

A cooperative evolutionary algorithm for classification

Stoean, C.; Stoean, R.; Preuss, M.; Dumitrescu, D.

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PREFACE

The second edition of the International Conference on Computers, Communications & Control¹, ICCCC 2006, was organized by Agora University of Oradea and was powered by IEEE Computer Society, Romania Section, and took place in Baile Felix - Oradea, Romania, June 1-3, 2006.

ICCCC 2006 provides a forum for scientist in academia and industry to present and discuss their latest research findings on a broad array of topics in Computer Science, Information Technology & Data Communications and Computer-based Control.

The scope of the conference covered the following topics: Artificial Intelligence, Automata and Formal Languages, Computational Mathematics, Cryptography and Security, E-Activities, Fuzzy Systems, Informatics in Control, Information Society - Knowledge Society, Natural Computing, Network Design & Internet Services, Multimedia & Communications, Parallel and Distributed Computing.

ICCCC 2006 and the the International Journal of Computers, Communications & Control (IJCCC, founded by I. Dziţac - Executive Editor, F.G. Filip - Editor in Chief and M.J. Manolescu - Managing Editor), celebrates, by two invited papers² published in IJCCC Vol. I, No. 1, 100 years from the birth of Grigore C. Moisil (1906-1973). Grigore C. Moisil was one of the great Romanian mathematicians who had a great impact in Computer Science. He received post-mortem, in 1996, the "Computer Pioneer Award" of IEEE Computer Society. He insisted and helped in the building of the first Romanian computer, by Victor Toma, at the Institute of Atomic Physics (1957). He also directed the first generation of graduate students in Mathematics to work with the team of Victor Toma, at the Institute of Atomic Physics; they were trained to learn programming at the new computers CIFA. He introduced Łukasiewicz algebras with three values and multiple values (which are known today as Łukasiewicz-Moisil algebras) and used them in the logic and study of commutation circuits. He developed new methods of analysis for finite automata and had valuable contributions in the filed of algebraic theory of automated mechanism.

The Program Committee received 142 submissions, originating from Algeria, France, Germany, Greece, Hungary, Italy, Japan, India, Ireland, Iran, Spain, Serbia & Montenegro, Moldova, Romania, Thailand, Tunisia and and USA. Each submission was reviewed by two Program Committee members, or other experts. Out of the 142 papers only 91 (64%) were accepted for presentation at the conference and for publication (7 papers in IJCCC, Vol. I (2006), No.1 and 84 papers in this supplementary issue of IJCCC).

The Program Committee gratefully acknowledges all authors who submitted papers for theirs efforts in maintaining the scientific standards of the second edition of ICCCC.

We would like to thank the members of the Program Committee, the additional reviewers and the members of the Organizing Committee for their work and support.

Also, we thank the authors that responded to our request for preparing invited papers: K. Chen, G. Ciobanu, P. D. Cristea, F. Dong, D. Dumitrescu, J. Fodor, A. Garrido, K. Hirota, I.D. Karamitsos, A. Roth, I. Rudas, M. Stanojevici, A.D. Stylidias, and D. Tufis. M. Vujosevici and D. I. Zacharoiu.

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Oradea, May 2006 I. Dziţac, F.G. Filip, M. J. Manolescu

¹The first edition of this conference, entitled "International Conference on Computers and Communications", ICCC 2004, has been founded and organized in 2004 by I. Dziţac, C. Popescu and H. Oros.

²"Grigore C. Moisil (1906 - 1973) and his School in Algebraic Logic", authors George Georgescu, Afrodita Iorgulescu, Sergiu Rudeanu and "Grigore C. Moisil: A Life Becoming A Myth", author Solomon Marcus

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A Cooperative Evolutionary Algorithm for Classification

Cătălin Stoean, Ruxandra Stoean, Mike Preuss, Dan Dumitrescu

Abstract: An evolutionary algorithm based on cooperative coevolution is applied to a classification problem, the Pima Indian diabetes diagnosis problem. Previous cooperative coevolution algorithms were developed for function optimization [1], optimizing agents behaviour [2] or modelling the behaviour of a robot in an unknown environment [3]. The aim of this paper is to integrate the cooperative approach into a learning classifier system and use it for solving a real-world problem of classification. To the best of our knowledge, there have been no attempts on applying cooperative coevolution specifically to classification. For each category of the classification problem, a sub-population evolves specific rules using a classical genetic algorithm. Sub-populations evolve simultaneously but independently; cooperation between them takes place only when the fitness of an individual in computed. Obtained experimental results encourage further investigation.

