An Improved Immune Genetic Algorithm for the Optimization of Enterprise Information System based on Time Property

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Abstract-In order to optimize enterprise information system's structure and improve its performance, this paper deals with the structure optimization problem based on an improved immune genetic algorithm (IIGA). First, a new immune genetic algorithm (IGA) is proposed, i.e., IIGA, which can overcome traditional genetic algorithm (GA)'s deficiency of slow convergence. In the new IGA, Niche algorithm is used to accelerate convergence speed, and measures such as convergence function, and "noise" chromosome are proposed to avoid Niche algorithm's deficiency of premature convergence. Then the structure and time property of enterprise information system (EIS) are discussed. And then optimization model of EIS structure is given. Finally, the IIGA and its application in EIS structure optimization are exemplified, and by comparing with self-adaptive Genetic Algorithm (SAGA) and traditional GA, the results verified IIGA's better convergence speed and optimization ability.

Index Terms—Niche Algorithm, Improved Genetic Algorithm, Enterprise information system, Structure optimization

I. INTRODUCTION

At present, various information systems in different enterprises have played increasingly important roles in the field of management and decision-making. So far, the corresponding research effort can be summarized as follows: researches on enterprise information system (EIS) mainly focus on the following aspects: (1) applications of information system in different fields, i.e., researches on various information systems' design and implementation. (2) integration of information systems with different technologies^[1-3]</sup>. (3) sub-technologies of EIS^[4-5]. (4) the property of EIS^[6-8]. As an example of (2), Li Qing^[3] studied the integration of workflow technology and EIS. In terms of (3), Heiner S^[5] studied check, aggregation and visualization of metadata in EIS. In terms of (4), Xue C G^[7] studies on EIS's reconfiguration property, and proposes a reconfiguration method for complex system

based on Agent and knowledge mesh (KM). Oyenan W H^[9] has studied the design and performance evaluation method for multi-Agent information systems.

Although there are many studies on EIS, there are few studies on its properties, especially time property optimization. Now studies on time property mainly focus on time performance evaluation approaches in workflow models and quantitative analysis^[10-12]. Even if there are researches on time property optimization, they mainly focus on software fields^[13], which can provide references for study on time property in EIS. However, differences exist between software and EIS on time property. First, although EIS is implemented though software system, EIS also includes key contents such as business process. Second, software system's environment means operation carrier and development platform, while EIS's environment means external market, policies and internal operation environment. So there are large differences between EIS and software system on main body and environment. Therefore, it's necessary to further study properties of EIS.

In order to improve EIS's time property, it's necessary to study its optimization method. Now studies on system performance optimization mainly focus on aspects as follows: (1) applications of the operations research to the manufacturing system, software field^[14-15], and so on. (2) studies on various optimization algorithms^[16-17]. As examples of (1), Xue Chaogai^[14] studies on automatic construction of the knowledge mesh, based on the user's functional requirement. Guseletova^[15] studies on the optimization with logical constraints for design of complex products. In terms of (2), Yannis Marinakis^[16] uses multi-swarm particle swarm optimization algorithm to solve the probabilistic traveling salesman problem. All these researches have gained remarkable achievements, and they can provide references for time property optimization.

So far, Genetic algorithm based on immune mechanism has become the new focus of this field. Compared with traditional GA, IGA's memory function can accelerate the search speed, shorten search time, thus can save the cost.

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IGA can overcome familiar premature phenomenon to a great extent, but it still has some deficiencies. For example, its convergence cannot meet the expected target. Fortunately, there are many ways to improve the deficiencies of IGA, such as promoting and inhibiting antibodies by calculating individual's affinity and concentration, taking similarity and vector distance as selection probability^[18-21], and so on. However, all these methods can effectively avoid premature phenomenon, but cannot get a better solution to convergence speed. For example, reference [19] can realize antibodies' self-adjustment and ensure population diversity, but cannot solve the problem of speeding up convergence speed. Reference [20] can accelerate convergence speed effectively, but there are limitations when applied in practice.

