

## Short Paper

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### Adapting Crossover and Mutation Rates in Genetic Algorithms\*

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It is well known that a judicious choice of crossover and/or mutation rates is critical to the success of genetic algorithms. Most earlier researches focused on finding optimal crossover or mutation rates, which vary for different problems, and even for different stages of the genetic process in a problem. In this paper, a generic scheme for adapting the crossover and mutation probabilities is proposed. The crossover and mutation rates are adapted in response to the evaluation results of the respective offspring in the next generation. Experimental results show that the proposed scheme significantly improves the performance of genetic algorithms and outperforms previous work.

**Keywords:** genetic algorithms, self-adaptation, progressive value, crossover rate, mutation rate

## 1. INTRODUCTION

Genetic Algorithms (GAs) are robust search and optimization techniques that were developed based on ideas and techniques from genetic and evolutionary theory [9, 19]. Beginning with a random population of chromosomes, a genetic algorithm chooses parents from which to generate offspring using operations analogous to biological processes, usually *crossover* and *mutation*. All chromosomes are evaluated using a fitness function to determine their "fitness." These fitness values are then used to decide whether the

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chromosomes are eliminated or retained. According to the *principle of survival of the fittest*, the more adaptive chromosomes are kept, and the less adaptive ones are discarded in the course of generating a new population. The new population replaces the old one, and the whole process is repeated until specific termination conditions are satisfied. Fig. 1 depicts a typical genetic process.

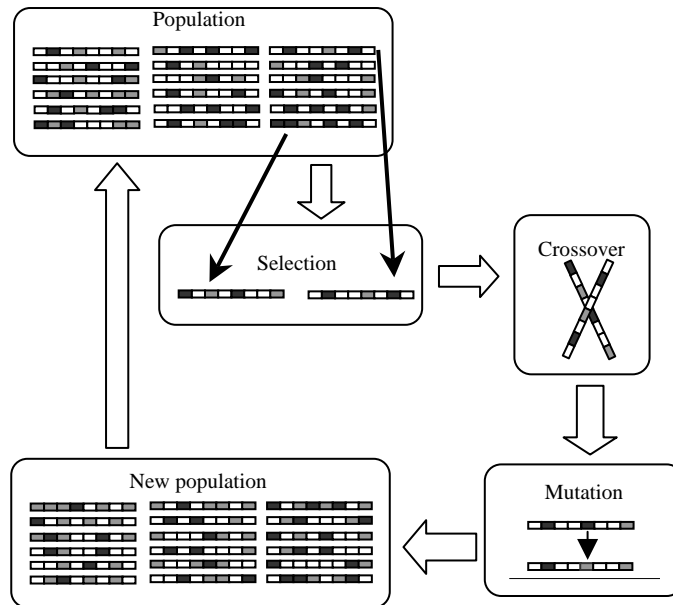


Fig. 1. A typical genetic process.

There is evidence showing that the probabilities of crossover and mutation are critical to the success of genetic algorithms [3-6, 12, 20]. Traditionally, determining what probabilities of crossover and mutation should be used is usually done by means of trial-and-error. The optimal crossover or mutation rates, however, vary along with the problem of concern, even within different stages of the genetic process in a problem. In the past few years, though some researchers have investigated schemes for automating the parameter settings for GAs, the problem of making GAs self-adaptive in choosing the optimal parameters remains an unexplored area.

In this paper, a generic scheme for adapting the crossover and mutation probabilities is proposed. The crossover and mutation rates are adapted in response to the evaluation results of the respective offspring in the next generation. Experimental results show that the proposed scheme significantly improves the performance of genetic algorithms and outperforms previous proposed methods.

The content of this paper is organized as follows. A brief review of operator rate adaptation in genetic algorithms and related works is given in section 2. Our scheme for adapting the crossover and mutation rates is proposed in section 3. There we also discuss its convergence property. Section 4 describes our experiments. Conclusion and future work are given in section 5.