Keywords: genetic algorithm, cooperative coevolution, classification, evolutionary rules, diabetes mellitus

1 Introduction

Evolutionary models based on cooperative coevolution have been recently developed and applied for the optimization of difficult multimodal functions [1] and agent behaviour [3] and they have proven to be very successful. In [1], the performance of the cooperative based algorithm proved to be higher than the one of a typical evolutionary algorithm, as the cooperative one did not remain blocked into local optima, but always found the global one.

When a cooperative coevolutionary algorithm is applied to a problem, the first step is to find a natural decomposition of the problem into subcomponents. Then, each sub-problem is assigned to a sub-population, such that the individuals in a certain sub-population represent the potential subcomponents of the greater solution. Each sub-population is evolved simultaneously, but independently from the others. Collaboration is achieved only at the level of fitness evaluation; when the fitness of an individual is computed, collaborators from each of the other sub-populations are selected in order to form a complete solution which is evaluated [4].

In present paper, a new learning classifier system for binary classification is proposed. Decomposition of the problem is conducted with respect to the two classes; consequently two sub-populations are considered: one *evolves* a rule for the one class and the other for the opposite class. Each individual represents one rule. In the end of the algorithm, the best individuals from each of the two sub-populations represent the final rules. The cooperative approach is motivated by recent work [6] which indicated that two rules —one for each outcome— are sufficient to achieve good classification results.

When an individual of one sub-population is evaluated, its fitness is computed in correspondence with one individual from the other sub-population. The former shall be more similar to the objects of the training set which have the same outcome, and, at the same time, as different as possible from the latter individual, which represents the rule for the other outcome. In a sense, both subpopulations each evolve substitutes for the training set objects with one designated outcome.

The paper is organized as follows: next section presents some basics regarding cooperative coevolution, section 3 contains the detailed description of the proposed algorithm for classification and sections 4 and 5 present the diabetes diagnosis problem and the experimental results. The paper closes with the conclusions and some ideas for future work.

2 Cooperative Coevolution. Basic Concepts

Individuals in nature evolve by means of adaptation to the environment, part of which consists of other living beings itself, in particular of different groups or species. From this viewpoint, evolution is actually coevolution. Coevolution can be competitive, cooperative or both. Similarly in the evolutionary computational area, a interest has recently grown towards the extension of the powerful evolutionary algorithms to coevolutionary architectures. They are interesting indeed because they bring along a new idea for the fitness evaluation of an individual, i.e. in

relation to the other individuals in the population. As in nature, two techniques have been proposed: competitive and cooperative models.

We will briefly discuss the concepts underlying the latter. The first step towards a cooperative coevolutionary algorithm for a given problem is to decompose the problem into subcomponents and assign each subcomponent to a sub-population. Each sub-population evolves separately but concurrently with the others. Sub-populations collaborate only at the level of fitness evaluation, since each of them represents only a subcomponent of the problem and therefore a potential solution for every component in turn cannot be assessed apart from those of the complementary components. Therefore, every individual of every sub-population is evaluated by selecting collaborators from every other sub-population; a complete solution to the problem at hand is thus reached and its performance is computed and returned as fitness value of the current individual.

The main question in this process is the choice of collaborators. There are consequently three attributes regarding this selection whose values have to be decided when building a cooperative coevolutionary algorithm [4].

Collaborator selection pressure is the degree to which highly fit individuals will be chosen to form the complete solution to the problem, i.e. pick the best individual according to its previous fitness score, pick a random individual or select individuals based on classic selection schemes from each of the other sub-populations. **Collaboration pool size** is the number of collaborators that will be selected from each sub-population. Since each of these collaborations will have their own fitness score, the **collaboration credit assignment** will decide the value for the fitness of the current individual. There are three methods for this assignment, i.e. *optimistic* - the fitness of the individual whose fitness is computed is the value of its best collaboration, *hedge* - the average value of its collaborations is returned as fitness score and *pessimistic* - the value of its worst collaboration is assigned to the current individuals.

3 Proposed Algorithm

A formal representation for the binary classification problem is considered: training data is denoted by $\{(x_i, y_i)\}_{i \in \{1, 2, ..., m\}}$; $x_i \in \mathbb{R}^n$ represents the input vector and $y_i \in \{0, 1\}$ is the *class* (or *outcome*).

