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Rule-based Classifier via Fitness Scaling Genetic Algorithm

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Abstract: The global optimization is the best choice for parameter extraction of rule-based classifier. Restricted methods have been published, and their limitations are concerned mainly on the slow convergence and being trapped into local minima. To resolve the matter, this paper introduced in the fitness scaling genetic algorithm (FSGA) which conducted the heuristic search as the parameter optimization for rule-based classifier. The FSGA rule-based classifier was compared with GA, SA, and ACA, and the results prove that the proposed FSGA rule-based classifier is the most robust and rapid.

Keywords: Pattern classification; Rule-based; Classifier; Fitness Scaling; Genetic Algorithm; Heuristic Search; Ant colony Algorithm; Simulated Annealing

1 Introduction

In machine learning and statistics, classification is the problem of identifying which of a set of categories a new observation belongs, on the basis of a training set of data containing observations whose category membership is known. [1-3]. Thus the requirement is that new individual items are placed into groups based on quantitative information on one or more measurements, traits or characteristics, etc., and based on the training set in which previously decided groupings are already established [4-6].

The most widely used classifiers are naïve Bayes classifier [7], maximum entropy classifier [8], artificial neural networks, support vector machine (SVM) [9], *k*-nearest neighbor classifier [10], ant coolly algorithm [11], random forest [12], radial basis function (RBF) classifier [13], and artificial bee colony (ABC) [14] . However, above classifiers perform feature transform implicitly, so their generated classifiers are not meaningful. It is difficult to extract meaningful rules to determine how conclusions are drawn [15].

Rule based approaches become the most popular techniques for pattern classification [16]. One advantage is that it is capable of extracting classification rules that are easy to realize for users [17]. However, to determine the parameters in the rule-based model is a difficult problem because the optimization function is a multi-model, non-differential, non-convex problem which can not be solved by traditional gradient-based techniques. Therefore, scholars tend to integrate global search techniques into the rule-based model. Immense global methods are used as follows.

Wu et al. [18] confirmed that the genetic algorithm (GA) has been widely applied as a soft computing technique in various fields, while the ant colony algorithm (ACA) is a rapidly developing tool used for optimization. Based on the combination of the fast global search ability of GA and the positive feedback mechanism of ACO, they proposed a novel algorithm, named genetic ant colony algorithm (GACA) in the domain of pattern classification. Experiments show that the classifier based on GACA can achieve better performance than that the normal GA and ACA does.

Zheng et al. [19] introduced in an adaptive chaotic particle swarm optimization (PSO), and utilized it to find the optimal parameters of the rule-based classifier. The ACPSO rule-based classifier was compared with those of GA, ACA, SA, and PSO, and the results prove that the proposed rule-based classifier by ACPSO is the most robust and rapid among all the algorithms.

Castro [20] gave an exact representation of SVMs as TSK fuzzy systems for every used kernel function. Restricted methods to extract rules from SVMs had been previously published. Their limitations were surpassed with the presented extraction method. The behavior of SVMs was explained by means of fuzzy logic and the interpretability of the system was improved by introducing the λ -fuzzy rule-based system (λ -FRBS). The λ -FRBS exactly approximated the SVM's decision boundary and its rules and membership functions were very simple, aggregating the antecedents with uninorms as compensation operators. The rules of the λ -FRBS were limited to two and the number of fuzzy propositions in each rule only depends on the cardinality of the set of support vectors. For that reason, the λ -FRBS overcomed the course of dimensionality and problems with high-dimensional data sets were easily solved with the λ -FRBS.

Lutu et al. [21] pointed out algorithms for feature selection in predictive data mining for classification problems attempt to select those features that are relevant, and are not redundant for the classification task. A relevant feature was defined as one which is highly correlated with the target function. One problem with the definition of feature relevance was that there is no universally accepted definition of what it meant for a feature to be highly correlated with the target function or highly correlated with the other features. A new feature selection algorithm which incorporated domain specific definitions of high, medium and low correlations was proposed in their paper. The proposed algorithm conducted a heuristic search for the most relevant features for the prediction task.

Cline et al. [16] proclaimed concept maps have been heralded as an effective learning tool to help students integrate new concepts into their existing set of knowledge. However, the concept maps are also useful

for evaluating student learning and helping to illuminate where learning has occurred and where invalid or incomplete ideas are held by the student. They had developed a web-based concept map construction and rule-based evaluation system called the Concept Mapping Tool (CMT) that was being deployed at the university level. After students used the drawing facility of CMT to construct individual concept maps for a particular topic that was presented in a course, they could then use the rule-based evaluation system to grade their concept maps against a criterion concept map created by the course instructor. Students were given immediate feedback on how to improve their concept maps, and they could use CMT iteratively to improve their understanding of the topic at hand. The rule-based evaluation or grading system was modeled in part on a manual system for the consistent scoring of concept maps. Their tests of the system showed that there was a strong positive correlation (>0.80) between the scores on students' concept maps given by the course instructor grading manually and by the CMT rule-based evaluation system.