Niche algorithm has the advantage of fast convergence, and has been integrated in many optimization algorithms, such as the combination of Niche algorithm and Ant algorithm^[21], and the combination of Niche algorithm and Particle Swarm Optimization algorithm^[22], which have been successfully applied in fields of job scheduling and robots. However, Niche algorithm also has the deficiency of too fast convergence, which can lead to premature phenomenon. Thus, it needs to be improved. In this paper, Niche algorithm is introduced into IGA to speed up convergence. By introducing adjusting fitness and convergence function, Niche algorithm is improved. And the self-adaptive operators are also adopted. All these improvements can overcome traditional GA's slow convergence, premature convergence and Niche algorithm's too fast convergence. And the improved algorithm can solve structure optimization problems in EIS.

The paper is organized as follows. The basic idea and procedure of IIGA are introduced in section II. The structure forms of EIS and definitions of time properties are given in section III, then how to calculate time property for each structure form are discussed. In addition, the structure optimization model of EIS is also given in this part. As an example, the corresponding results and analysis are included in section IV. Finally, the conclusions of this paper are presented in section V.

II. IMPROVED IMMUNE GENETIC ALGORITHM

A. Immune Genetic Algorithm

Immune system is the defensive structure that body protects itself. It can detect and remove foreign bodies and factors, which fluctuates internal environment. After a series of process, pathogenic microorganism is cleared, in order to protect the body from attacks by viruses, bacteria and so on. The working mechanism of immune system enlightens scholars to have its ideas used in GA. i.e., immune genetic algorithm.

IGA is an improved algorithm based on biologic immune mechanism. It has functions of self-adaptive recognition, learning from biologic immune system and excluding foreign bodies. In the process of solving practical problems, objective function and constraints are input as antigen, then initial antibody population is generated. Finally, after a series of genetic manipulation, the antibody against the antigen, which is optimal solution to the problem, is obtained.

Compared with genetic algorithm based on immune principle and standard GA, IGA has the following advantages: (1) immune memory function; (2) maintaining antibody diversity function; (3) self-adjustment function. So IGA has its own unique advantages, while maintaining traditional GA's feature of global parallel search. Therefore, studies on IGA have important guiding significance.

B. Improved Niche Algorithm

When fitness in IIGA is calculated, Niche algorithm can be used to select the best chromosome, and maintain the diversity of population. Improvements proposed in this paper are as follows:

1) Adjusting fitness

Each fitness is adjusted according to (1).

$$sh(d) = \begin{cases} 1 - \frac{d}{\sigma_{share}} & d \le \sigma_{share} \\ 0 & d > \sigma_{share} \end{cases}$$
(1)

Where σ_{share} is the radius of Niche, and generally $\sigma_{share} = 0.1$; d is calculated according to (2).

$$d = \frac{d(opi, opj)}{m \times popsizel}$$
(2)

Where d(opi, opj) is the *Hamming* distance between opi and opj, m is the number of genes in each chromosome, popsize1 is the number of chromosomes in each sub-group. Then the new method of calculating fitness is shown in (3).

$$\varepsilon(x_{opi}) = \frac{\varepsilon'(x_{opi})}{\sum_{opj=1}^{N} sh(x_{opi}, x_{opj})}$$
(3)

2) Introducing convergence function

To overcome Niche algorithm's deficiency of fast convergence, which leads to premature convergence, convergence function is introduced as follows.

$$f = \frac{\log(sum)}{\log(sum - 0.02)} \tag{4}$$

Where,
$$sum = \sum_{opj=1}^{N} sh(x_{opi}, x_{opj}).$$

3) Excluding "noise" chromosomes

To prevent "degradation" phenomenon, "noise" chromosomes will be excluded.

Definition 1. The chromosomes with fast convergence in continuous several generations are regarded as "noise" chromosomes, and will be excluded from the alternative chromosome set.

C. Self-adaptive operators

In order to avoid the crossover and mutation probability's dependence on the initial value, the following improvements on the probability are proposed.

1) Self-adaptive crossover probability

$$p_{c} = \begin{cases} p_{c1} - \frac{(p_{c1} - p_{c2})(\varepsilon' - \varepsilon_{avg})}{\varepsilon_{max} - \varepsilon_{avg}} & \varepsilon' \ge \varepsilon_{avg} \\ p_{c1} & \varepsilon' < \varepsilon_{avg} \end{cases}$$
(5)

Where, $\varepsilon_{\rm max}$ is the best fitness in current population, $\varepsilon_{\rm avg}$ is the average fitness in current population, ε' is the greater fitness of the two crossover individuals, and generally $P_{\rm c1} = 0.9$ and $P_{\rm c2} = 0.6$.

