

## Estimation of Average Hitting Time in Genetic Algorithms by Markov Chain

QingLian Ma, Yu-an Zhang, Makoto Sakamoto, Hiroshi Furutani  
Faculty of Engineering, University of Miyazaki  
Miyazaki City 889-2192 Japan

### Abstract

The hitting time  $T$  is an important topic in the theory of Genetic Algorithms (GAs). In this paper, we develop a new approach to estimate the mean first hitting time of optimum solution in GA. We consider the success probability  $S$  of GA on the multiplicative landscape and study the relation between  $S$  and  $T$  by Markov chain. The success probability  $S$  is defined as that there is at least one optimum solution in a population at the stationary distribution. We performed numerical experiments with and without crossover, and found that crossover accelerates the speed of evolution. The mean first hitting time becomes very short when crossover is included in GA calculation.

### 1 Introduction

Recently, there have been many theoretical attempts for obtaining the mean first hitting time of optimum solution(s) in Evolutionary Computation [1]. Researchers consider this quantity is very important measure for the evaluation of applied methods. Among these studies, the analysis adopting Markov chain model is most promising one. However, there should be done a lot of attempts to obtain more quantitative results. In this paper, we develop a new approach to estimate the mean first hitting time of optimum solution  $T$  in Genetic Algorithm (GA) on the multiplicative landscape.

First, we define the success probability of GA  $S$  as the one that there is at least one optimum solution in a population at the stationary distribution [2]. We have developed a method to calculate the success probability by using Markov chain as the function of the string length  $L$ . In this approach, we assume that the population is in linkage equilibrium through the effect of crossover, and the population is fully represented by the distribution of the first order schema. The frequency distribution of the first order schema can be obtained by using Wright-Fisher model, which also adopts the Markov chain changing with gener-

ation  $t$ . The analytical expression of the transition matrix  $P$  can be obtained for the GA on the multiplicative landscape, and we calculate the distribution of the first order schema  $\mu(t)$ . The success probability  $S$  is given by using this distribution  $\mu(t)$  at the stationary stage of Markov chain.

Next, we use this  $S$  for the estimator of the mean first hitting time  $T$  with the relation  $T = 1/S$ . The rationale of this equation is that there are populations containing the optimum solution with probability approximately given by  $1/S$ , and the mean first hitting time is also given by  $1/S$ .

In this study, we performed numerical experiments with and without crossover, and found that crossover accelerates the speed of evolution. The mean first hitting time becomes very short when crossover is included in GA calculation. We will discuss the mechanism of this phenomenon.

### 2 Model and Methods

#### 2.1 Model

We studied the GA on the multiplicative landscape with selection, crossover and mutation. The analysis of GA evolution was done by using Markov chain theory.

An individual is represented by a binary string of fixed length  $L$ . The genotype is given by the integer  $i$ , and  $i(k)$  is the  $k$ th bit of the binary string. Thus there are  $n = 2^L$  genotypes.  $N_i(t)$  represents the frequency of the  $i$ th genotype at generation  $t$ , and  $x_i(t)$  its relative frequency. The population size  $N$  is assumed to be time-independent.

If a population is in linkage equilibrium, the distribution of individuals depends only on the frequencies of the first order schema[3]. Therefore, the relative frequency  $x_i$  is represented by

$$x_i = \prod_{k=1}^L h_{i(k)}, \quad (1)$$

where  $h_{i(k)}$  is the frequency of the first order schema corresponding to  $i(k)$ . This decomposition enables us to treat the population by using the schema theory [2].

We study the evolution of the GA on the multiplicative landscape. The fitness function is

$$f_i = \prod_{k=1}^L \{1 + s i(k)\}, \quad (2)$$

where  $s$  is a parameter representing selection strength.

## 2.2 Markov Chains

We consider a population having two alleles  $A$  and  $a$ . We assume that the  $A$  genes have selective advantage  $1 + s$  while  $a$  genes have selective advantage unity. The number of  $A$  genes in any generation is a Markovian variable with the transition matrix  $P$  give by

$$P_{ij} = P(j|i) = \binom{N}{j} a^j (1-a)^{N-j}, \quad (3)$$

$$a = \frac{(1+s)i}{(1+s)i + N - i}. \quad (4)$$

The matrix element  $P_{ij}$  is the probability that the number of  $A$  individuals selected at the  $t + 1$  th generation is  $j$ , given that the number of  $A$  individuals in the  $t$  th generation is  $i$ . To take into account the effect of mutation with mutation rate  $p_m$ , we replace  $a$  by  $b$  in equation (3)

$$b = (1 - 2p_m)a + p_m, \quad (5)$$

and we have

$$P(j|i) = \binom{N}{j} b^j (1-b)^{N-j}. \quad (6)$$

The evolution of GA population is given by

$$\mu_j(t+1) = \sum_{i=0}^N \mu_i(t) P_{ij}, \quad (7)$$

where  $\mu_i(t)$  is the probability that there are  $i$   $A$  individuals in the population. The stationary distribution  $\pi$  is given by

$$\lim_{t \rightarrow \infty} \mu(t) = \pi. \quad (8)$$

## 2.3 Calculation of success probability

In the following, we give a short description for calculating the success probability  $S$  [4]. We call the  $(\ell \leq L)$  bit string of  $\langle 1, 1, \dots, 1, 1 \rangle$  as the partial

optimum solution. The random number  $X_\ell$  represents the number of partial optimum solution of length  $\ell$  in the population. The probability that there are  $j$  units of optimum solution is  $S_j^{(\ell)} = \Pr \{X_\ell = j\}$ . We can get the success probability  $S$