## 2. OPERATOR RATE CONTROL IN GENETIC ALGORITHMS AND RELATED WORK

When genetic algorithms are applied to solve a problem, the first step is to define a representation that describes the problem states. The most commonly used representation is the bit string. An initial population is then defined, and three genetic operations (crossover, mutation, and selection) are performed to generate the next generation. This procedure is repeated until the termination criterion is satisfied. This so-called Simple Genetic Algorithm (SGA) [9] is described in Algorithm 1.

**Algorithm 1. A simple Genetic Algorithm.**

```

Initialize the parameters;
Generate a population  $P$  randomly;
 $generation \leftarrow 1$ ;
while  $generation \leq max\_gen$  do
    Clear the new population  $P'$ ;
    Use a fitness function  $f(\cdot)$  to evaluate each individual in  $P$ ;
    while  $|P'| \leq N$  do
        Select two parents from  $P$ ;
        Perform crossover with rate  $p_c$ ;
        Perform mutation with rate  $p_m$ ;
        Insert the offspring to  $P'$ ;
    endwhile
     $P \leftarrow P'$ ;
     $generation \leftarrow generation + 1$ ;
endwhile

```

The power of genetic algorithms arises primarily from crossover and mutation. The crossover operation is used to generate offspring by exchanging bits in a pair of individuals (parents) chosen from the population, with the possibility that good solutions can generate better ones. Crossover occurs only with a probability  $p_c$  (the *crossover rate* or *crossover probability*). When individuals are not subjected to crossover, they remain unmodified. The mutation operator is used to change some elements in selected individuals with a probability  $p_m$  (the *mutation rate* or *mutation probability*), leading to additional genetic diversity to help the search process escape from local optimal traps.

The choice of  $p_c$  and  $p_m$  is known to critically affect the behavior and performance of GAs. The crossover rate controls the capability of GAs in exploiting a located hill to reach the local optima. The higher the crossover rate, the quicker exploitation proceeds. A  $p_c$  that is too large would disrupt individuals faster than they could be exploited. The mutation rate controls the speed of GAs in exploring a new area. Small  $p_m$  values are commonly adopted in GAs. A number of guidelines exist in the literature for setting the values for  $p_c$  and  $p_m$  [3, 6, 9, 23]. Typical values of  $p_c$  are in the range 0.5~1.0, while typical values of  $p_m$  are in the range 0.001~0.05. These general guidelines were drawn from empirical studies on a fixed set of test problems, and were inadequate because the optimal use of  $p_c$  and  $p_m$  is specific to the problem under consideration. Some studies

focused particularly on finding optimal crossover or mutation rates [3, 11, 12, 22]. These heralded the need for self-adaption in the crossover or mutation rates [7].

Fogarty [8], to our knowledge, was the first to use a varying mutation rate. He concluded that a mutation rate that decreased exponentially over generations had superior performance. His idea is quite similar to simulated annealing, where the mutation rate takes on a role analogous to that of *temperature*. Indeed, a mutation-only GA that evolves at a constant mutation rate is analogous to simulated annealing at a constant temperature [22] (which corresponds to the Metropolis process). Bäck [2] followed Fogarty's investigation and devised a deterministic formula for adjusting the mutation rate to dynamically approach the optimal value. An analogous way of cyclically varying the mutation rate reported in [13] exhibited a similar effect.

In [24], Srinivas and Patnaik proposed a mechanism for adapting operator probabilities in a generational GA. Each chromosome has its own crossover probability  $p_c$  and mutation probability  $p_m$  necessary for it to undergo crossover and mutation, respectively. During the execution of GAs, both  $p_c$  and  $p_m$  are adapted in proportion to the population maximum and mean fitness, with probabilities being larger when the mean fitness is near the maximum, and smaller for particular chromosomes with larger fitnesses. Similar concepts were adopted and further explored in [16, 25].

