Designing Radial Basis Function Neural Networks with Meta-Evolutionary Algorithms: The Effect of Chromosome Codification

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Abstract. In this paper a study of two approaches of a meta-algorithm, Meta_CHC_RBF, is presented. The main goal of this algorithm is to automatically design Radial Basis Function Networks (RBFNs) finding a suitable configuration of parameters (automatically adapted to every problem) necessary for the algorithm EvRBF, an evolutionary algorithm for the automatic design of asymmetric RBFNs. The principal difference between two proposals is the type of codification, in the fist one, the meta-algorithm uses binary codification, while in the second one, it implements real codification; affecting this influence of the codification kind in the carried out experimentation. Finally, results show that the first approach yields good marks reducing the computation time, with respect the second one.

Keywords: Radial Basis Function Neural Networks, evolutionary meta-algorithms, CHC algorithm, chromosome codification.

1 Introduction

Radial Basis Function Networks (RBFNs) [2] are two-layer, fully-connected, feed-forward networks, in which hidden neuron activation functions are Radial Basis Functions (RBF), usually Gaussian. They have been successfully used in many areas such as pattern classification, function approximation, and time series prediction, among others. RBFNs have interesting characteristics such as their simple topological structure and the fact that outputs can be easily explained.

Scientists have applied data mining techniques to the tasks of finding the optimal RBFNs that solves a given problem. Thus, many methods have been developed to face this problem, all of them sharing the same disadvantage: they need to be given a good parameter setting in order to work properly. To overcome this problem, the meta-algorithm Meta_CHC_RBF has been developed to fully configure Radial Basis Function Networks (RBFNs) adapted to every given problem.

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In this paper, two different versions of Meta_CHC_RBF have been tested in order to find out the influence of the chromosome representation, discovering similarities and differences between both proposals. To do this, two kind of codification for chromosomes have been used: binary and real codification, since the CHC algorithm [1] was originally designed to work with binary-coded solutions although can be adapted to real codification.

The rest of the paper is organized as follows: section 2 explains the Meta_CHC_RBF codified under the two approaches, section 3 shows the experimentation carried out and the results obtained; and finally, section 4 describes some conclusions and future works.

2 Method Overview

This section describes the two approaches of Meta_CHC_RBF, a meta-algorithm developed to find a suitable configuration of parameters necessary for the EvRBF algorithm [3] [4].

The two proposals use the CHC algorithm [1], in order to get an appropriate balance between diversity and convergence. The CHC algorithm was developed in order to solve the problems of premature convergence that genetic algorithms frequently suffer, and it uses a conservative strategy of selection. CHC is based on four components [1]: Elitist selection, HUX crossover operator, incest prevention and restart.

Binary Codification Approach. Every individual of the meta-algorithm in this proposal is a binary string representing a set of 8 parameters for the method EvRBF, as the size of the population, the size of the tournament for the selection of the individuals or the maximum number of generations.

The number of bits for integer parameters allows to represent any of the allowed values. The number of bits for real parameters gives the algorithm a wide variety of values to be used along the execution. Minima and maxima values for ranges have been established according to previous experience accumulated over the last year using EvRBF.

In order to set the *fitness* of an individual, the chromosome is decoded into the set of parameters it represents. Then, these parameters are used to perform a complete execution of EvRBF. Once EvRBF has finished, the percentage of training patterns correctly classified by the best net found, is used as *fitness* for the individual.

Real Codification Approach. For this second versionMeta_CHC_RBF has a real codification scheme where each individual is formed of a string of real values which represent a set of 8 parameters for the method EvRBF. The crossover operator is also different from the one used in the binary-coded approach. Thus, real-coded meta-algorithm implements BLX-α, specially designed for real values, and it is applied twice in order to generate two new individuals. On the other hand, the binary version uses the original HUX crossover operator based on Hamming distance.

Regarding to the incest prevention property of CHC algorithm, real codification meta-algorithm compares the two fathers which are going to cross, variable to variable by means of the absolute value of the difference ($|x_i^1 - x_i^2|$). Only when this difference is lower than a threshold δ_i the two genes are considered equals. After this, the number of genes that differ across the whole two chromosomes is established as the Hamming distance for real codification.

