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Study on the Method of Association Rules Mining Based on Genetic Algorithm and Application in Analysis of Seawater Samples

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Abstract: Based on the data mining research, the data mining based on genetic algorithm method, the genetic algorithm is briefly introduced, while the genetic algorithm based on two important theories and theoretical templates principle implicit parallelism is also discussed. Focuses on the application of genetic algorithms for association rule mining method based on association rule mining, this paper proposes a genetic algorithm fitness function structure, data encoding, such as the title of the improvement program, in particular through the early issues study, proposed the improved adaptive P_c, P_m algorithm is applied to the genetic algorithm, thereby improving efficiency of the algorithm. Finally, a genetic algorithm based association rule mining algorithm, and be applied in sea water samples database in data mining and prove its effective. *Copyright © 2014 IFSA Publishing, S. L.*

Keywords: Data mining, Association rules, Genetic algorithm, Fitness function, Effective.

1. Introduction

Recently, because of improving of applying of databases, more and more databases store huge amount of data. It is special difficult to get valuable information from those databases which involve in huge number of different data in order to service for deceives. Data mining and knowledge discovery in databases (KDD) is an international frontier and has already become a hotspot in R&D field [1].

Data Mining (Data Mining) in the database can be said that knowledge discovery. Now people think that it is from a large, incomplete, noisy, fuzzy, random data, the extraction of implicit in them, people do not know in advance, but is potentially useful information and knowledge [2]. It utilization of statistical methods, fuzzy recognition technology, artificial intelligence, artificial neural network technology and other related technologies, and all walks of production data, data management and data processing operations, organization, analysis, synthesis and interpretation with a mined from these data reveal the objective laws reflect the intrinsic link and predict trends knowledge to help companies develop their marketing strategy, reduce risk and increase market share.

Data mining technology research is still immature, there is a large limitation of its application; it is these limitations generated a lot of growing points, prompting further development of data mining research [3].

The formation and development of genetic algorithm genetic algorithm on biological systems originated in the computer simulation studies conducted [4]. University of Michigan professor and his students in Holland doors being inspired biological simulation technology to create an approach based on genetic and evolutionary mechanisms for complex adaptive system optimization probabilistic optimization techniques - genetic algorithms. Professor Holland using genetic algorithms thoughts on natural and artificial adaptive systems studied, the fundamental theorem of genetic algorithms - schema theorem (Schema Theorem), and in 1975 published the first systematic exposition of genetic algorithms and artificial self-adaptive systems monograph "Adaptation in Natural and Artificial Systems" [5].

This genetic algorithm to association rule mining is proposed to extract association rules using genetic algorithm approach, and discuss genetic algorithm encoding method and fitness function construct genetic operators improvements. Currently based on genetic algorithm method for data mining, research focuses on aspects of the classification system. For the extraction of association rules, the application of genetic algorithm is also less.

Basing on the research of data mining, this paper brings forward a data-mining method base on genetic algorithm (GA). In order to understand genetic algorithm preferably, this paper deeply comments genetic algorithm, introduces the history of genetic algorithm research, recently condition of research, main concept and main process of genetic algorithm. In the same time, this paper introduces tow basic concepts of genetic algorithm: schemata theory and implicit parallelism, importantly, this paper analysis the implement of data mining basing on genetic algorithm. According with the differences of associate rule, this paper improves the construction of function of fitness, coding method of data, crossover operator, selection operator, and mutation operator and so on. Especially, basing on the research of inadequacies of evaluation, this paper put the algorithm of improved adaptive P_c, P_m in use. At last, this paper brings forward an algorithm of mining of associate rule base on genetic algorithm and prove its effective by an example.

2. Algorithm Improvement

Genetic algorithms as an effective global search tool parallel optimization has long been accepted by many applications, it is in the application of data mining has also been a great deal of attention. Genetic algorithm is applied to decision tree classifiers and fuzzy rules for other aspects of the emerging literature, so genetic algorithm is an important area of data mining research.

Genetic algorithms to solve the problem because of its chaotic, random and non-linear characteristics are typical for other science and technology can't solve complex problems difficult to solve or provide a new computing model. For large amounts of data characteristic of post mixed disorder, genetic algorithms are effective methods to solve such problems.

Genetic algorithms simulate natural evolution generic global search algorithm, the search process to avoid local optima, with the rules of discovery in a hope to find really useful rules.

