

Adaptive genetic algorithm with the criterion of premature convergence

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Abstract: To counter the defect of traditional genetic algorithms, an improved adaptive genetic algorithm with the criterion of premature convergence is provided. The occurrence of premature convergence is forecasted using colony entropy and colony variance. When premature convergence occurs, new individuals are generated in proper scale randomly based on superior individuals in the colony. We use these new individuals to replace some individuals in the old colony. The updated individuals account for 30% – 40% of all individuals and the size of scale is related to the distribution of the extreme value of the target function. Simulation tests show that there is much improvement in the speed of convergence and the probability of global convergence.

Key words: genetic algorithm; premature convergence; adaptation

The genetic algorithm (GA) was proposed by inspiration from the theory of evolutionism, and it regards optimization as a process of evolution. In early 1960's, professor Holland in Michigan University first proposed the genetic algorithm^[1]. Recently, the GA has drawn lots of attention and has emerged as practical in engineering. But the GA still has some defects, such as ① Premature convergence cannot always get the most optimal result; ② Difficulty in confirming some important parameters such as the size of the colony, probabilities of crossover and mutation (P_c and P_m). These defects prevent the popularity of the GA.

To counter the defects of the GA, an improved adaptive GA with the criterion of premature convergence is provided. The results of tests show that there is great improvement in both convergence speed and the probability of global convergence, and it has a lower request in confirming P_c and P_m .

1 Principle of the Genetic Algorithm

1.1 Specialty of the genetic algorithm

Genetic algorithm is a search algorithm based on the mechanisms of evolution and natural genetics. It simulates the propagation, copulation and mutation in natural selection and natural inheritance. In detail, it regards each solution as one individual of a colony (the set of all solutions), and encodes each individual into string form. The GA evaluates each individual according to a preconcerted target function and gives

out a fitness value. Using selection, crossover and mutation operators, these new individuals inherit superior specialties from the previous generation and obviously are superior to them. During inheritance from one generation to another generation, each generation moves towards the most optimal solution.

Three operators of the GA express the evolution process of individuals. Selection is the process of selecting one new individual according to the fitness value of each one. The bigger the fitness value of the individual is, the bigger the probability of being selected is, and the number of its offspring is bigger too. Crossover selects one random position N on the gene codes of the parents using the probability P_c , then exchanges the code parts of two individuals that are behind the position. Mutation changes the value of one position with very small probability P_m randomly. The combination of three operators ensures that the whole algorithm can search every point of space and insure the global convergence of the algorithm.

1.2 Standard genetic algorithm and its defects

The standard genetic algorithm selects parents using the ratio-select mechanism. In general, the ratio-select mechanism suits the individual whose fitness value is much bigger than the others' in the colony. While during the anaphase of the GA, the distinctions among individuals are very narrow, and probabilities to individuals based on ratio-select mechanism are nearly equal; this prevents the generation of new individuals. So people propose a fitness-scale transform and individual selection method based on order. The fitness-scale transform uses a linear transform to adjust the fitness values of

Received 2002-07-01.

Foundation item: The Natural Science Foundation of Jiangsu Province (BK99011).

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individuals, and its purpose is to enlarge the distinctions among individuals. The method, based on order, orders the fitness value from small to big or vice versa, then selects parents according to the situation of ordering; its purpose is to save as many superior individuals as possible.

The standard genetic algorithm has two modes in crossover operation: one mode randomly selects one or two positions on the gene codes of individual. If one position is selected, the code parts of the two individuals behind this position will exchange; if two positions are selected, the code parts of the two individuals between the two positions will exchange. This operator has weak split power, but when the individuals in colony are similar to each other, it is hard to create new individuals with this method. So this method is generally used in large colonies. The other mode selects some bits using fixed probability and exchanges the codes on those positions. This operator has strong split power and helps to create new individuals. This method is used in small colonies generally.

Standard genetic algorithm changes the values on some positions using a fixed mutation rate in mutation operation. The value of the mutation rate is decided on the basis of the size of the colony^[2]. If the size is larger than 100, the mutation rate equals 0.001; if the size is smaller than 30, the mutation rate equals 0.01.

In prophase and anaphase of evolution, the specialties are not the same. While the standard genetic algorithm uses a fixed selection rate, crossover rate and mutation rate, all these are prone to cause premature convergence. So in the prophase of evolution, we take the individual mode into account and augment the crossover rate to abundantly combine existing modes. While in the anaphase of evolution, the distinctions among individuals are very narrow, and abundant recombination is not necessary. So in the anaphase of evolution, the crossover rate should be reduced and the mutation rate should be augmented to introduce new individual modes to avoid relapsing into the local min-point. Thus the crossover rate and mutation rate should be dynamic in the process of evolution.