### 3. SCHEME FOR ADAPTING CROSSOVER AND MUTATION RATES

In the classic genetic algorithm, the involved genetic operators, such as crossover and mutation, work at an a priori, constant probability. Different crossover and mutation rates can, however, traverse different search directions in the state space, thus affecting the performance of the applied genetic algorithm. In fact, the overall performance of a genetic algorithm depends on it maintaining an acceptable level of productivity throughout the process of evolution. It is, thus, essential to design a genetic algorithm that adapts itself to the appropriate crossover and mutation rates. Our intuition is to dynamically adjust the operator's applied probability according to its "contribution" (or productivity); thus, there is the potential to produce children of improved fitness. In this section, we propose a rate-adapting scheme to achieve this goal.

The rationale behind this approach is as follows: It may be advantageous to employ a method that dynamically adjusts the genetic algorithm's settings according to a measure of the performance of each operator. To measure the performance of an operator, we develop a scheme involving the ability of an operator to produce new, preferably fitter, children. The purpose of the dynamic operator adapting methods is to exploit information gained regarding the current ability of each operator to produce children of improved fitness.

#### 3.1 Description

The first step in our approach is determining an initial  $p_c$  and  $p_m$  pair. For classic genetic algorithms, the general rule is to use a high crossover rate and a low mutation probability. However, inspired by previous works [3, 8], a large initial mutation rate is employed to help explore more local hills and locate a prospective area quickly. During

this time, crossover should occur with a small probability to retain diversity. For these reasons, we set the initial crossover rate and mutation rate at 0.5 and 0.5, respectively, and adjust them using the *progress-value* concept [15] described in the following.

Consider the offspring generated from two parents after a crossover operation is performed. Let  $f_{sum_S}$  be the fitness sum of the two offspring, and let  $f_{sum_P}$  denote the fitness sum of the parent individuals. We define the progress value of crossover  $CP$  as the gain obtained by

$$CP = f_{sum_S} - f_{sum_P}. \quad (1)$$

For a generation that undergoes  $n_c$  crossover operations, the average crossover progress value  $\tilde{CP}$  is

$$\tilde{CP} = \frac{1}{n_c} \sum CP \quad (2)$$

Thus,  $\tilde{CP}$  measures the overall performance of the crossover operator within a generation run.

Similarly, consider the resulting offspring after a mutation operation is performed; the progress value of the mutation  $MP$  is

$$MP = f_{new} - f_{old}, \quad (3)$$

where  $f_{new}$  is the fitness of the new offspring and  $f_{old}$  the fitness of the original individual. For a generation that undergoes  $n_m$  mutation operations, the average mutation progress value  $\tilde{MP}$  is

$$\tilde{MP} = \frac{1}{n_m} \sum MP \quad (4)$$

Before the end of each generation, the crossover and mutation rates are adjusted using these average progress values. The operator that performs better in the previous run (with a larger average progress value) should participate more frequently (increase its probability) in the next generation run, and vice versa. The adjustment is executed as shown below:

$$\begin{aligned} p_c &= p_c + \theta_1 & \text{if } \tilde{CP} > \tilde{MP}, \\ p_c &= p_c - \theta_1 & \text{if } \tilde{CP} < \tilde{MP}, \\ \text{and} \\ p_m &= p_m + \theta_2 & \text{if } \tilde{CP} < \tilde{MP}, \\ p_m &= p_m - \theta_2 & \text{if } \tilde{CP} > \tilde{MP}, \end{aligned}$$

where  $\theta_1$  and  $\theta_2$  represent the amount of adjustment of  $p_c$  and  $p_m$ , respectively. Now we are confronted with another problem: What values of  $\theta_1$  and  $\theta_2$  should be chosen? Should

$\theta_1$  and  $\theta_2$  be identical or different? And, should they be constant values or adapting functions? We will examine these aspects later through experiments.