2) Self-adaptive mutation probability

$$p_{m} = \begin{cases} p_{m1} - \frac{(p_{m1} - p_{m2})(\varepsilon_{avg} - \varepsilon)}{\varepsilon_{max} - \varepsilon_{avg}} & \varepsilon \ge \varepsilon_{avg} \\ p_{m1} & \varepsilon < \varepsilon_{avg} \end{cases}$$
(6)

Where, ε_{max} is the best fitness in current population, ε_{avg} is the average fitness in current population, ε is the fitness of mutation individual, and generally $P_{m1} = 0.1$ and $P_{m2} = 0.001$.

Self-adaptive crossover and mutation probability can improve genetic operation's efficiency and accelerate convergence speed.

D. Flow of IIGA

Based on the improved Niche algorithm, the process of IIGA is shown in Fig.1.

The steps of IIGA based on improved Niche algorithm are as follows:

Step1: Initializing the parameters of IIGA and generating initial population pop_0 (made up of *popsize* chromosomes).

Step2: Dividing population into q_s sub-spaces uniformly, which includes the following operations.

- (1) Calculating and adjusting fitness according to above (1) and (2).
- (2) Taking the first five optimal chromosomes as initial vaccine bank.

(3) Crossover operation. The P_c of any two chromosomes in pop_i ($i = 1, 2, \dots, s$) is calculated according to (3), then the pair with maximum P_m will be selected to perform crossover operation, and the first two optimal chromosomes will be reserved.

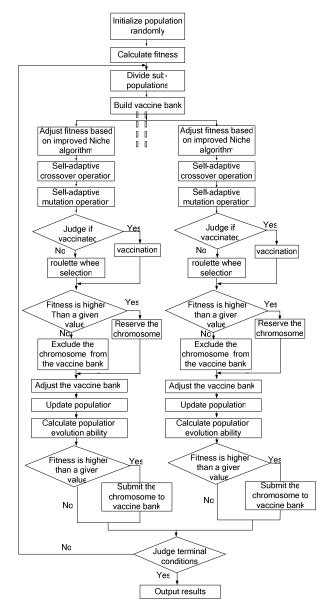


Fig.1 Flowchart of IIGA

- (4) Mutation operation. The P_m of each chromosome in pop_i is calculated according to (4), then the one with maximum P_m will be selected to perform mutation operation, and the optimal chromosome will be reserved.
- (5) Judging evolution generation, if the maximum generation is divisible by present generation, then one chromosome is selected from *pop_i*, and will be vaccinated. Or the chromosomes are selected via a

simulated roulette wheel selection. Here the chromosome's selection probability P_{opi} is in direct proportion to fitness value ε_{opi} , as in (7), and *popsize* chromosomes are selected from the current sub-population, and coped into its child population.

$$P_{opi} = \frac{\varepsilon_{opi}}{\sum_{opi=1}^{popsize} \varepsilon_{opi}} \quad opi = 1, 2, \cdots, popsize$$
(7)

- (6) Adjusting vaccine bank. When the chromosomes' fitness values are lower than a given threshold ϕ , then the corresponding chromosomes will be preserved, or will be excluded from the bank.
- (7) Updating sub-population and vaccine bank. Any chromosome's fitness is higher than a given value δ in *pop*_i, the corresponding chromosome is submitted to vaccine bank, and when the size of vaccine bank has been reached, the chromosome being submitted will replace the one with the lowest fitness in the bank.

Step3: After each sub-population is calculated in sequence, judging the present generation, if it's greater than the maximum generation, then end the process, else n = n + 1, and go to step 2.

Step4: End.

III. EIS'S STRUCTURE AND TIME PROPERTY

A. EIS's structures

Though the structure of information systems is various, there are four basic types of structure for them, i.e., sequential order, parallel order, selective order and circular order, represented by \rightarrow , \Rightarrow , \prec , \dashv respectively. The four structures are shown in Fig.2.