Dressler et al. [22] described a programming scheme for massively distributed systems that were assumed to self-organize according to a given set of simple rules. The focus of this investigation was operation and control in sensor and actor networks (SANETs). The main issues addressed by self-organization techniques were scalability, network lifetime, and real-time support. In the literature, biological principles are often cited as inspirations for technical solutions, especially in the domain of self-organization. We developed a system named rule-based sensor network (RSN) according to the observed communication and control behavior in cellular communication. Cellular signaling cascades allowed the event-specific reaction initiated by individual cells in collaboration with their direct neighbors. Information between cells were transmitted via proteins and resulted in the cascade of protein-protein or protein-DNA interactions to produce a specific cellular answer, e.g. the activation of cells or the transmission of mediators. These processes were programmed in every individual cell and lead to a coordinated reaction on a higher organization platform. We transferred these mechanisms to operation and control in SANETs. In particular, a rule-based processing scheme relying on the main concepts of cellular signaling cascades had been developed. It relies on simple local rules and provides problem specific reaction such as local actuation control and data manipulation. We described this RSN technology and demonstrate comparative simulation results that show the feasibility of our approach.

Those aforementioned methods had suffered from such shortcomings as slow convergence and being trapped into l local minima [23-25]. In this paper, we introduced in the fitness scaling genetic algorithm (FSGA) [26]. It can avoid being trapped into local minima and had a faster and steady speed. The structure of this paper is organized as follows: Next section 2 gives the rule-based model for classification; section 3 introduces the genetic algorithm; section 4 gives the detailed description of FSGA; experiments in section 5 demonstrate that FSGA method is more effective and swift than GA[27], SA [28], and ACA [29]; final section 6 is devoted to conclusion and discussion.

2 Model

Assume the classification problem contains c classes in the n dimensional data space, and there are p vectors $X_i = [x_{i1}, x_{i2}, \ldots, x_{in}]$ (i=1, 2,…, p) [30]. The rule-based classifier is represented as [31]:

IF $(T_{1\min} \le x_{i1} \le T_{1\max})$ AND $(T_{2\min} \le x_{i2} \le T_{2\max})$ AND $\cdots$ AND $(T_{n\min} \le x_{in} \le T_{n\max})$
THEN $X_i \in$ Class j

where R_j denotes a rule label, n is the number of attributes, $T_{k\min}$ and $T_{k\max}$ are the minimum and maximum thresholds of the kth attribute x_{ik}, respectively. The rule R_j is then encoded as Tab. 1. A default rule is added at the end of the rule list. It has an empty antecedent with consequent as a class that represents maximum of uncovered class, which is not covered by any of the discovered rules.

Tab. 1 Encoding of Rule

Antecedent Element 1		…	Antecedent Element n		Consequent Element
$T_{1\min}$	$T_{1\max}$	…	$T_{n\min}$	$T_{n\max}$	j

To measure the accuracy and coverage of the rule, the fitness function was chosen as the misclassification error depicted as

$$\begin{aligned} f(\mathbf{T}) &= f(T_{1\min}, T_{1\max}, \ldots T_{n\min}, T_{n\max}) \\ &= 1 - \frac{\text{Number of cases find}}{\text{Number of all cases}} \times \\ &\quad \frac{\text{Number of accurately classified cases}}{\text{Number of cases find}} \\ &= 1 - \frac{\text{Number of accurately classified cases}}{\text{Number of cases find}} \end{aligned} \tag{1}$$

where “Number of cases find/Number of all cases” measures the coverage of a rule, and “Number of accurately classified cases/Number of cases find” measures the accuracy of a rule. The objective is defined as a total measure of accuracy and coverage, which provides an effective selection strategy to find a rule for the class with the highest hit ratio if rules were to be fined across all cases. Our task is to minimize the fitness function, and construct the classifier by the rule model with corresponding threshold $\boldsymbol{T}^*$.

$$\mathbf{T}^* = \arg\min_{T} \left(f(\mathbf{T}) \right) \tag{2}$$

3 Genetic Algorithm

For the genetic algorithm (GA), a population of strings called chromosomes which encode candidate solutions to an optimization problem, and evolves toward better solutions [32]. The evolution usually starts from a population of randomly generated individuals and happens in generations. In each generation, the fitness of every individual in the population is evaluated [33]. Multiple individuals are stochastically selected from the

current population based on their fitness and modified to form a new population. The new population is then used in the next iteration of the algorithm. Commonly, the algorithm terminates when either a maximum number of generations has been produced, or a satisfactory fitness level has been reached for the population. If the algorithm has terminated due to a maximum number of generations, a satisfactory solution may or may not have been reached [34].

The GA includes three standard operators:

(a) Selection. This operator selects chromosomes in the population for reproduction. The smaller the fitness of the chromosome, the more times it is likely to be selected to reproduce [35].

(b) Crossover: This operator randomly chooses a locus and exchanges the subsequences before and after that locus between two chromosomes to create offspring [36]. There are three different types of cross over functions: scatter, single point, and two-points. The scatter crossover creates a random binary vector and selects the genes where the vector is a 1 from the first parent, and the genes where the vector is a 0 from the second parent, and combines the genes to form the child. Single-point crossover chooses a random integer n and then selects vector entries numbered less than or equal to n from the first parent and vector entries numbered greater than n from the second parent. Afterwards, it concatenates these entries to form a child vector [37]. Two-point crossover selects two random integers m and n. It selects vector entries numbered less than or equal to m from the first parent, vector entries numbered from m+1 to n from the second parent, and vector entries numbered greater than n from the first parent [38, 39].