The main subject is the study of genetic algorithm to association rule mining is proposed to extract association rules using genetic algorithm approach, and discuss genetic algorithm encoding method and fitness function structure and improvement of genetic operators and other issues. Given based on genetic algorithm of association rules extraction algorithm.

Currently based on genetic algorithm method for data mining research focuses on aspects of the classification system. For the extraction of association rules, the application of genetic algorithm is also less. The topics proposed using genetic algorithms for mining association rules, not only in association rule extraction methods, a new attempt. But also for solving practical problems related to a new approach.

First, let us take it and several major traditional search methods to make a brief comparison. Genetic algorithms in order to see where strong robustness in the end? As a search method. Its superiority in the end reflected in where?

Analytical method is commonly used search methods. It is normally the gradient of the objective function by solving a set of linear equations of zero to be searched. In general, if the objective function continuously differentiable. Solution space equation is relatively simple, analytical method can still be used. However, if the equation there are thousands or hundreds of variables when it powerless. Climbing method is also commonly used search method. It belong to the same analytical method and find local optimal solution method for climbing purposes of the law. Only in a better solution in the vicinity of the current solution under the premise that in order to continue to search for optimal solutions. Obviously this method has a unimodal distribution for the nature of the solution space in order to conduct an effective search. And get the optimal solution, and for multimodal space, climbing method (including analytical method) even local optima are rare to the root.

Another typical exhaustive search method is that the method is simple, the search space in a continuous or discrete infinite limited search space, the calculation of each point in space is the objective function value, and calculate a time. Obviously, the low efficiency of this method is not strong robustness. Many practical problems are large search space corresponds, not solved slowly little by little.

Random search method compared to an improvement of the search method, is a commonly used method, but it is still not high search efficiency. Generally, the only solution is formed compact in the search space distribution, its search to be effective, but this condition is difficult to meet in practice. It should be noted that we have the random search method and randomization techniques to distinguish. Is the use of a genetic algorithm to guide the randomization technique an efficient encoding parameter space search method. And the other search methods - simulated annealing (simulated annealing) method is the use of randomization techniques to guide the search for the minimum energy state. Thus, randomized search technique does not mean no search direction, which is different from the random search.

The advantage of GA:

1) Genetic Algorithm for Solving Complete Works from the start the search, rather than start from a single solution.

2) The use of genetic algorithm paucity of information on specific issues, easy to form a common algorithm.

3) Genetic algorithm has strong fault tolerance

4) Genetic algorithm selection, crossover and mutation operation are random, rather than determine the precise rules.

5) Genetic algorithm has implicit parallelism can be massively parallel computing to speed up calculations.

6) For the genetic algorithm optimization function to be basically unlimited, it neither requires a continuous function, but does not require the function differentiable; mathematical expression can be both expressed an explicit function, but the mapping matrix and even neural networks implicit function, and thus wider range of applications.

7) Is more suitable for large-scale genetic algorithm optimization of complex problems.

The disadvantage GA:

1) Genetic algorithm is easy to premature convergence.

2) Because of the variability of the individual optimal solution is easy to eliminate.

3) Not to determine the population size, too small is bad, too converges very slowly.

Association rule discovery problem is that in a given set of transactions to produce all meet the minimum support and minimum confidence association rules in the process. Therefore, for the characteristics of this association rule mining on the basic genetic algorithm improvements made the following basis.

2.1. Coding and Improvement of the Fitness Function

Based on the characteristics of mining for association rules, this article makes the following improvements on genetic algorithm.

1) Coding.

We use a coding method of an array of real numbers because of the genetic operators, association rule mining and project needs. This encoding method has high precision, easy space advantage of search, and most importantly related to this issue, implement relatively simple. In the process of encoding method use an array of real numbers. The number of elements of an array of real numbers corresponds to the number of fields in a database with a transaction, and real numbers elements of an array value represent the property value for the filed.

We use an array of N tuples to represent such as transactional database that is shown on individual coding. A [1] indicates that the Field 1, and A [2] indicates that the Field 2, and A [n] indicates that the field N; and we property value expressed as a numeric value, for example, we use the Value 1 indicates that the attribute Value 1, and use Value 2 indicates that the attribute Value 2, and use value E indicates that the attribute Value E, so we can use array A [N] element value to represent the property value for the filed that corresponds to. At the same time, we need to use the Value 0 indicates that the property is not associated with other properties.

2) Calculation of individual fitness.