2 Adaptive GA with Criterion of Premature Convergence

The adaptive genetic algorithm^[3] uses a dynamic crossover rate and mutation rate, and their values change with the schedule of evolution. In this algorithm, the individual whose fitness value is greater than the average value of the colony has a high crossover rate and a low mutation rate, and its purpose

is to combine excellent modes; the individual whose fitness value is smaller than the average value of the colony has a low crossover rate and high mutation rate, and its purpose is to introduce new modes. All these prevent the occurrence of premature convergence in some way. But if we want to further eliminate premature convergence, we must forecast the occurrence of premature convergence and update the individuals in the colony to ensure new individuals' entrances. So we propose an improved adaptive genetic algorithm with a criterion of premature convergence that can improve the ability of convergence to the global optimal point.

2.1 Criteria of premature convergence

Criterion 1 Big colony entropy can forecast the occurrence of premature convergence.

The occurrence can be forecasted by the diversity of colony fitness. Because the survival of the individual is in direct proportion to its fitness in the GA, so the diversity of individual fitness can be measured by the probability of individual survival. The probability of individual survival P_i is defined as

$$P_i = P\{X = i\} = f(x_i) / \sum_{j=1}^N f(x_j) \quad (1)$$

where $\{X = i\}$ expresses the event of "individual i will occur"; $f(x_i)$ expresses the fitness value of individual i ; N expresses the number of individuals in this colony. As formula (1) expresses, when the distinction among P_i is big enough, the probability of random variable X selecting the bigger one of P_i is high. That is to say, the uncertainty of X is small. And the uncertainty is big when the distinction among P_i , so the diversity of P_i is the embodiment of uncertainty of random variable X . According to information theory, we can use the entropy of information to measure the uncertainty of information^[4]. So we can use colony entropy to forecast the occurrence of premature convergence. Colony entropy is defined as

$$E(x) = - \sum_{i=1}^N P_i \ln(P_i) \quad (2)$$

Big colony entropy expresses the small diversity of colony fitness values. That is to say, individuals have close fitness values. So when E is big enough, we can consider premature convergence has occurred.

Criterion 2 Small colony variance can forecast the occurrence of premature convergence.

Variance can also reflect the distinctions among the individuals in the colony, so variance can also be used to forecast the occurrence of premature convergence. Variance E is defined as

$$E = \sum_{i=1}^N (f(x_i) - \bar{f})^2 / N \quad (3)$$

where $\bar{f} = \sum_{i=1}^N f(x_i) / N$. To simplify computation, the absolute value operator can be used to replace the square operator.

$$E = \sum_{i=1}^N |f(x_i) - \bar{f}| / N \quad (4)$$

When E shrinks consistently or maintains its value, premature convergence has occurred.

2.2 Treatment of premature convergence

The fitness values of individuals in the colony are close to each other when premature convergence occurs, and new individuals need to be used to skip the local min-point. We can use a high mutation rate to introduce new individuals, but this may introduce some inferior modes. So we generate new individuals in proper scale randomly based on superior individuals in colony. We use these new individuals to replace some individuals in the old colony. The updated individuals take 30% – 40% of all individuals and the size of scale is related to the distribution of extreme values of target function. If we can obtain the average distances among extreme values of the target function, we can use twice the average distance as a scale. According to our experience, 1% of the biggest scope of all variables contained in individuals can also be used as a scale. The results of tests show that this method is superior to standard method.

3 Analysis of Test Results

To evaluate this adaptive genetic algorithm, we compared 4 kinds of genetic algorithms to each other in tests and used 3 kinds of target functions to examine^[3,5].

1) Calm single-modal parabola function F_1

$$y = (x_1 - 2)^2 + (x_2 + 1)^2 \quad (5)$$

2) Sin-spreading function F_2

$$y = 0.5 + (\sin^2 \sqrt{x_1^2 + x_2^2} - 0.5) / [1.0 + 0.001(x_1^2 + x_2^2)]^2 \quad (6)$$

3) Multi-modal function F_3

$$y = 0.002 + \sum_{j=1}^{25} \frac{1}{j + \sum_{i=1}^2 (x_i - a_{ij})^6} \quad (7)$$

The four kinds of genetic algorithms used in tests are:

1) Simple genetic algorithm: Using fixed crossover rate and mutation rate, P_c between 0.8 and 0.85. To maintain the specialty of superior individuals

and to introduce new individuals, we use the following strategy to select the mutation rate: $P_m = 0.05$ when fitness value is smaller (target function F_1 , F_2) or bigger (target function F_3) than average fitness value or $P_m = 0.5$ vice versa.