3.1 Representation of Individuals

For each of the two classes, a sub-population of individuals is considered. The individuals in each sub-population represent IF-THEN rules; a rule contains n genes for each attribute of the input vectors and a last one which represents the class (0 or 1, in the binary case). All individuals in one sub-population have the same outcome, so the last gene does not suffer any modification during evolution.

3.2 Fitness Function

The distance between an object from the training set $x_i = (x_{i1}, x_{i2}, ..., x_{in}, y_i)$ and an individual $c = (c_1, c_2, ..., c_n, y_c)$ does not depend on the outcome and is given in (1).

$$d(c,x_i) = \sum_{j=1}^{n} \frac{|c_j - x_{ij}|}{b_j - a_j}$$
(1)

where a_j and b_j represent the lower and upper bounds of the *j*-th attribute. As usually the values for the attributes belong to different intervals, the distance measure has to refer their bounds.

When computing the quality of an individual c, a *collaboration* between c and **only one** individual e from the other sub-population - the best one from the previous generation or one randomly taken - is envisaged. The goal of the fitness function is to minimize the distance between c and all objects x_i of the training set with equal outcome and, at the same time, maximize the distance between the same objects and e. Consequently, the criteria are aggregated into the maximization problem in (2).

$$eval(c) = \frac{\sum_{i=1}^{m} h_c(e, x_i)}{1 + \sum_{i=1}^{m} h_c(c, x_i)}$$
(2)

where h_c is defined as follows:

 $h_c: \mathbf{R}^{n+1} \times \mathbf{R}^{n+1} \to \mathbf{R}_+,$

$$h_c(a,b) = \begin{cases} d(a,b), & class(c) = class(b), \\ 0, & \text{otherwise.} \end{cases}$$
(3)

3.3 Algorithm Description

An evolutionary algorithm that learns characteristics for each of the two classes from the training data is further on presented. The rules that result after termination –the two individuals selected from each of the two classes– are applied to the test data.

Algorithm 1 Proposed evolutionary algorithm

t = 0; initialize both sub-populations P₁(t) and P₂(t); randomly select an individual from each of the sub-populations (b_1 and b_2) **repeat** P₁(t + 1) = evolve(P₁(t)); update b_1 P₂(t + 1) = evolve(P₂(t)); update b_2 **until** stop condition

The method "evolve" contains one generation from a typical genetic algorithm. Selection and then variation operators are applied to the population; resulted population is returned. The method could be described as follows:

function evolve(P) evaluate population P; apply selection for P; apply recombination to the selected population; mutate obtained population; return resulting population; end function

If collaboration selection pressure envisages the best individuals in each sub-population to be chosen for collaboration, then these best ones, denoted above by b_1 and b_2 , will be determined as follows. At first, when the two subpopulations are initialized, b_1 and b_2 are randomly selected. Then, at generation t, the fitness of every individual from the first sub-population is computed in relation with b_2 , while that of the individuals of the complementary sub-population is calculated with respect to b_1 . Two individuals, one from each sub-population, that obtain the highest value for the fitness evaluation will now replace the b_1 and b_2 found at generation t - 1.

Selection and Variation Operators

Tournament selection is employed. Mutation with normal perturbation and intermediate crossover are used. Naturally, crossover takes place only between individuals within the same sub-population. Mutation does not apply to the last gene (the outcome).

Stop Condition

The stop condition may refer to a predefined number of generations or a previously set number of generations that may pass without any improvement. The final b_1 and b_2 in Algorithm 1 represent the two rules that are to be applied to the test set.

4 Diabetes Diagnosis Problem

The Pima-Indian Diabetes data set comes from the UCI repository of machine learning databases [5]. All objects in the data set represent females of at least 21 years age, of Pima Indian heritage, living near Phoenix, Arizona,

USA. For each object in the data set there are eight attributes (either discrete or continuous) containing personal data, e.g. age, number of pregnancies, and medical data, e.g. blood pressure, body mass index, result of glucose tolerance test etc. The outcome is binary, either 0 (negative) or 1 (positive). 34.9% of the cases in the data set are assigned diabetes positive. The total number of cases is 768. No replacement or deletion of these values was undertaken in present paper.

The data is split into training and test sets. The task for proposed algorithm is to evolve two rules based on objects in the training set (one rule per outcome); these rules are then applied to the test set and the accuracy is computed as the percent of the patients from the test set correctly classified by the algorithm.

As an evolved rule represents a vector with eight values that correspond to the eight attributes, when a new object (a similar vector with eight attributes) from the test set is to be classified, the distance between that object and each of the two rules is computed. The outcome of the object coincides with the one of the closest rule to it.