In the evolution of genetic algorithms in search generally does not require other external information, but only requires fitness function with values to access the merits of the individual or solutions, and the genetic algorithms as the basis for later genetic manipulation. On its only requirement is that the input can be calculated can be non-negative result of the comparison. In special issues, the design of the fitness function should be connected with the question.

For the mining association rules based on genetic algorithm, support is a measure of the importance of association rules. We consider support of association rules to define its fitness function. And such we can filter the rules. First with support to filter rule, and then meet the minimum level of support set out in the rules of its associated and relevance. So the adaptation of the rule values such as (1)

$$fitness(R_i) = s'/s\begin{cases} p & s' > s \\ q & s' < s \end{cases} \tag{1}$$

In the formula, *S'* to go through genetic manipulation in support of the formation of a new rule, and *S* given threshold of support for the user. When the R_i to meet the requirements of the rule, its Adaptive function value should be greater than 1; Otherwise the adaptability function value will be less than 1, so this rule will be eliminated in the next - generation genetic.

2.2. The Application of the Improved Adaptive P_c and P_m

This article provides an analysis of a new population of "precocious" evaluation indicators, and finally combining genetic algorithm with adaptive adjustment of control parameters of the mind, have come up with a modified adaptive genetic algorithm. Experimental results show that the algorithm can not only speed up the speed of genetic evolution, but also enhanced global convergence algorithm performance, to be satisfied with the globally optimal value.

Early evaluation index. Set t's population made up of individuals $X_t^1, X_t^2, \ldots\ldots, X_t^M$, fitness respectively $F_t^1, F_t^2, \ldots\ldots, F_t^M$, and population average fitness of the individual.

$$F_{av} = \frac{1}{M}\sum_{i=1}^{M} F_t^i \tag{2}$$

Optimum fitness for the individual $F_{\max}, \overline{F_{t\max}}$, fitness is greater than the average fitness of the F_{av} individual representative, defines the difference between $F_{\max}$ and $\overline{F_{t\max}}$:

$$\Delta' = F_{\max} - \overline{F}_{t\max} \tag{3}$$

So the index Δ' it can be used for characterization of population "premature" level.

Improved P_c and P_m Adaptive Algorithm

Crossover probability and mutation probability of genetic algorithms convergence performance has a material effect. We describe P_c and P_m Adaptive Algorithm as follows: First, when the Group's largest fitness F_{max} and fitness F_{av} approached the Group tends to average convergence then should be increased P_c and P_m, Otherwise, strong group diversity, should be reduced P_c and P_m, that means P_c and P_m is inversely proportional to the value of (F_{max} - F_{av}). Secondly, to prevent the good gene structure is compromised, must make fitness solution for smaller P_c and P_m, so that fitness is larger P_c and P_m, and small solutions, P_c and P_m, proportional to the value (F_{max} - F_{av}). In the following, for a time X_1 involved in crossover operation of larger of the two individual fitness, Y fitness to participate in the variation of the individual.

$$P_c = \begin{cases} P_c * \dfrac{F_{\max} - X_1}{F_{\max} - F_{av}} & X_1 > F_{av} \\ P_c \quad X_1 < F_{av} \end{cases} \tag{4}$$

$$P_m = \begin{cases} P_m * \dfrac{F_{\max} - Y}{F_{\max} - F_{av}} & Y \geq F_{av} \\ P_m \quad Y < F_{av} \end{cases} \tag{5}$$

Type (4) and (5) showed that the smaller the (F_{max} - F_{av}) reach, Groups reach likelihood of local optimization, and greater the likelihood of early, let P_c and P_m the larger, to enhance the Group's ability to produce new individual. On the other hand, the larger the (F_{max} - F_{av}) reach, the population divergence, then should lower P_c and P_m to improving the convergence of individual capacities, to maintain its convergence, we should let P_c and P_m and (F_{max} - F_{av}) is inversely proportional.

2.3. Improvement of Genetic Manipulation

1) Selecting (copy) operation

Fitness proportional selection mechanisms used in this article and the best individual retention mechanisms with the collection of methods. First fitness value to individual selection probability proportional to copy individual, set group size M, individual i fitness value of f_i, then i selected the probability is

$$P_{s_i} = f_i / \sum_{j=1}^{M} f_i \tag{6}$$

Select full, we can let the next - generation compared to the best of the best individual and parent individual, full of individual institutions to adapt to most of them copied to a new generation.