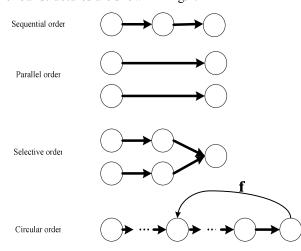


Fig.2 Enterprise information system's structure expression

These four structure types can be represented by the model as follows:

$$\mathbf{M} = S_1 \oplus S_2 \oplus S_3 \cdots \oplus S_n \tag{8}$$

Where $S_1, S_2, S_3, \dots, S_n$ represent sub-systems, n is the number of sub-systems, \oplus is the connection between sub-systems, and $\oplus \in \{\rightarrow, \Rightarrow, \prec, \downarrow\}$.

Assuming $S = \{S_1, S_2, S_3, \dots, S_n\}$, and $P_1, P_2 \in S$, then definitions are:

- (1) The sequential order of two points: $P_1 \rightarrow P_2$ and the order cannot be exchanged.
- (2) The parallel order of two points: $P_1 \Rightarrow P_2$ and the order can be exchanged, that's $P_1 \Rightarrow P_2$ equals $P_2 \Rightarrow P_1$.
- (3) The selective order of the two points: $P_1 \prec P_2$ and the order can be exchanged, that's $P_1 \prec P_2$ equals $P_2 \prec P_1$.
- (4) The feedback order of two points: $P_1 \downarrow P_2$ and the order cannot be exchanged. P_1 is the principle knowledge point, and P_2 is the feedback knowledge point.
- B. EIS's time property

Time property is the executing time of an event. To be mentioned, the event can be one or more, such as a process of order management, a process of raw materials into storage, etc.

Lemma: Assuming that X_1, X_2 are two independent random variables, and X_1, X_2 obey normal distribution, that is, $X_1 \sim N(\mu_1, \sigma_1^2), X_2 \sim N(\mu_2, \sigma_2^2)$ respectively, then $X_1 + X_2 \sim N(\mu, \sigma^2)$, and $\mu = \mu_1 + \mu_2$, $\sigma^2 = \sigma_1^2 + \sigma_2^2$.

(1) The equivalent property analysis of sequential order

Theorem 1. Assuming that time properties of n knowledge points obey sequential order, they are independent and obey normal distribution $N_1(u_1, \sigma_1^2), \dots, N_n(u_n, \sigma_n^2)$ respectively, so their average time properties are u_1, u_2, \dots, u_n respectively and the total

executing time is
$$\sum_{r=1}^{r} u_r$$
.

(2) The equivalent property analysis of parallel order

Theorem 2. Assuming that time properties of n knowledge points obey parallel order, they are independent and all obey the same normal distribution $N(u, \sigma^2)$. So their total time property is T approximately, as in (9).

$$T = \frac{n\sigma}{\sqrt{2\pi}} \int_{-\infty}^{+\infty} t \left[\Phi_0(t) \right]^{n-1} e^{-\frac{t^2}{2}} dt + \frac{nu}{\sqrt{2\pi}} \int_{-\infty}^{+\infty} \left[\Phi_0(t) \right]^{n-1} e^{-\frac{t^2}{2}} dt \quad (9)$$

(3) The equivalent property analysis of selective order

Theorem 3. Assuming that *n* knowledge points z_1, z_2, \dots , z_n obey selective order. The probability of selecting z_i ($i = 1, 2, \dots, n$) is $P\{I = z_i\} = \beta_i$, and the sum of β_i is 1. The execution times of z_1, z_2, \dots , z_n are $E(z_i)$ respectively. So the expected execution time of this selective relationship is E(Z), as in (10).

$$E(Z) = \sum_{i=1}^{n} \beta_i E(z_i)$$
(10)

(4) The equivalent property analysis of feedback order

Definition 2. Assuming that α is the probability of entering cycling process, $1-\alpha$ is the probability of exiting cycling process. α declines by $\Delta \alpha$ and $\alpha = n\Delta \alpha$. Commanding once per cycle, α declines by $\Delta \alpha$ while $1-\alpha$ increases $\Delta \alpha$. It doesn't exit the cycling process until α declines to zero and $1-\alpha$ increases to 1. Known from this definition, the cycling number n is determined by $\alpha / \Delta \alpha$, and $1-\alpha + n\Delta \alpha = 1$.

