演化式基因演算法應用於平行測驗之建構

An Evolutionary Genetic Algorithm for Parallel Test Construction

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Abstract

In this paper, we proposed a new approach "evolutionary genetic algorithm" that called improves the efficiency and the quality of the simple genetic algorithm (GA) in constructing parallel tests. The basic principle of this evolutionary genetic algorithm combines two theories. One is that of genetic diversity, which is beneficial to species evolutionary existence. The other is eugenic theory, which can increase the probability of finding better offspring. Experimental results show that our approach is much better than the simple genetic algorithm in terms of time efficiency and solution quality. The evolutionary genetic algorithm would be a more powerful tool than the simple genetic algorithm for parallel test construction.

Keywords: genetic algorithm, parallel test construction, time efficiency, solution quality.

本研究將提出一新的演算方法"演化式基因 演算法(evolutionary genetic algorithm)"應用於平 行測驗建構上。此演算方法主要結合兩個概念:即 生物多樣性(genetic diversity)以及優生學理論 (eugenic theor)。自然界中,生物多樣性有利於物 種演化綿延不絕;優生學概念則強調產生更佳的下 一子代。結合這兩個概念於本研究所提出之演化式 演算方法,其實驗結果顯示,此演算方法比起傳統 基因演算法具有更高的效率以及得到更佳的解。同 時也證明此演化式基因演算法將成為平行測驗建 構更有效的工具。

關鍵詞:基因演算法,平行測驗建構,時間效率, 解答品質

1. Introduction

In the past decades, test construction methods (Lord, 1953; Lord & Novick, 1968; Lord, 1980; Weiss, 1982; Hambleton & Swaminathan, 1985; Theunissen, 1985; Baker, Cohen, & Barmish, 1988; van der Linden & Boekkooi-Timminga, 1989) were simple and inflexible due to the lack in popularity of personal computers. Recently, related research (Luecht & Hirsch, 1992; Stocking, Swanson, & Pearlman, 1993; Armstrong, Jones, & Rutgers, 1996; Armstrong, Jones, & Kunce, 1998; van der Linden & Adema, 1998; Csöndes & Kotnyek, 2002; van der Linden, 2005; van der Linden, Ariel & Veldkamp, 2006) has proposed various techniques and methods construction successfully test due on to improvements in the efficiency of computers. However, since test construction is an NP-hard problem (van der Linden, 1998), the execution time presents exponential growth with growth in problem size. An efficient technique is still required to find better solutions. The genetic algorithm is based on the Darwinian Theory that has a powerful ability to find the optimal or near optimal solutions from a huge pool (Goldberg, 1989), and has also been designed to solve the parallel test problem (Sun, 2000), obtaining very good results. In this paper, we combine genetic diversity (Fisher, 1930; Hubbell, 2001) with eugenic theory (Barrett & Kurzman, 2004) to improve the efficiency and quality of the simple genetic algorithm for parallel test construction.

First, we briefly introduced the concept of parallel test construction by the simple genetic algorithm. To solve the parallel test construction problem by a genetic algorithm, we first transformed this problem into an optimized form. The formula of test information function can be represented by a linear math model as follows.

$$\begin{aligned} \text{Maximize} \quad O_{j} &= \sum_{i=1}^{n} I_{i}(\theta_{j}) \, x_{i}, \end{aligned} \tag{1} \\ \text{Subject to } k_{q} &\geq \sum_{i \in Cq} A_{i,q} x_{i} \geq k_{q}^{'}, q = 1 \sim p, \end{aligned}$$

where p is the number of total constraints, $A_{i,q}$ is the q^{th} content attribute value of item i, C_q is the q^{th}

constraint and k_q and k'_q are the constraint values.

When we want to construct a test, Eq. (1) would be maximized and would satisfy all constraints (Eq. (2)). However, in the construction of parallel tests, several tests need to be constructed and the deviation between them (the sum of squared errors) needs to be minimized. If we choose one of the parallel tests as a standard (denote by d_i), then the other test information (denoted by O_j) of the two parallel tests should have the minimum deviation from the standard test by using the following equation.