(c) Mutation: This operator randomly flips some of the bits in a chromosome. Mutation can occur at each bit position in a string with some probability, usually very small [40, 41]. The common mutations contain single-point and two-points.

4 Fitness Scaling Genetic Algorithm

Fitness scaling converts the raw fitness scores that are returned by the fitness function to values in a range that is suitable for the selection function [42]. The selection function uses the scaled fitness values to select the particles of the next generation. Then, the selection function assigns a higher probability of selection to particles with higher scaled values [43]. There exist bundles of fitness scaling methods [44].

4.1 Linear Scaling

One of the most common scaling techniques is traditional linear scaling, which remaps the fitness values of each bee using the following equation

$$f_{linear} = a + b \times f_{raw} \tag{3}$$

where a and b are constants defined by users.

4.2 Rank Scaling

Another option is the rank scaling, which is obtained by sorting all the bees by their raw fitness values

$$f_{rank} = r \tag{4}$$

where r denotes the rank of the individual particle.

4.3 Power Scaling

The third option is the power scaling method which are instead computed with

$$f_{power} = f_{raw}^{k} \tag{5}$$

Where k is a problem-dependent exponent that might require change during a run to stretch or shrink the range as needed.

4.4 Top Scaling

Top scaling is the 4th option and probably the most simply scaling method [45]. Using this approach, several of the top individuals have their fitness set to the same value, with all remaining individuals have their fitness values set to zero. This simple concept yields [46]

$$f_{top} = \begin{cases} s & f_{raw} \geq c \\ 0 & f_{raw} < c \end{cases} \tag{6}$$

Where s is the user-defined constant, c is the threshold.

4.5 Power-Rank Scaling Method

Among those fitness scaling methods, the power scaling finds a solution nearly the most quickly due to improvement of diversity but it suffers from instability [47, 48], meanwhile, the rank scaling show stability on different types of tests. Therefore, power-rank scaling method was depicted as follows

$$fit_i = \frac{r_i^k}{\sum_{i=1}^{N} r_i^k} \tag{7}$$

where r_i is the rank of ith individual, N is the number of population. Our strategy contains a three-step process. First, all individuals are sorted to obtain the ranks. Second, powers are computed for exponential values k. Third, the scaled values are normalized by dividing the sum of the scaled values over the entire population.

5 Experiment

We implement several classifiers running on two benchmark data sets (the housing data and diabetes data) which are available in the UCI machine learning repository. Here we let k equals to 5 by trial-and-error method [49]. The results are all averaged over 10 runs. Besides, we compared the FSGA method with GA, ACA, and SA .

5.1 Housing Data

The results of different algorithms on housing data are listed in Tab. 2. For the convergence iterations, the FSGA takes the least of only 103.1, GA takes 108.3 epochs, ACA takes 115.4 epochs, and SA takes 204.3 epochs. For the misclassification Error, the proposed

FSGA is 45.2% as the smallest among all algorithms, conversely, misclassification errors of GA, ACA, and SA are 46.7%, 46.1%, and 48.6%, respectively.

Tab. 2 Comparison on housing data

Algorithm	Generation	Misclassification Error	Classification Rate
GA	108.3	46.7%	53.3%
ACA	115.4	46.1%	53.9%
SA	204.3	48.6%	51.4%
FSGA	**103.1**	**45.2%**	**54.8%**

Tab. 3 Comparison on diabetes data

Algorithm	Generation	Misclassification Error	Classification Rate
GA	198.3	29.8%	70.2%
ACA	172.0	28.3%	71.7%
SA	284.9	31.5%	68.5%
FSGA	**173.1**	**27.6%**	**73.4%**

5.2 Diabetes Data

The results of different algorithms on diabetes data are listed in Tab. 3. For generations, the FSGA only uses 173.1 epochs to find the global minimum, and other algorithms uses much more generations: GA uses 198.3 epochs, ACA uses 172.0 epochs, and SA uses 284.9 epochs. For misclassification error, the FSGA reaches the smallest amount (**27.6%**) again compared to GA of 29.8%, ACA of 28.3%, and SA of 31.5%.

From the above two benchmarks, it is obvious that the FSGA method can find the best parameters of rule-based classification model among all the algorithms. Besides, the FSGA uses the least epochs to find the solution. Therefore, the proposed method is efficient and speedy.

6 Conclusion

In this paper, a novel classifier was proposed for pattern classification. The classifier was based on rule model and its parameters were determined by Fitness Scaling Genetic Algorithm (FSGA) algorithm. Simulation results on housing and diabetes data sets proved the proposed FSGA method is superior to those based on GA, ACA, and SA. Moreover, the calculative iteration of the FSGA is the least. The future work involves application of the introduced FSGA based classifier to other industrial fields such as image processing [50], call recognition [51], signal processing, and etc.

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