Theorem 4. Assuming that the execution time of knowledge points z_1, z_2 are two independent variables, and obey normal distribution $N_1(u_1, \sigma_1^2), N_2(u_2, \sigma_2^2)$ respectively. Assuming that after executing z_1 , the probability of returning to z_2 is α , and in one cycle, α declines by $\Delta \alpha$ while $1-\alpha$ increases $\Delta \alpha$, then the total execution time of these two cycling knowledge points is T, as in (11).

$$T = \sum_{i=1}^{n} \left[i \times (u_1 + u_2) + u_1 \right] \times P(I = i)$$
(11)

Where, P(I = i) is the probability of exiting cycling process after *i* times circulation.

C. The structure optimization model of EIS

As is known, system's structure determines its performance, and this paper optimizes enterprise information system's structure based on time property by IIGA. The model is shown below.

The EIS's structure representation is taken as a chromosome and coded. The objective is to obtain the optimal chromosome with best fitness, i.e., the least execution time. Thus, the objective function is shown in (12).

$$J = \min_{f_{in} \atop s \in s} \varepsilon \left(f_{mn} \left(x \right) \right)$$
(12)

Where, ε is the chromosome corresponding to EIS's execution time; f_{mn} is a fitness determined by the *n* th chromosome in the *m* th generation, which varies with the chromosomes; *x* is a chromosome, which is arranged by EIS's sub-system genes and operator genes alternately.

When optimizing the above model, real-coding method is adopted in this paper, and each chromosome (e.g., the chromosome is called A below) includes two types. One

type (e.g., called A_1 below) consists of sub-systems and connection methods, which are arranged alternately. The other (e.g., called A_2 below) is used to describe forcing operational sequence, which is a random permutation with numbers from 1 to n-1. What's more, the four types, i.e., $\rightarrow, \Rightarrow, \prec, \dashv$ are represented by 0, 1, 2, 3 respectively. The calculation method for each chromosome is shown in Fig.3.

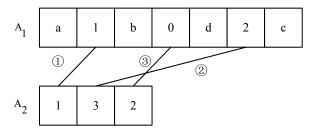


Fig.3 The representation of A chromosome

As in Fig.3, the chromosome is A_1 : a 1 b 0 d 2 c A_2 : 1 3 2 , when calculating fitness, the first operational symbol is calculated firstly, i.e., a 1 b, then the third operational symbol is calculated, i.e., d 2 c , and so forth.

IV. EXAMPLES

A. Example settings

There are ten sub-systems a b c d e f g h j k needed to be assembled in an enterprise information system, and the assembling ways are: sequential order, parallel order, selective order and circular order, which can be represented with 0,1,2,3 in sequence.

Assuming that the distribution each sub-system obeys is below:

Whatever method knowledge points are connected,

$$a \sim N(1, 0.1^2), b \sim N(2, 0.1^2), c \sim N(3, 0.1^2),$$

 $d \sim N(4, 0.1^2), e \sim N(5, 0.1^2), f \sim N(6, 0.1^2),$
 $g \sim N(7, 0.1^2), h \sim N(8, 0.1^2), j \sim N(9, 0.1^2),$
 $k \sim N(10, 0.1^2)_{\circ}$

To be mentioned, when the relationship between sub-systems is parallel order, the execution time property

is u_0 , which is the larger time value of sub-systems involved.

In the example, either two sub-systems or two sub-system modules are involved in each calculation, so the equation rules for time property calculation are: Rule1:

- (1) When the connection between two sub-systems is sequential, the equivalent time performance is $T_{m1} + T_{m2}$.
- (2) When the connection between two sub-systems is parallel, the equivalent time performance 0.2

is
$$\frac{1}{\sqrt{\pi}} + T_{\text{max}}$$
, and T_{max} is the larger value of T_{m1}

and T_{m^2} .

- (3) When the connection between two sub-systems is selective, the equivalent time performance $is \frac{1}{2} \sum_{i=1}^{2} T_{mi}$.
- (4) When the connection between two sub-systems is circular, the equivalent time performance $2T_{m1} + T_{m2}$. Rule 2:

The smaller final fitness value is, the better the result is.