Minimize
$$E = \sum_{j=1}^{s} (d_j - O_j)^2$$
 (3)

Equation (3) would be used in the fitness function of the genetic algorithm.

The detailed steps of applying a genetic algorithm to create parallel tests can be described as follows.

First, set the initial population of chromosome strings X. Each chromosome string X^{k} represents a constructed test k, which contains n bits (n is the number of items in the item bank), among which, m bits are 1 and the rest are 0, for a test with m items. Each bit x_i represents whether an item is included or not in the test ($x_i=1$, Yes; $x_i=0$, No). For each chromosome, we can calculate the fitness function as follows:

$$fitness(X^{k}) = \sum_{j=1}^{s} (d_{j} - O_{j}^{k})^{2}, \qquad (4)$$

where O_j^k is the value of the test information function at ability level *j* for the k^{th} parallel test. The lower the fitness value (deviation) is, the better the result obtained. When constraints are considered, the *fitness*(X^k) is modified as in Equation (5):

$$fitness(X^{k}) = fitness(X^{k}) + r, \quad \text{if} \quad r \quad \text{of} \quad p$$

satisfie $\sum_{i \in C_{q}} A_{i,q} x_{i} > k_{q} \text{ or} \sum_{i \in C_{q}} A_{i,q} x_{i} < k_{q}$ (5)

where r is the number of constraints which have not satisfied the constraints in Equation (2). Then, complete the following genetic operations for generating P offspring from current chromosomes in the population.

(1) Two-point crossover operation: two offspring for each pair of parents are generated with the probability p_c . A section of the chromosome string in the offspring is the same as one parent and else is the same as the other parent.

(2) Two-point mutation operation: randomly select

some chromosomes with probability p_m from the population and randomly choose two positions. Mutation occurs when 0 is changed to 1 and 1 is changed to 0 in the selected chromosome, and it then becomes the offspring.

(3) Reproduction operation: the best chromosome string is found in the "parent" population having the reproduction probability p_r . These then become the offspring which make up the new population (also called elitism selection).

Repeat the above steps $(1) \sim (3)$ for generating n new chromosomes (tests) and replace the old ones in the population until a generated chromosome (solution) fits the expected result or the number of generations reaches the predefined value.

Finally, a chromosome (test) with the minimum deviation within the population would be the solution of the parallel test construction problem.

The simple genetic algorithm can deal with parallel test construction simply and easily with constraints and obtain very good results, but the efficiency and quality could be improved by the further inclusion of some useful theories. In this paper, we propose an "evolutionary genetic algorithm" to improve the test quality of evolution which combines two theories, genetic diversity and eugenic theory.

In a natural life system, there are similar or different characteristics making up each individual. This variation is the meaning of bio-diversity or 1958). polymorphism (Fisher, In general, bio-diversity is the basic characteristic of a life system, but diversity does not arise from natural selection. Most of the time, crossover and mutation are important processes in creating genetic diversity. Therefore, genetic diversity in the interlocking nature of the system guarantees species continuous evolution in natural selection and the species should evolve to fit with its environment more easily (Fisher, 1930).

We will apply the concepts of the above-mentioned theories to the simple genetic algorithm. The basic concept is to examine the diversity between two new offspring and compare that against the diversity between the new offspring and the chromosomes included in population. If the diversity was greater than the threshold value, then the new offspring would be selected into the population. Else, the offspring is eliminated through competition. As a result, it ensures the diversity of intra-population in the environment. Corresponding this to the parallel test construction problem, we can find a set of tests having the greatest difference to find the best parallel test form.

According to eugenic theory, there is a higher probability of generating better offspring if two of the better individuals are selected to mate (Barrett & Kurzman, 2004). Therefore, we can find better results efficiently if we select only the better individuals to mate at each evolutionary generation. The concept is similar to selecting the stud in animal husbandry. However, the local minimum often occurs during the evolutionary process.