Notice that after each adjustment, we should make sure that the crossover and mutation operations have the chance to work continuously. For this reason, we set the minimum crossover and mutation rates to 0.001. If the crossover or mutation rate is less than or equal to 0.001, the adjustment operation stops decreasing the probability.

The refined genetic algorithm incorporating this adaptation approach (called the *progress rate genetic algorithm*, or PRGA) is described in Algorithm 2.

**Algorithm 2. Progress Rate Genetic Algorithm.**

```

Initialize the parameters;
Generate a population  $P$  randomly;
 $generation \leftarrow 1$ ;
while  $generation \leq max\_gen$  do
    Clear the new population  $P'$ ;
    Use a fitness function  $f(\cdot)$  to evaluate each individual in  $P$ ;
    while  $|P'| \leq N$  do
        Select two parents from  $P$ ;
        Perform crossover and accumulate the crossover progress value  $CP$ ;
        Perform mutation and accumulate the mutation progress value  $MP$ ;
        Insert the offspring to  $P'$ ;
    endwhile

    Compute  $\tilde{CP}$  and  $\tilde{MP}$ , and adjust the crossover rate  $p_c$  and mutation rate  $p_m$ ;
     $P \leftarrow P'$ ;
     $generation \leftarrow generation + 1$ ;
endwhile

```

### 3.2 Convergence Property of PRGA

Since genetic algorithms are stochastic search processes, there is no convincing theory that can completely deduce the convergence rate for GAs to reach the optimal solution. Nevertheless, we can examine a sort of convergence in probability.

Let  $N$  be the population size, and let  $n$  be the length of each individual. Given a probability  $\alpha$ , we may ask what the smallest number of generations  $g(\alpha)$  required to obtain an optimal solution is. Aytug and Koehler [1] modeled genetic algorithms with the Markov chain and derived the following bound:

$$\begin{aligned}
 \text{INT} \left[ \max_j \left\{ \frac{\ln(1-\alpha)}{\ln(\delta(Q - Qu_j u_j^T))} \right\} \right] &\leq g(\alpha) \\
 &\leq \text{INT} \left[ \frac{\ln(1-\alpha)}{\ln(1 - \min\{(1 - P_m)^{nN}, p_m^{nN}\})} \right],
 \end{aligned} \tag{5}$$

where  $\text{INT}[x]$  denotes the smallest integer greater than or equal to  $x$ , for  $x \geq 0$ ;  $Q$  is the Markov chain transition matrix;  $u_j$  is the  $j$ th unit vector;  $\rho(A)$  is the spectral radius of a matrix  $A$ ; and  $p_m$  is the mutation probability. The lower bound is difficult to evaluate because the maximum is taken over all states of the Markov chain. Greenhalgh and Marshall [10] showed that the upper bound can be improved further as

$$g(\alpha) \leq \text{INT} \left[ \frac{\ln(1-\alpha)}{N \ln(1-\min\{P_m(1-P_m)^{n-1}, P_m^n\})} \right], \quad (6)$$

and that the bound holds independent of the crossover and selection schemes.

The above result can be further refined in the case where the mutation rate is adapted. Note that the mutation rate  $p_m$  under the proposed adaptation scheme is always bounded between 0 and 1. Without loss of generality, let  $p_1 \leq p_m \leq p_2$  for  $p_1 > 0$  and  $p_2 < 1$ . Then, it is easy to show that, following the derivation in [10],

$$g(\alpha) \leq \text{INT} \left[ \frac{\ln(1-\alpha)}{N \ln(1-\min\{P_1(1-P_1)^{n-1}, P_2^n\})} \right]. \quad (7)$$

Note that the above derivation is based on the simple GAs, without taking into account the effect of repairing chromosomes. Because the degree of population diversity is reduced after repairing is performed, we can expect that the population will converge more quickly. The question of what the exact bound on the number of generations will be when the repairing effect is considered deserves further investigation.