2) Interlace Operation

This article uses one cross: Individuals will be selected in the previous step out for pairs, and with the probability of a random set in each individual P_s cross point. Consider before or after the point part of the structure of two individual swaps to generate a new individual. For example,

Pairing individual A 1001|111-→1001000 new individual A

Pairing individual B 0011|000-→0011111 new individual B

Crossing points are located in between the fourth and fifth loci. Intersections are random set. When L is length of the chromosome may have L-1 Cross and the location. One point cross may implement L-1 different cross results.

3) Mutation in Operation

Mutation

This article is based on the improved method of uniform variations. We use the mutation operator is designed for:

Consider to a certain mutation probability random variations in the populations of individual. After you select it, turn it at every level of the individual loci variation, and gene's is in its turn within the range of allowed values. So this mutation in turn ensures that after each property values will exist.

2.4. Algorithm Description

GA program design should take into account the versatility, but also have a strong ability to adapt to the new operator. Class inheritance in OOP provides us this possibility.

The following Fig.1 shows the improved genetic algorithm flow graph.

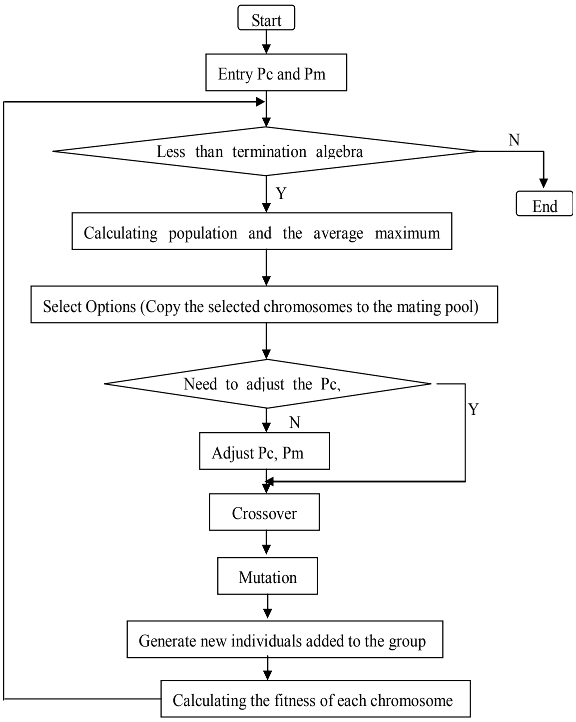

Fig. 1. Improved genetic algorithm flow graph.

Define two basic structure: gene (ALLELE) and individual (INDIVIDUAL), with a collection of individuals as a group class Tpopulation data members, and there are groups TSGA derived class, which defines the basic operation of the GA. For any one application can be derived in TSGA class, and define a new operation.

Tpopulation class contains two important processes:

Fill Fitness: evaluation function for each individual decoding (decode) and calculate the fitness value.

Statistic: the current population statistics, such as for the overall fitness sumfitness, average fitness average, the best individual f_{max}, the worst individual f_{min} and so on.

TSGA class Tpopulation derived on the basis of class to the GA system parameters as constructor arguments; it has four important member functions:

Select: Select the operator, the basic model selection strategy using roulette. Any rotation of the wheel is stopped by the pointer region is selected; the fitness value of the individual large probability of being selected is large.

Crossover: crossover, crossover probability in the two genes in a random position on chain exchange string.

Mutation: mutation operator to chain gene mutation probability for each gene random interference.

Generate: the next generation, including evaluation, statistics, selection, crossover, mutation and so the whole process, each run once, resulting in a new generation.

GA structure and class defined as follows: (written in C + +):

```
Typedef char ALLELE;
Typedef struct{
ALLELE * chroom;
Float fitness;
} INDIVIDUAL;

class Tpopulation:public BackProp{
public:
int size;
int lchrom;
float sumfitness, average;
INDIVIDUAL * fmin, * fmax;
INDIVIDUAL * pop;
Tpopulation(int popsize, int strlength);
~Tpopulation ();
inline INDIVIDUAL & Individual (int i){return
pop[i];};
void FillFitness ();
virtual void Statistics ();
};

class TSGA: public Tpopulation{
public:
float pcross;
float pmutation;
int gen;
TSGA (int size, int strlength, float pm, float pc);
Tpopulation (size, strlength)
{gen=0; pcross=pc; pmutation=pm;};
virtual INDIVIDUAL & Select ();
virtual void Crossover (INDIVIDUAL &
parent 1, INDIVIDUAL & parent 2,
INDIVIDUAL & child 1, INDIVIDUAL &
child 2);
virtual ALLELE Mutation (ALLELE alleleval);
virtual void Generate ();
};
```

3. Applications

Based on Bohai seawater samples database, this article set up an association rules mining system, and through the establishment of the system of seawater samples in information management and analysis, in which application of association rule mining algorithm based on genetic algorithm for data mining. Look forward to the establishment and implementation of systems to help related departments manage seawater information. And also in the seawater information from related departments, the mining association rule has practical significance;

you can use these rules to guide the industry, manufacturing and life, and makes recommendations for them.