We have, therefore, incorporated the advantages of these two theories into the simple genetic algorithm. Experimental results show that our proposed method can construct parallel tests with a smaller margin of error than the simple genetic algorithm.

2. Evolutionary genetic algorithm for parallel test construction

To verify the effectiveness of our evolutionary genetic algorithm, we first compared the performance of three techniques: genetic diversity, eugenic theory, and the mix of genetic diversity and eugenic theory. The concept of each technique as applied to parallel test construction is stated as follows.

(1) Genetic Diversity Method (GDM): The items selected for inclusion in each test are as far as possible different. Each test is represented by a one dimensional chromosome which is selected to evolve for the next generation when the distance between it and tests already included in the population is great enough (i.e., the distance beyond a predefined threshold value). This technique generates a set of offspring (tests) of the greatest difference for evolution.

(2) Eugenic Theory Method (ETM): This technique considers only the fitness value of each test (offspring). Tests with the smaller number of errors would be selected to mate by the crossover operation generating two new tests (offspring) which have a higher probability of finding the better solutions.

(3) Evolutionary Genetic Algorithm (EGA): This approach combines the above two techniques, GDM and ETM. In the first half of the execution of EGA, we apply the GDM which makes the chromosomes (tests) as diverse as possible in the initial evolution thus avoiding having the results fall into a few local optimal solutions. Then, the selection pool is made as wide as possible by the genetic diversity method in the first half of the process of evolution. After the first half of the process, we apply the ETM to search for the optimal solution from a set of better solutions (candidates) to in turn evolve better offspring in the next generation. Then, optimal or near optimal solutions would be generated rapidly.

The detailed execution of the steps of each approach to parallel test construction is stated as follows.

(1) Genetic Diversity Method

The principle of GDM is based on the concept of the genetic diversity of nature. In nature, diversity is critical for the stable existence of a species. In other words, individuals need to maintain a degree of variation (diversity) to confront challenge for natural selection (Endler, 1986). So if we maintain the diversity of selected items during the selection process, it is useful in finding various combinations of items for test construction.

For reaching genetic diversity, the selection process of two generated offspring after the crossover operation of the simple genetic algorithms is designed as follows.

(1) When two offspring are both infeasible solutions, neither of them is selected into the population for the next generation; (2) when one offspring is a feasible solution and another is an infeasible solution, the selection is made by computing the distance between the feasible solution and other selected solutions in the population. If the distance is greater than the predefined threshold value, then this offspring is included in the population for the next generation; (3) when two offspring are both feasible solutions, we first compute the distance between the two offspring. If the distance is less than the threshold value, then the distance of the offspring with the greater distance between it and other selected solutions would be computed. This offspring is then selected into the population if the computed distance is also greater than the threshold value. If the distance between the two offspring is greater than or equal to the threshold value, then the distance between each one of the offspring and other selected solutions is computed. The offspring is selected into the population if this distance is also greater than the threshold value. The algorithm of GDM could be stated as follows.

/* The selection process of GDM for two offspring

 $P_1^{'}$ and $P_2^{'}$ after the crossover operation of GA */

(1) Set the threshold value of distance: d_{θ} .

(2) Selecting offspring $P_1^{'}$ or $P_2^{'}$

(2.1) if $P_1^{'}$ and $P_2^{'}$ are both infeasible

then regenerate two offspring $P_1^{'}$ and $P_2^{'}$

(2.2) if only
$$P_1^{'}$$
 (or $P_2^{'}$) is feasible

then

compute the distance between $P_1^{'}$ (or $P_2^{'}$) and other solutions P_k in population P

$$d_1^{\min} = \min\{\text{distance}(P_1, P_k), \forall P_k \in P\}$$

$$d_{2}^{\min} = \min\{\text{distance}(P_{2}^{'}, P_{k}^{'}), \forall P_{k} \in P\}$$

if d_{1}^{\min} (or d_{2}^{\min}) $\geq d_{\theta}$
then select $P_{1}^{'}$ (or $P_{2}^{'}$)