With respect to the setting of the individuals *fitness*, and as every gene of the chromosome represents a parameter, this set of parameters is used to perform a complete execution of EvRBF. Once EvRBF has finished, the percentage of training patterns correctly classified by the best net found, is used as *fitness* for the individual.

3 Experiments and Results

In order to test the behavior of the approaches, both of them have been evaluated with the following data sets taken from UCI data set repository[1]: Flag, German, Glass, Haberman, Ionosphere, New-thyroid, Pima, Postoperative, Sonar, Vehicle, and WDBC. Then, a 10-crossfold validation method has been used for every data set, so that every one has been divided into 10 different sets of training-test patterns.

Table 1 shows the results of Meta_CHC_RBF with binary and real codification. The results show that both chromosome representations yield similar results according to the percentage of classification and the number of nodes. With respect to the execution time, differences appear as the model size increases, so that almost no differences are found for the first five databases. On the other hand, the real-coded version takes half the time to find the solution in the case of the Vehicle database, which turns to be the most difficult problem to solve (taking into account the number of nodes needed to classify the patterns).

Table 1. Results in the classification of different databases for both binary and real codifications

Processed	Binary codification			Real codification		
	Nodes	Test(%)	Time (mins)	Nodes	Test(%)	Time (mins)
Postoperative	**02** ± 01	**82.96** ± 6.99	**05** ± 01	**02** ± 01	80.13 ± 3.05	**05** ± 00
Haberman	**07** ± 03	**82.55** ± 5.28	**57** ± 12	**07** ± 04	82.10 ± 5.16	59 ± 18
New-thyroid	**06** ± 04	**98.61** ± 2.46	63 ± 08	07 ± 05	98.47 ± 3.25	**61** ± 13
Glass	**01** ± 01	92.22 ± 2.19	**11** ± 02	**01** ± 00	**92.39** ± 2.55	12 ± 03
Flag	**01** ± 00	**87.39** ± 15.56	10 ± 02	**01** ± 01	**87.39** ± 15.39	**09** ± 05
Pima	**09** ± 06	80.06 ± 3.24	**309** ± 53	11 ± 06	**80.38** ± 2.22	337 ± 48
Ionosphere	13 ± 07	**97.45** ± 2.39	316 ± 82	**12** ± 06	96.99 ± 2.75	**204** ± 40
Sonar	**06** ± 04	71.79 ± 6.66	130 ± 32	09 ± 10	**73.98** ± 7.83	**86** ± 16
Vehicle	49 ± 20	**94.99** ± 1.80	1903 ± 442	**42** ± 15	94.32 ± 2.05	**875** ± 499
WDBC	08 ± 06	95.02 ± 3.29	310 ± 55	**07** ± 03	**95.03** ± 3.19	**243** ± 32
German	**06** ± 05	**73.20** ± 2.43	**259** ± 36	10 ± 09	**73.20** ± 2.77	286 ± 51

[1] http://www.ics.uci.edu/~mlearn/MLRepository.html

The Wilcoxon test was carried out to study whether the above conclusions where correct or not. With respect to the number of nodes and classification ability, the test showed that no differences could be found between binary and real codifications. No differences were found even when only the first five ("easy") or the last six ("difficult") databases were considered. Regarding to the execution time, the Wilcoxon test shows no differences between the codifications when the whole set of databases or only the "easy" databases are considered. Nevertheless, when only the "difficult" databases are studied, then significant differences exist in favor of the real codification (Wilcoxon test shows a p-value of 0.058). This leads to conclude that the real-coded scheme should be used in any case, independently of the size of the problem to solve. For small problems, the time would be similar to the binary-coded scheme; for larger problems, the real codification would get the solution in a shorter time.

4 Conclusions and Future Research

Results show that the two approaches can be used to automatically design RBFNs finding a suitable configuration of parameters for the method EvRBF. Both of them yield similar results with respect to the size of the nets and the classification ability. But on the other hand, the codification type affect to the method with respect to the computation time, since Meta_CHC_RBF with real codification is able to reduce the execution, specially as the complexity of the database been classified increases.

Future research lines will center on applying Meta_CHC_RBF to function approximation and time series prediction.

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