#### 4. EXPERIMENTS

To examine the performance of the progress rate genetic algorithm (PRGA), we compared it with four variants of GAs. They included the simple genetic algorithm (SGA) with fixed crossover and mutation rates; the decreasing mutation rate genetic algorithm (DMRGA) proposed by Bäck [2]; the cyclic-parental, low-offspring mutation (CPLO) in [13]; and the adaptive genetic algorithm (AGA) proposed by Srinivas and Patnaik [24]. The test problem was the 0/1 knapsack problem, which belongs to the class of knapsack-type problems and is well known to be NP-hard [17].

The 0/1 knapsack problem is as follows: given a set of objects,  $a_i$ , for  $1 \leq i \leq n$ , together with their profits  $P_i$ , weights  $W_i$ , and a capacity  $C$ , find a binary vector  $\mathbf{x} = \langle x_1, x_2, \dots, x_n \rangle$ , such that

$$\sum_{i=1}^n x_i \cdot W_i \leq C \quad \text{and} \quad \sum_{i=1}^n x_i \cdot P_i \quad \text{is maximal.}$$

Because the difficulty of knapsack problems is greatly affected by the correlation between profits and weights [18], we employed the three randomly generated sets of data used in [18]:

- (1) uncorrelated  
 $W_i$  and  $P_i$ : random(1.. $v$ );
- (2) weakly correlated  
 $W_i$ : random(1.. $v$ );  
 $P_i$ :  $W_i + \text{random}(-r..r)$ ;
- (3) strongly correlated  
 $W_i$ : random(1.. $v$ );  
 $P_i$ :  $W_i + r$ .

The data were generated with the following parameter settings:  $v = 10$ ,  $r = 5$ , and  $n = 250$ . Following a suggestion made in [17], we adopted two different types of capacity  $C$ : 1)  $C = 2v$ , for which the optimal solution contained very few items; and 2)  $C = 0.5\sum W_i$ , in which about half of the items were in the optimal solution.

The test suit represented two different types of problem instances. Those data sets in Group 1 under the constraint  $C = 2v$  were more difficult than those in Group 2 under the constraint  $C = 0.5\sum W_i$ , because the fitness landscape in Group 1 abounded with local hills. This increased the difficulty for GAs to locate the global optimum. The instance difficulty in each group was further classified by means of the correlation between profits and weights.

To be consistent with the crossover and mutation operators considered, we used the binary encoding scheme: each bit represented the inclusion or exclusion of an object. It was, however, possible to generate infeasible solutions with this representation. That is, the total weights of the selected objects would exceed the knapsack capacity. In the literature, two different ways of handling this constraint violation [18] have been proposed. One way is to use a penalty function to penalize the fitness of the infeasible candidate to diminish its chance of survival. Another approach is to use a repair mechanism to correct the representation of the infeasible candidate. In [18], the repair method was more effective than the penalty approach. Hence, we adopted the repair approach in our implementation.

The repair scheme that we used was a greedy approach. All the objects in a knapsack represented by an overfilled bit string were sorted in decreasing order of their profit weight ratios. The last object was then selected for elimination (the corresponding bit of "1" was changed to "0"). This procedure was executed until the total weight of the remaining objects was less than the total capacity.

The common parameters set in this experiment were those listed below:

crossover: one-point crossover;  
 mutation: bit-flip mutation;  
 selection: random selection;  
 replacement:  $(\mu + \lambda)$  replacement;  
 population size: 100;  
 generations: 500;  
 experimental runs: 10.



In a preliminary experiment, we noticed that the original AGA algorithm [24] that adopted proportional selection with generational replacement was inferior to all of the other methods that used random selection and  $(\mu + \lambda)$  replacement. For this reason, the AGA algorithm was changed to use random selection with  $(\mu + \lambda)$  replacement as well.

