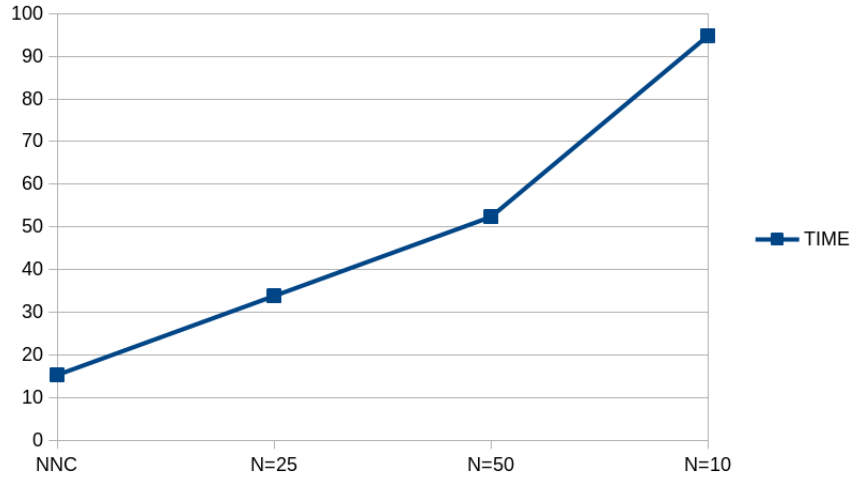

Figure 12. Average execution time for the NNC machine learning model using different values of the N_{cr} value.

The average execution time increases dramatically as the critical parameter N_{cr} increases, something that is expected since the crossings increase significantly with the increase of this parameter, as well as the evaluation of the fitness function. This dramatic increase in required execution time can be significantly reduced by using parallel techniques, such as using the MPI interface [96] or the OpenMP library [97].

4. Conclusions

A new genetic operator for tasks based on Grammatical Evolution is introduced in this article. This operator is applied to randomly selected chromosomes of the genetic population. On each application, a group of randomly selected chromosomes is formulated for every chromosome and one - point crossover is executed between each member of the group and the selected chromosome, aiming to reduce the associated fitness value. In order to measure the effectiveness of the new operator, it was applied with success in two machine learning models from the recent bibliography that utilize the Grammatical Evolution method:

- A rule construction method, that constructs rules in a C - like language for data classification or regression problems.
- A method that constructs artificial neural networks.

The methods were applied on a wide series of classification and regression datasets used in the recent literature. In the vast majority of cases, the application of the new genetic operator resulted in a drastic reduction of the corresponding classification or data fitting error. Furthermore, to assess the effect of changing the values of the critical parameters of the genetic operator on the performance of the machine learning methods, more experiments were conducted in which these critical parameters were changed over a wide range of values. Boosting these values improves the performance of machine learning methods by applying the new genetic operator, but up to a point. Moreover, the increase in the number of chromosomes involved in the above genetic operator has a direct increase in a direct increase of the significant increase in the required execution time, as was also seen in the performed experiments. However, with the use of new techniques that take advantage of modern parallel computing structures, this additional time can be significantly reduced.

Future improvements to the method may include the application of the new crossover in other machine learning methods based on Grammatical Evolution, a parallel implementation of the operator or even the usage of this operator in other tasks involving Genetic Algorithms.

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