else regenerate offspring $P_1^{'}$ and $P_2^{'}$

(2.3) if
$$P_1'$$
 and P_2' are both feasible

then

compute the distance d_{12} between P_1

and P_2

co

mpute the distance
$$d_1^{min}$$

between $P_1^{'}$ and other solutions P_k in population P

compute the distance d_2^{min}

between $P_2^{'}$ and other solutions P_k in population P

if $d_{12} < d_{\theta}$ then if $d_1^{min} > d_2^{min}$ and $d_1^{min} \ge d_{\theta}$ then select P_1' elseif $d_2^{min} \ge d_1^{min}$ and $d_2^{min} \ge d_{\theta}$ then select P_2'

else regenerate offspring

$$P_{1}^{'} \text{ and } P_{2}^{'}$$
if $d_{12} \ge d_{\theta}$
then
if $d_{1}^{min} \ge d_{\theta}$ then select $P_{1}^{'}$
if $d_{2}^{min} \ge d_{\theta}$ then select $P_{2}^{'}$
if $d_{1}^{min} < d_{\theta}$ and $d_{2}^{min} < d_{\theta}$
then regenerate offspring $P_{1}^{'}$ and

$$P_2$$

(2) Eugenic Theory Method

The concept of the eugenic theory method is to select the better solutions into the population such that there is a higher probability to generate better offspring after the crossover operation. However, the probability of trapping at local minimum is also increased. The selection process for two offspring by the ETM is designed as follows. (1) When two offspring are both infeasible solutions, neither of them is selected into the population; (2) when one offspring is a feasible solution and another is an infeasible solution, select the feasible (better) solution into the population; (3) when two offspring are both feasible solutions, select the better (smaller fitness value) one into the population. The algorithm of ETM could be stated as follows.

/* The selection process of ETM for two offspring $P_1^{'}$ and $P_2^{'}$ after the crossover operation of GA */ if $P_1^{'}$ and $P_2^{'}$ are both feasible then select the smaller of $P_1^{'}$ and $P_2^{'}$

elseif only $P_1^{'}$ (or $P_2^{'}$) is feasible, then select the feasible solution $P_1^{'}$ (or $P_2^{'}$) else regenerate offspring $P_1^{'}$ and

 P_2

(3) Evolutionary Genetic Algorithm

This method combines the advantages of the genetic diversity method (GDM) and eugenic theory method (ETM). Initially, we adopted the genetic diversity method to search a wide ranging problem space and in this way avoided falling into localized optimal solutions. Then, we expanded the search space making it as wide as possible in the first half stage. Now, after the search for diversity, we apply the eugenic theory method and select better solutions to continue the intensive search for the optimal solution regardless of diversity any more (e.g., if the number of generations was set to 1000, then the first 500 generations would adopt GDM, and the last 500 generations would adopt ETM). In this way, we consider both genetic diversity and eugenic theory and obtain results that were better than the simple GA. The algorithm of EGA could be stated as follows.

/* The selection process of EGA for two offspring $P_1^{'}$ and $P_2^{'}$ after the crossover operation of GA */

(1) Initially, set gener_no to 1

(2) Repeat

if gener_no < 1/2 generation_number /* gener_no is the index of generations */

then apply the GDM

else apply the ETM

gener_no = gener_no + 1

Until gener_no = generation_number

3. Performance comparison

To compare the performance of the proposed three techniques, we used a computer to generate a virtual 1000-item bank. The parameters of each item are randomly generated and their scopes are shown in Table 1. The parameters set for evolution were defined as follows: n = 1000, $m = \{30, 40, 50\}$, P = 100, $p_c = 86.3\%$, $p_m = 0.4\%$, $p_r = 13.3\%$, gener_no = 300 ~ 5000, and $d_{\theta} = 6$.

For experiments of 300-generations, EGA had the least number of errors in 5 out of 9 cases, and ETM had the least number of errors for the remaining 4 cases (as shown in Table 2).