The crossover and mutation rates employed for each variant are shown below:

SGA:  $p_c = 0.65, p_m = 0.01$ ;

DMRGA:  $p_c = 0.65$ ,

$$p_m(t) = \left( 2 + \frac{L-2}{T} \cdot t \right)^{-1},$$

where  $t$  is the generation count,  $L$  the length of chromosomes, and  $T$  the maximum generation;

CPLO:  $p_c = 0.65, p_m = 0.1$  for parent mutation, and 0.001 for offspring mutation;

AGA: the expressions for  $p_c$  and  $p_m$  were

$$p_c = (f_{\max} - f) / (f_{\max} - f_{\text{avg}}), \quad f \geq f_{\text{avg}},$$

$$p_c = 1.0, \quad f < f_{\text{avg}},$$

and

$$p_m = 0.5 (f_{\max} - f) / (f_{\max} - f_{\text{avg}}), \quad f \geq f_{\text{avg}},$$

$$p_m = 0.5, \quad f < f_{\text{avg}},$$

where  $f_{\max}$  represents the maximum fitness value of the population,  $f_{\text{avg}}$  the average fitness value of the population,  $f$  the fitness value of the solution undergone mutation, and  $f^*$  the larger of the fitness values of the solutions to be crossed.

We first examined the effects of different step sizes for adaptation of  $p_c$  and  $p_m$ . To understand the effect of varying  $\theta_1$  and  $\theta_2$  under constant step sizes, we first measured the PRGA performance using four different settings: 1)  $\theta_1 = \theta_2 = 0.01$ ; 2)  $\theta_1 = 0.01$  and  $\theta_2 = 0.001$ ; 3)  $\theta_1 = 0.001$  and  $\theta_2 = 0.01$ ; 4)  $\theta_1 = 0.001$  and  $\theta_2 = 0.001$ . The results are presented in Table 1.

**Table 1. Best fitness obtained by PRGA using different constant step sizes of  $\theta_1$  and  $\theta_2$ .**

	$\theta_1 = 0.01$ $\theta_2 = 0.01$	$\theta_1 = 0.01$ , $\theta_2 = 0.001$	$\theta_1 = 0.001$ , $\theta_2 = 0.01$	$\theta_1 = 0.001$ $\theta_2 = 0.001$
Uncorrelated, $C = 2v$	114	89	87	78
Uncorrelated, $C = 0.5\Sigma W_i$	1078	983	1089	1069
Weakly, $C = 2v$	54	54	58	54
Weakly, $C = 0.5\Sigma W_i$	1063	962	1079	947
Strongly, $C = 2v$	60	65	65	65
Strongly, $C = 0.5\Sigma W_i$	1470	1435	1500	1460

As Table 1 shows, no combination was superior to the others in all test suits. This observation led us to seek a self-adaptive control of the step sizes. Inspired by [24], we tuned the values of  $\theta_1$  and  $\theta_2$  according to the population convergence. When the population converged, we increased the step sizes to reduce the probability of the GA getting stuck in a local optimum. The resulting self-adapting function is expressed as follows:

$$\theta_1 = \theta_2 = 0.01 \frac{f_{\max} - f_{\text{avg}}}{f_{\max} - f_{\min}}, \text{ if } f_{\max} > f_{\min},$$

$$\theta_1 = \theta_2 = 0.01, \text{ if } f_{\max} = f_{\text{avg}},$$

where the convergence is measured as the difference between the maximum and average population fitness,  $f_{\max} - f_{\text{avg}}$ , and normalized by  $f_{\max} - f_{\min}$ .

We next compared the other four methods with our PRGA algorithm using the adaptive step size function. The results are shown in Figs. 2 to 7. Our PRGA outperformed the competitors in all test cases except for the weakly correlated case  $C = 0.5 \sum W_i$ , where AGA led. For the most difficult problem, as shown in Fig. 2, SGA converged quickly to a local optimum and failed to perform further exploration. CPLO, with cyclic-rate mutation, exhibited the ability to escape from local traps, but the resulting improvement was not clear. DMRGA and AGA performed well initially but failed to perform further exploration when the population began to converge. Similar phenomena were observed for the other two instances in Group 1, as shown in Figs. 4 and 6.