The system combination way with the shortest running time should be optimized.

B. Experimental design and resultss

In the experiment, population size is 50, the maximum evolutionary generation is 200, $q_m = 5$, $P_{c1} = 0.9$, $P_{c2} = 0.6$, $P_{m1} = 0.1$, $P_{m2} = 0.001$, $\phi = \delta$ =10. The results of IIGA, SAGA and GA are shown in Fig.4 and Fig.5.

From the figures, such conclusions can be drawn: IIGA has faster convergence than SAGA and GA. Although there is oscillation phenomenon, "degradation" phenomenon can be effectively prevented by excluding "noise" chromosomes. What's more, SAGA and GA will be in "stalemate" state, IIGA can effectively avoid the occurrence of this phenomenon.

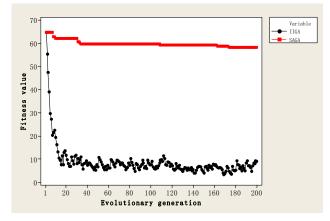


Fig.4 The comparison of SAGA and IIGA

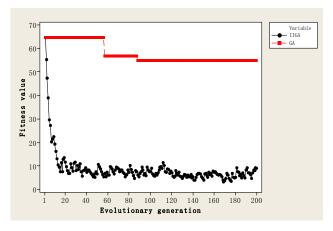


Fig.5 The comparison of GA and IIGA

C. Discussions

Each chromosome corresponds to a certain system structure. In this experiment, the final better chromosome is:

$$A_{1}: f 2 a 1 j 2 e 3 h 0 g 1 c 2 d 1 b 0 k$$
$$A_{2}: 6 1 9 2 4 8 5 7 3$$

So the corresponding system structure is:

$$((f \prec a) \Rightarrow j) \prec (((e \dashv h) \rightarrow (g \Rightarrow c) \prec (d \Rightarrow (b \rightarrow k))))$$

This structure can be described as follows:

- (1) g and c are connected in a parallel order, constituting module B1, i.e., B1 \Leftrightarrow g \Rightarrow c.
- (2) f and a are connected in a selective order, constituting module B2, i.e., B2 \Leftrightarrow f \prec a.
- (3) b and k are connected in a sequential order, constituting module B3, i.e., $B3 \Leftrightarrow b \rightarrow k$.
- (4) module 2 and j are connected in a parallel order, constituting B4, i.e., B4 ⇔ (f ≺ a) ⇒ j.
- (5) e and h are connected in a circular order, constituting B5, i.e., B5 ⇔ e, ⊥h.
- (6) d and module B3 are connected in a parallel order, constituting module B6, i.e., B6 ⇔ d ⇒ (b → k).
- (7) module B5 and module B1 are connected in a sequential order, constituting module B7, i.e., $B7 \Leftrightarrow (e \dashv h) \rightarrow (g \Rightarrow c)$.
- (8) module B7 and module B6 are connected in a selective order, constituting module B8, i.e., $B8 \Leftrightarrow (((e \dashv h) \rightarrow (g \Rightarrow c) \prec (d \Rightarrow (b \rightarrow k)))).$
- (9) module B4 and module B8 are connected in a selective order, i.e., the final better system structure ((f ≺ a) ⇒ j) ≺(((e⊥h) → (g ⇒ c) ≺ (d ⇒ (b → k))))

Such structure has less executing time, thus has better time property.

V. CONCLUSIONS

This paper mainly studied the improved immune genetic algorithm and its application in time property optimization of EIS, and the conclusions are as follows:

- (1) The improved immune genetic algorithm can ensure population's diversity, prevent premature phenomenon, accelerate convergence speed and improve the final performance.
- (2) The four structure forms in an information system are expressed. The expression is beneficial to understand the relationship and difference among them.
- (3) IIGA can solve optimization problems in information systems, and obtain better performance. In this paper, we mainly discuss optimization based on time property, and the final optimization system can meet needs. Structure optimization can reduce enterprise's time cost, so it can improve enterprise's competitiveness in the market.
- (4) To be mentioned, the method proposed in this paper, may be a preprocessing method before the system design when used in practice, but it can play a guiding role in enterprise system structure optimization. How to use IIGA in the whole designing process is one of our future researches.

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