From Table 2, we can see that the ETM and EGA techniques obtained similar results. For further comparison of these two methods, more experiments proceeded with the number of generations changing from 300 to 5000. Simulations were divided into two parts. The first part (PART 1) included cases generated by ETM that were better than those of EGA at 300 generations (shown in Table 3). The other part (PART 2) composed the remaining five cases (cases generated by EGA that were better than those of ETM (shown in Table 4)).

From experimental results, we found that the proposed EGA method obtained the best results among the three proposed approaches. We will now compare it with the previously proposed SGA method (Sun, 2000) of parallel test construction.

4. Performance Evaluation

In this section, we will compare the performance of EGA and SGA to verify the hypothesis that combining genetic diversity and eugenic theory into the SGA is useful for evolving better solutions. Nine hundred target tests were randomly generated by computer, and results were generated by the execution of EGA and SGA, respectively.

Figure 3 (a) \sim (c) shows that in one-peak cases EGA had better solutions if the number of generations was beyond 1000. Figure 4 (a) \sim (c) shows that in two-peak cases EGA had better solutions if the number of generations was beyond 500. Figure 5(a) ~ (c) shows that in uniform distribution cases EGA had better solutions for 30-item and 40-item cases if the number of generations was beyond 1000 and for 50-item cases if the number was beyond 1500. Figures 3 ~ 5 also show that SGA often got trapped in a local minimum (horizontal periods of lines). Then, the results were worse for larger generations. Experimental results satisfied our postulation that the combination of genetic diversity and eugenic theory is useful for evolving better results.

5. Conclusions

This paper proposed three techniques, GDM, ETM, and EGA, to improve the performance of the simple genetic algorithm. The basic principles behind these techniques are: genetic diversity, eugenic theory, and the mixing of the two. Based on the constructed 1000-item bank, 900 different target tests were simulated to compare the performance of these three techniques. Experimental results show that the EGA had the best performance for the cases with the larger number of generations. Then, another 900 different target tests were used to compare the performance of EGA and SGA, and the EGA was also better than the SGA after a large number of evolutionary generations. The phenomenon confirmed our hypothesis that "the combination of genetic diversity with eugenic theory could improve the performance of SGA." The proposed evolutionary genetic algorithm would be more effective in parallel test construction than the SGA.

In the future, we will reinforce our method and expect to solve more complex problems such as item duplication and item exploration.

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Attributes	Th	ree paramet	ters	Constraints				
Information	а	b c		Content Topic		Skill	Length	
Range	0.8 ~ 3.0	-3.0 ~ +3.0	0.1 ~ 0.3	1 ~ 10	1 ~ 5	1~6	20 ~ 50	
Туре	real	real	real	integer	integer	integer	integer	
Mean	1.916	-0.013	0.201	5.396	2.989	3.515	34.854	
SD	0.627	1.740	0.059	2.893	1.381	1.675	8.909	

Table1. The ranges of item parameters and constraints used in the 1000-item bank

Table 2. The averages of the deviations (sum of squared errors) of the experimental results in different cases of 300 generations

Algorithms Cases	GDM	ETM	EGA
one-peak-30	0.693828	0.638656*	0.656910
one-peak -40	0.934632	0.813931	0.801122*
one-peak -50	1.881100	1.601764	1.527370*
two-peak -30	0.961837	0.860859*	0.961165
two-peak -40	1.157878	1.053346*	1.114947
two-peak -50	2.112837	1.843338*	1.863328
uniform-30	0.035137	0.035211	0.030991*
uniform -40	0.014054	0.014899	0.012977*
uniform -50	0.015825	0.015395	0.013020*

(*: the best results among three algorithms)

Table3. The averages of the deviations (sum of squared errors) of the experimental results for different cases and algorithms (PART 1)