For the cases within Group 2, we found that the performance gap between PRGA and the competitors was smaller. Note that the ranking of SGA, CPLO, DMRGA, and AGA, however, was different. CPLO ranks lower in Fig. 3, while SGA ranks last in Fig. 5, and DMRGA ranks last in Fig. 7. This phenomenon reveals that when the interaction between crossover and mutation is not considered, solely adapting the mutation rate can guarantee no performance gain.

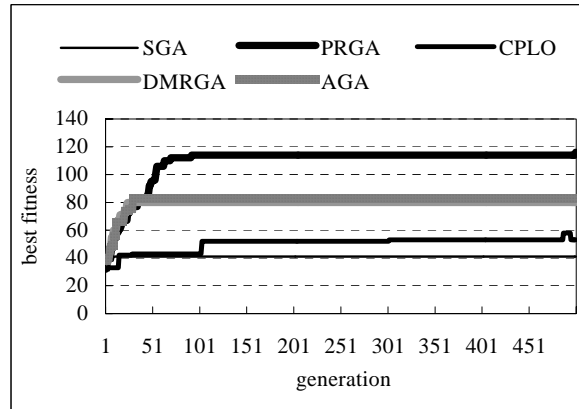


Fig. 2. Experimental results for the uncorrelated 0/1 knapsack problem with  $C = 2v$ .

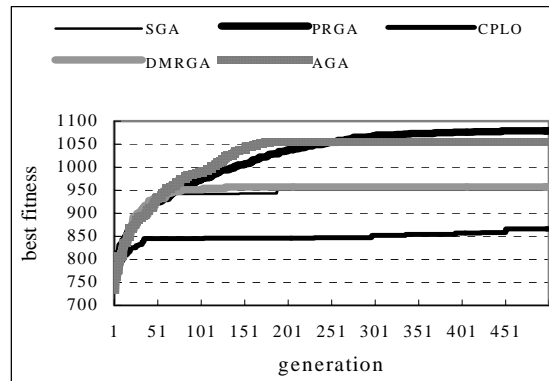


Fig. 3. Experimental results for the uncorrelated 0/1 knapsack problem with  $C = 0.5 \sum W_i$ .

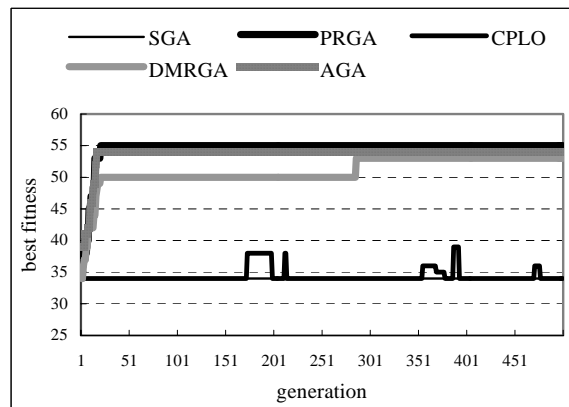


Fig. 4. Experimental results for the weakly correlated 0/1 knapsack problem with  $C = 2v$ .

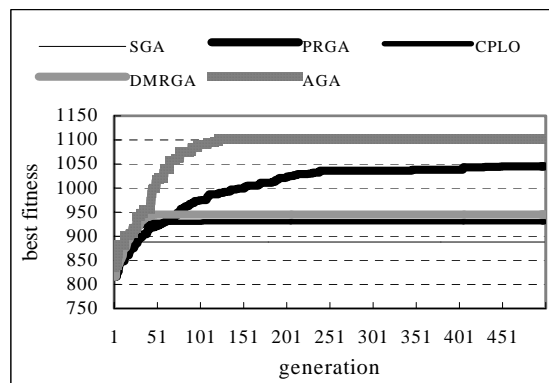


Fig. 5. Experimental results for the weakly correlated 0/1 knapsack problem with  $C = 0.5 \sum W_i$ .