3.1. System Design

Through top-down hierarchical analysis, we will divide the entire association rule mining system is shown in Fig. 2 modules. The following will detail the function of each module.

The main modules are described as follows:

Information Query Module: provides standard information query.

Information modification module: according to user permissions to the user the appropriate modification.

Security Maintenance Module: change user permissions, passwords.

Rule mining modules: the focus of this study, the application of genetic algorithm based on association rule mining algorithm for data mining.

Rule output modules: including general information output and output association rules in two parts.

3.2. Data Preprocessing

There are many database incomplete data sets, therefore, for the data collected from the database must have a series of initialization processing.

First, the missing value for processing, where the main use: Ignore tuples and be filled with the most common value. For a large number of vacancies attribute value tuples ignore deleted, but for only a small amount of vacant property value tuples to fill.

Secondly, the number of data conversion, the different attribute values with the corresponding interval integers instead.

Then, the processed data set is similar to adding a key attribute of the ID attribute, ID attribute's primary role is to distinguish between any two records in the dataset, a record corresponds to an ID value, any two record ID values are not repeated. Such as: In a 3000 recording of the data set, ID value field is 1-3000.

After the database tables data extraction, we get the following Table 1, that as the basis for mining of association rules.

Table 1. Mining Table.

Field Names	Data Type	Explanation
FLQD	String	Storm intensity
TMD	String	Water transparency
YYY	String	Nutrients
WSW	String	Microorganism
YPH	String	Oxygen balance
SYYT	String	Water Usage

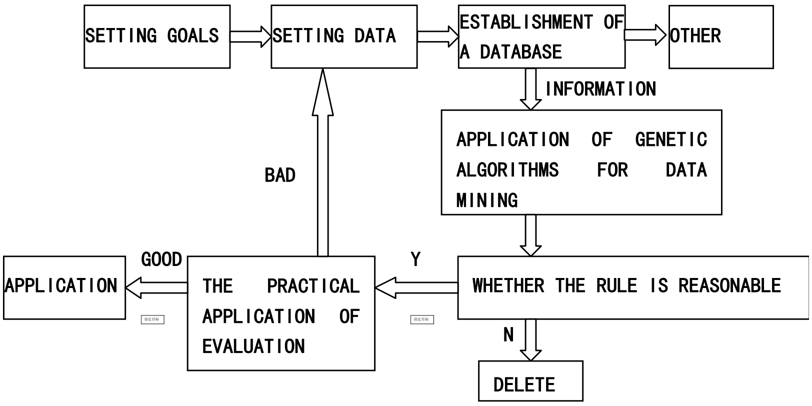

Fig. 2. Overall system flow chart.

3.3. Genetic Algorithm Coding

According to the actual needs of the algorithm, the storm intensity is divided into: high, medium and low three cases, the field values are shown in Table 2 and the corresponding coding; transparency into the sea: high, medium and low three cases, the field values and the corresponding coding Table 3; the water use categories are divided into: Aquaculture, living area, three cases of industrial water, field values are shown in Table 4 and the corresponding coding; nutrients, microorganisms, oxygen balance factor of three kinds of numerical rounding, according to the standard record field Table 5 the corresponding code value.

Table 2. Storm intensity field.

Field	Corresponding coding
HIGH	1
MIDDLE	2
LOW	3

Table 3. Water transparency field.

Field	Corresponding coding
HIGH	1
MIDDLE	2
LOW	3

Table 4. Water Usage.

Field	Corresponding coding
HIGH	1
MIDDLE	2
LOW	3

Table 5. Nutrients.

Field	Corresponding coding
HIGH	1
MIDDLE	2
LOW	3

Table 6. Microorganism.

Field	Corresponding coding
HIGH	1
MIDDLE	2
LOW	3

Table 7. Oxygen balance factor.