5 Experimental Results

The first 75% of the cases represent the training set and the last 25% compose the test set; test sample cross-validation is conducted. As stated in previous section, two ways of establishing collaboration between an individual from one sub-population and one from the complementary sub-population are considered. In each of the two cases, same parameters of the evolutionary algorithm were considered - they are outlined in Table 1.

Population size*	No. of generations	Mutation strength	Mutation prob.	Crossover prob.
100	1000	100	0.1	0.4

* population size refers to only one subpopulation.

Table 1. Parameters of proposed evolutionary algorithm

The value of the mutation strength for a gene *i* directly depends on the size of the interval of the *i*-th attribute; in order to determine the value of the mutation strength for a gene, the size of the interval is divided into steps, the number of which corresponds to the value written in Table 1.

Figure 1 illustrates the progress of the accuracy obtained for both training and test sets when the best individual is considered for collaboration when fitness is computed.

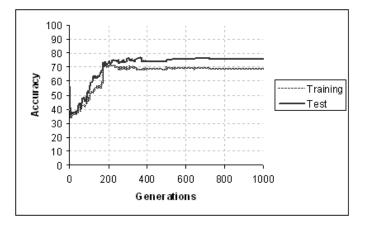


Figure 1: Accuracy obtained on training and test sets when collaboration is performed with the best individual in the complementary sub-population

Interestingly, the algorithm seems to work better when a random individual is selected for fitness evaluation (Figure 2). Support for the affirmation is not necessarily based on the weak start in Figure 1 - where it is probably just an unlucky initialization of the sub-populations - but on the accuracies reached during evolution and even on the final results (Table 2). The higher value of 77.08% on the test set is reached at generation 361 (Figure 2), while in the other case (Figure 1) the highest value reached in generation 364 is 76.56%. Another aspect that indicates the supremacy of the *random collaboration* choice refers to the number of fitness evaluations; in 30 runs, the average number of evaluations reached 879.992, while when collaboration was performed with the best one from

the complementary sub-population the average number of fitness evaluations again in 30 runs was 1.080.745. On the other hand, in both situations, the algorithm does not seem to need more than 400 generations to reach the optimum (see Figures 1 and 2), so if we set the number of generations parameter to 400 instead of 1000, the number of evaluations could be significantly decreased.

Searching for an explanation concerning the superior performance of *random collaboration*, we may conclude that for this problem, it is advantageous to let each sub-populations adapt to a set of individuals of the other sub-population instead of a probably rarely changing single best one.

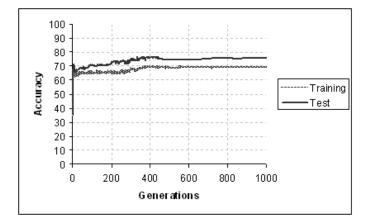


Figure 2: Accuracy obtained on training and test set when collaboration is performed with a random individual from the complementary sub-population

Pima Indian diabetes diagnosis task represents a largely used benchmark problem so, naturally, there are many results for comparison of the accuracy. Some of the best results found for the considered problem are outlined in Table 2.

Algorithm	Repeats	Accuracy (%)
Proposed algorithm & collaboration with best individual	30	75.27
Proposed algorithm & collaboration with a random individual	30	75.4
Best accuracy reached by proposed algorithm	1	77.08
EGGC algorithm in [6]	100	75.08
Neural Network (NN) in [7] with Prechelt's rules	30	65.5
Evolved NN in [8]	30	77.6

Table 2. Comparison to resulting accuracies of other methods for the diabetes diagnosis problem

Except the NN model with Prechelt's rules, all the others models used test sample cross-validation for the separation of training and test sets. Prechelt's rules regarding this separation imagine four ways of setting the training and test sets (in a percentage of 75% and 25%, respectively).

6 Conclusions and Future Work

In present paper, an evolutionary algorithm based on cooperative coevolution is integrated into a learning classifier system for binary classification and is applied for a real-world problem. The preliminary results indicate the high-quality of the proposed classifier.

Work in the near future envisages the generalization of the evolutionary classifier from binary to multi-class classification problems. At the same time, different strategies for collaboration between individuals from different sub-populations will be tested.

Another possibility to significantly improve proposed classifier regards the evolution of more than one rule for one class; this involves the use of a multimodal algorithm instead of a classical genetic algorithm for each sub-population.

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