Case-Algorithm Generation	one-peak-30 -ETM	one-peak-30 -EGA	two-peak-30 -ETM	-	two-peak-30 -ETM	two-peak-40 -EGA	two-peak-50 -ETM	two-peak-50 -EGA
300	0.294235*	0.352977	1.397940*	1.606557	1.648128*	1.736090	3.511364*	3.720442
500	0.146861	0.106376*	1.065808	0.921360*	1.148937	1.106961*	2.340203	2.271899*
1000	0.063355	0.039203*	0.666984	0.521564*	0.861645	0.822929*	1.769672	1.755672*
1500	0.043929	0.015314*	0.602135	0.456566*	0.793820	0.775836*	1.676363	1.619012*
2000	0.030154	0.012043*	0.464633	0.385998*	0.771476	0.754100*	1.590481	1.563328*
2500	0.029399	0.010050*	0.407228	0.375111*	0.756032	0.725187*	1.560231	1.524355*

3000	0.028657	0.009740*	0.400260	0.370656*	0.742678	0.710264*	1.529342	1.517970*
3500	0.027882	0.009243*	0.397096	0.366944*	0.734097	0.699263*	1.522353	1.510788*
4000	0.026648	0.007492*	0.397096	0.365606*	0.734097	0.695098*	1.522353	1.500471*
4500	0.025520	0.007492*	0.388716	0.365606*	0.726330	0.693452*	1.520028	1.491408*
5000	0.025462	0.007492*	0.388716	0.364780*	0.718295	0.693415*	1.512261	1.490924*

(*: better results)

Table4. The averages of the deviations (sum of squared errors) of the experimental results for different cases and algorithms (PART 2)

Case-algo										
rithm	one-peak	one-peak	one-peak	one-peak	uniform	uniform	uniform	uniform	uniform	uniform
Genera	-40-ETM	-40-EGA	-50-ETM	-50-EGA	-30-ETM	-30-EGA	-40-ETM	-40-EGA	-50-ETM	-50-EGA
tion \										
300	0.180489	0.123472*	0.361709	0.250442*	0.024498	0.020462*	0.020808	0.018451*	0.011552	0.009039*
500	0.067727	0.047424*	0.102525	0.041080*	0.015097	0.012225*	0.012205	0.011719*	0.006650	0.005922*
1000	0.024944	0.017714*	0.026007	0.016006*	0.007920	0.003653*	0.005724	0.004079*	0.003527	0.003317*
1500	0.013203	0.011885*	0.017511	0.010248*	0.006816	0.003000*	0.004874	0.003123*	0.002409	0.002362*
2000	0.009769	0.008141*	0.013882	0.007206*	0.005903	0.002423*	0.003013	0.002364*	0.002203	0.002090*
2500	0.008722	0.007485*	0.012254	0.006813*	0.005798	0.002131*	0.002855	0.002004*	0.002051	0.002030*
3000	0.008377	0.006138*	0.011000	0.006084*	0.005440	0.002131*	0.002589	0.001859*	0.002018	0.001719*
3500	0.008166	0.005758*	0.009715	0.006084*	0.005440	0.002131*	0.002465	0.001859*	0.001948	0.001719*
4000	0.008166	0.005758*	0.009477	0.005809*	0.005440	0.002131*	0.002366	0.001795*	0.001948	0.001532*
4500	0.008166	0.005287*	0.009326	0.005012*	0.005284	0.002131*	0.002279	0.001795*	0.001786	0.001488*
5000	0.008166	0.004952*	0.008972	0.004951*	0.005065	0.002131*	0.002278	0.001795*	0.001785	0.001460*

(*: better results)

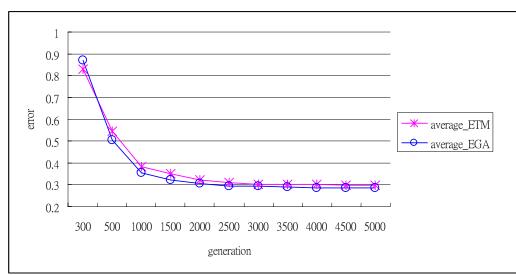
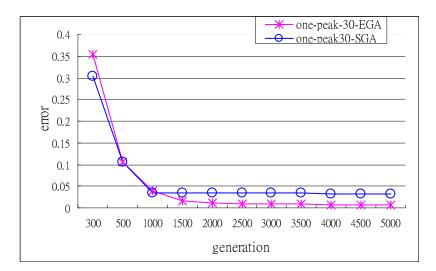
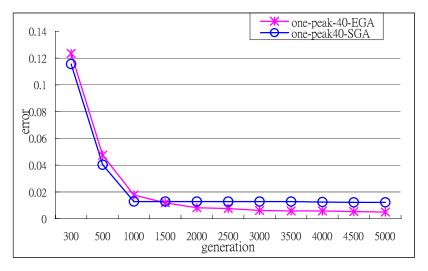