Field	Corresponding coding
HIGH	1
MIDDLE	2
LOW	3

In the actual process of encoding, the encoding for each field we added a "0", O means that this property is not associated with other attributes (such users do not associate with other items). Application of Genetic Algorithm in constraints randomly generated rules, such as rules generated 03, 400, 23, 455 and 23, 431 are examples covered by the rule, and not by the rule examples 34432 covered. In addition, in this paper, the rounding of the encoding process is named field.

If necessary, classification merge too small to delete the unwanted field, and the attribute data in the Table 8 the correspondence relation according to the above mapping results are as follows:

Table 8. Mapping Results.

xh	FLQD	TMD	YYY	WSW	YPH	SYYT
0202001	1	1	3	3	1	1
0202002	1	2	2	2	1	3
0202003	2	2	3	3	3	3
0202004	2	2	2	3	2	2
0202005	3	2	1	1	3	2
……	……	……	…	……	…	……

In order to facilitate the operation, use an array of real numbers to encode genetic operators. For such a code, the crossover and mutation operation becomes the operation of the array. Correspondence between the array and the field are shown in Table 9.

Table 9. Correspond Relations.

FLQD	TMD	YYY	WSW	YPH	SYYT
A[0]	A[1]	A[2]	A[3]	A[4]	A[5]

3.4. Setting the Operating Parameters

Genetic algorithms need to select individual parameters are encoded string length L, population size M, crossover probability P_c, mutation probability P_m, terminate algebra T.

Class code length L: coding of L monitor on the length and the coding methods used. In this paper, the length is equal to the number of code to related fields in the database, it is to find the relationship between the 8 fields in a table, so L=8.

Population size M: population size M denotes the number of groups contained in the individual. When M whichever is less, it can improve the computational speed of genetic algorithm, but reduces the diversity of the population, may cause genetic algorithm premature; when M's, whichever is greater, it will make the operation efficiency of genetic algorithm. So integrate these two factors and consider. The topics selected as the initial population 100.

Crossover probability P_c: genetic algorithm crossover operation is the main method of generating new individuals, so the crossover probability should generally be whichever is greater, but if too large, it will undermine the group's excellent model for evolutionary computing adversely affected; if we take value is too small, resulting in slower new individual. In this selection the initial crossover probability is 0.8.

Mutation probability P_m: variant determines the diversity of species. However, if the mutation probability bit too large, although able to produce more new individuals, but may undermine a lot better model, making the performance of GA approximate random search algorithm performance; if the mutation probability is too small, then the variation operation produces a new individual capabilities and the ability to inhibit the premature poor, the algorithm selects the initial mutation probability is 0.05.

3.5. Algorithm Description Based on Genetic Algorithm Association Rule Mining

Step 1: Initialization.

1) Generate a random initial population $P = \{\}$.

2) Get the support given by the user *S*, credibility *C*.

Step 2: The current population *P* is calculated for each individual fitness value, F (A) = S'/S; based on the individual fitness value filter: If F (A) > 1 is retained into the next generation of the rule otherwise, the deletion, and calculate the number of individuals retained M.

Step 3: According to the adaptive and principles, determine whether you need to adjust and make the appropriate action.

Step 4: If M < N is randomly generated (NM) individuals, otherwise skip to Step 3.

Step 5: Initialize the mating pool M and offspring Q, M =; Q =.

Step 6: Copy for i = 1 to v do

The current population of all individuals are copied to the mating pool, M = MUA.

Step 7: Cross for i = 1 to v / 2 do

M from the mating pool randomly select individual A' and A", in a crossover probability cross, M = M-(A', A").

Q = Q ∪ (A ', A" in accordance with the probability of crossing the offspring).

Step 8: Variation in the current population mutation probability of selection according to the mutation operation M individuals.

Step 9: Algebra terminated with the termination condition is determined by comparing the termination condition is reached, then the termination, and outputs the result; otherwise go to Step 2.

Step 10: For rule extraction.

3.6. Equations

Rule 20200030 noted that 86 % of water samples showed that aquaculture areas storms and medium strength, microbes, 56 % support for this situation in the actual proportion of high waters; rule 00030003 with 90 % transparency poor seawater oily factor more, 2 % support is because of their poor transparency relatively small percentage of the sample's sake; rule 00100330 Description waves small marine waters nutrient content of many factors, microbial content of many; 00303000 Description waves large marine waters of oxygen content and balance factor, but supports only 2 %, indicating that the share of such samples lower proportion of samples; rule 30020300 Description seawater poor transparency majority of industrial water, nutrient content of many factors. These applications show that the algorithm is effective.

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