2) Adaptive genetic algorithm: It uses dynamic crossover rate and mutation rate whose values change with the fitness value of the individual. In this method, the crossover rate is

$$P_c = \begin{cases} \sqrt{(f - f^*) / (\bar{f} - f^*)} & f > \bar{f} \\ k_1 & f \leq \bar{f} \end{cases}$$

and the mutation rate is

$$P_m = \begin{cases} (f - f^*) / (\bar{f} - f^*) & f > \bar{f} \\ k_2 & f \leq \bar{f} \end{cases}$$

3) Adaptive genetic algorithm with the criterion of premature convergence: It introduces the criterion for judging the premature convergence based on adaptive genetic algorithm. If no premature convergence occurs, method 2) is used; if premature convergence occurs, some individuals are updated in time.

4) Simple genetic algorithm with the criterion of premature convergence: Its strategy is similar to method 3). While no premature convergence occurs, fixed crossover rate and mutation rate are used.

In tests, to reduce the effect of the initial colony, we selected six different initial states. We used four algorithms to run each initial state twenty times. In each time, the repeated times were five hundred. We considered the average repeated times as the repeated times of this algorithm in such initial state.

The results are shown in Tab.1 – Tab.4.

Tab.1 Comparison on capability of target function F_1 influenced by different GAs (repeated times)

Initial state	Algorithm 1	Algorithm 2	Algorithm 3	Algorithm 4
1	8	14	25	5
2	> 500	> 500	17	5
3	> 500	17	13	20
4	> 500	18	14	11
5	> 500	> 500	25	23
6	> 500	> 500	8	8

Tab.2 Comparison on capability of target function F_2 influenced by different GAs (repeated times)

Initial state	Algorithm 1	Algorithm 2	Algorithm 3	Algorithm 4
1	91	89	20	17
2	27	20	5	17
3	62	115	53	23
4	75	105	11	35
5	120	184	29	16
6	50	36	28	20

Tab.3 Comparison on capability of target function F_3 influenced by different GAs (repeated times)

Initial state	Algorithm 1	Algorithm 2	Algorithm 3	Algorithm 4
1	129	94	28	53
2	> 500	91	32	8
3	120	> 500	12	68
4	120	367	41	29
5	> 500	38	72	80
6	201	8	54	44

Tab.4 Comparison on criterions of premature convergence

Initial State	Criterion	
	Colony entropy	Variance
1	20	40
2	5	8
3	53	10
4	11	17
5	29	26
6	28	23

According to the test results, we can obtain:

- 1) Comparison on repeated times of GA1, GA2 (Tab.1 - Tab.3) reflects that the use of a dynamic crossover rate and mutation rate can reduce the occurrence of premature convergence but can't eliminate this defect. Compared to the simple genetic algorithm with proper parameters, the speed of convergence has not been obviously improved.
- 2) According to the results of GA3, GA4 (Tab.1 - Tab.3), we can say that the method of introducing the criterion of premature convergence and updating individuals in time eliminates the possibility of premature convergence and obviously improves the speed of convergence. On the other hand, the selection of a crossover rate and mutation rate is not so important because the algorithm can detect the premature

convergence and update similar individuals in time to ensure the introduction of new individuals.

3) Tab.4 shows that colony entropy is a good method of measuring diversity of random variables. Colony entropy can be used to forecast the occurrence of premature convergence. And tests show that entropy can be replaced by variance as the computation of entropy is complicated. Using variance is a simple and efficient means forecasting of the occurrence of premature convergence.

4 Conclusion

To counter the defect of the traditional genetic algorithm, an improved adaptive genetic algorithm is proposed. The results of tests show that this algorithm can improve the speed of convergence and the probability of converging to a global optimal point. At the same time, it can eliminate difficulties in selecting a crossover rate and mutation rate.

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具有成熟前收敛判断的自适应遗传算法

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摘 要 针对传统的简单遗传算法的缺陷,提出了改进的具有成熟前收敛判断的自适应遗传算法. 用群体熵值和均方差来预报成熟前收敛的发生.当成熟前收敛发生时,提出以群体中的最优个体为基础,在其一定大小领域内随机产生若干个体,取代原种群中的部分个体,其中更新的个体数占群体中个体总数的 30% ~ 40%,领域大小与目标函数极值点分布有关.仿真实验证明,算法的收敛速度和全局收敛概率都有显著的提高.

关键词 遗传算法;成熟前收敛;自适应

中图分类号 TP183