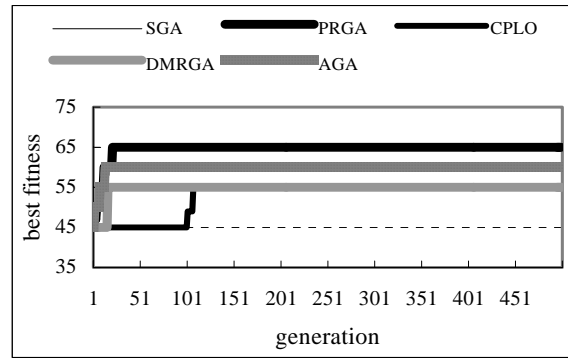


Fig. 6. Experimental results for the strongly correlated 0/1 knapsack problem with  $C = 2v$ .

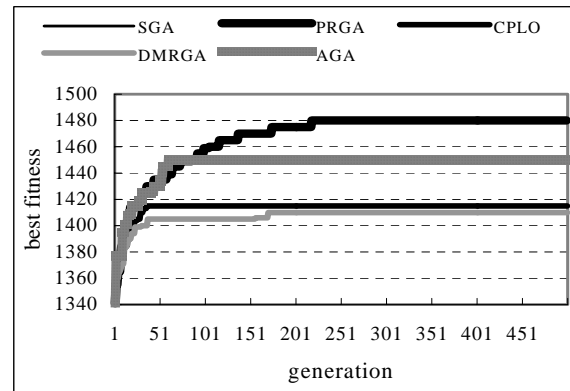


Fig. 7. Experimental results for the strongly correlated 0/1 knapsack problem with  $C = 0.5 \sum W_i$ .

To understand how  $p_c$  and  $p_m$  evolved when our method was employed, we also recorded the rates at the end of each generation. We only show the results for the uncorrelated case with  $C = 2v$ ; similar results were observed for the other cases.

Fig. 8 depicts the results, where  $p_m$  rises aggressively throughout evolution to reach the upper bound, while  $p_c$  behaves in the opposite manner. Note that the evolution map of  $p_m$  contradicts the conventional suggestion made by most researchers [2, 3, 8, 12] that  $p_m$  should behave as a descending curve. These results also confirm the necessity of using operator rate adaptation scheme to locate prospective solution.

## 5. CONCLUSIONS AND FUTURE WORK

In this paper, we have presented an adaptive genetic algorithm for automatically adjusting suitable crossover and mutation rates to reduce the effort of searching for

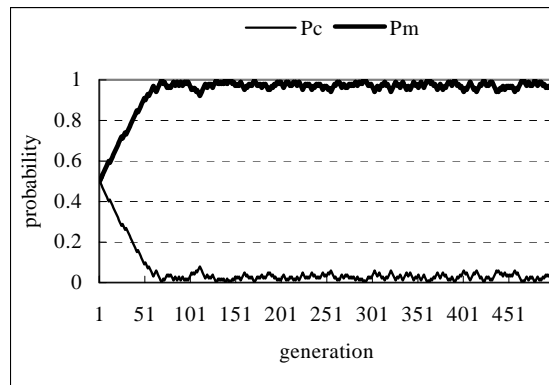


Fig. 8. Evolution of  $p_c$  and  $p_m$  for the uncorrelated 0/1 knapsack problem with  $C = 2v$ .

appropriate crossover and mutation rates. Our approach takes into account the interaction between crossover and mutation in adapting the operator rates. The performance of the proposed genetic algorithm has been empirically shown to be better than that of previous schemes. In the future, we will attempt to design other sophisticated adaptation schemes that include other parameters, such as the population size and the replacement rate.

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