Figure 2. The averages of errors for ETM and EGA at different generations



(a) One-peak 30-item cases



(b) One-peak 40-item cases

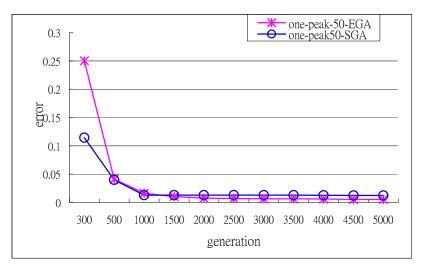
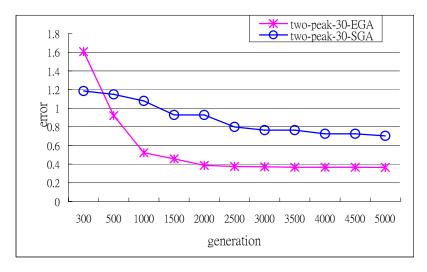
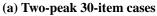
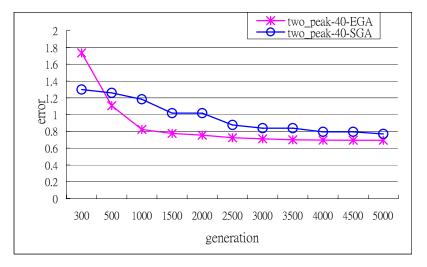




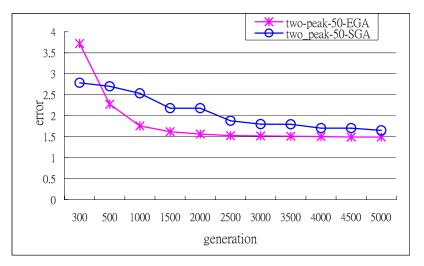
Figure 3. The performance of EGA and SGA for one-peak cases at different generations





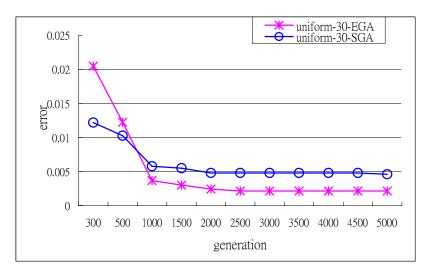


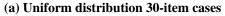
(b) Two-peak 40-item cases

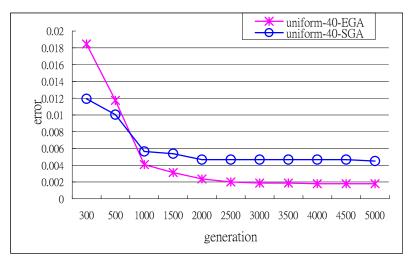


(c) Two-peak 50-item cases

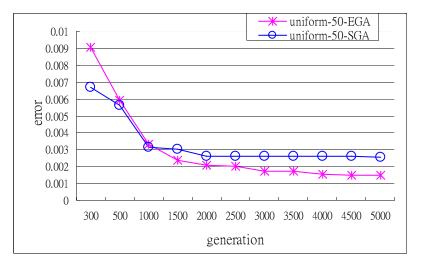
Figure 4. The performance of EGA and SGA for two-peak cases at different generations







(b) Uniform distribution 40-item cases



(c) Uniform distribution 50-item cases

Figure 5. The performance of EGA and SGA for uniform distribution cases at different generations