$$S = \sum_{j=1}^N S_j^{(L)}. \quad (9)$$

To obtain  $S$ , we have to calculate  $S_j^{(\ell)}$ , and this is done by iteration. The initial condition is

$$S_j^{(1)} = \pi_j, \quad (0 \leq j \leq N). \quad (10)$$

The transition probability from  $j$  units of partial optimum solution of length  $\ell - 1$  to  $j$  units of optimum solution of length  $\ell$  is

$$Q_{i,j}^{(\ell)} = \Pr \{X_\ell = j | X_{\ell-1} = i\}.$$

The transition probability  $Q_{i,j}^{(\ell)}$  can be calculated by using the distribution of the first order schema  $\pi$ . If  $j > i$ ,  $Q_{i,j}^{(\ell)} = 0$ . For  $j \leq i$ , we have

$$Q_{i,j}^{(\ell)} = \sum_{m=j}^{N-i+j} \binom{N}{m}^{-1} \binom{i}{j} \binom{N-i}{m-j} \pi_m. \quad (11)$$

Here  $\binom{0}{0} = 1$ . The probability  $S_j^{(\ell)}$  of having  $j$  units of  $\ell$ -bit partial optimum solution can be calculated by

$$S_j^{(\ell)} = \sum_{i=0}^N S_i^{(\ell-1)} Q_{i,j}^{(\ell)}. \quad (12)$$

## 3 Results

In this paper, we study the relation between success probability  $S$  and the mean first hitting time  $T$  by experiment. We performed numerical calculations of GA with roulette wheel selection on the multiplicative landscape. Population size  $N = 50$  and string length  $L = 20$ , selection strength with  $s = 0.04$ . Crossover was done with the uniform crossover of crossover rate  $p_c$ . We used mutation rates  $p_m$  from 0.02 to 0.09 and compared their results. The initial value of the first order schema was  $h_1 = 1/2$ . The calculations were performed repeatedly, and results were averaged over 10000 runs.

Figure 1 shows the distribution of generations finding optimum solution with crossover.

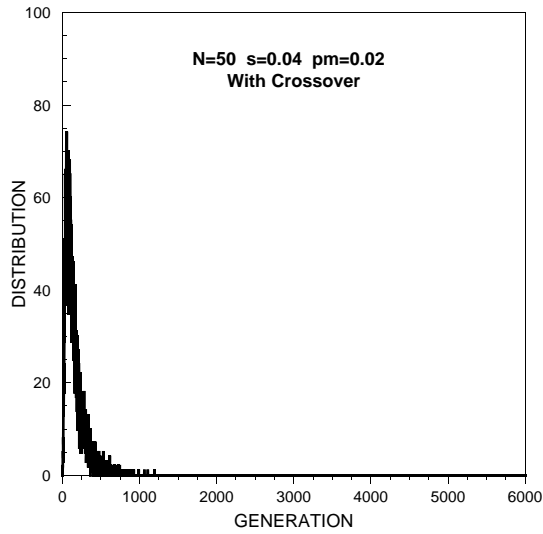


Figure 1: Distribution of generations finding optimum solution with crossover. Population size  $N = 50$  and selection strength  $s = 0.04$ .

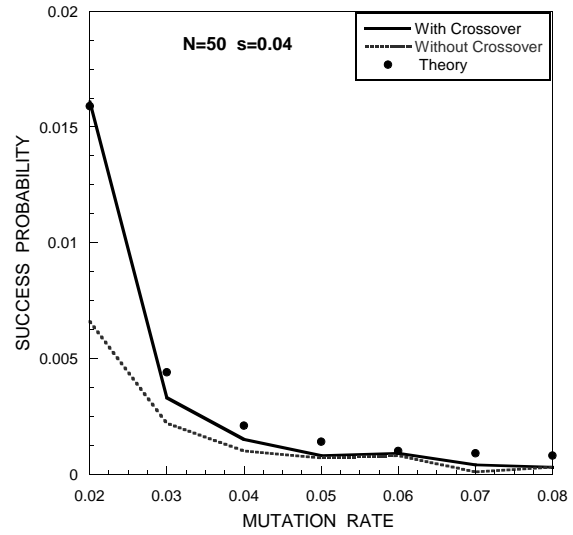


Figure 3:  $p_m$ -dependence of success probability  $S$  with  $N = 50$  and  $s = 0.04$ . Crossover rate are  $p_c = 1, 0$ . The horizontal axis represents mutation rate  $p_m$ .

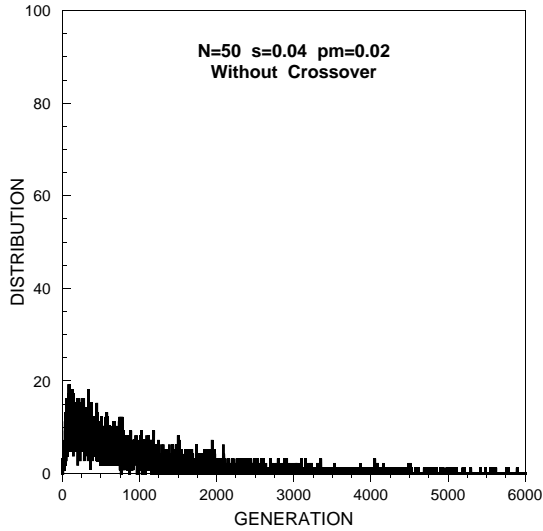


Figure 2: Distribution of generations finding optimum solution without crossover.  $N = 50$  and  $s = 0.04$ .

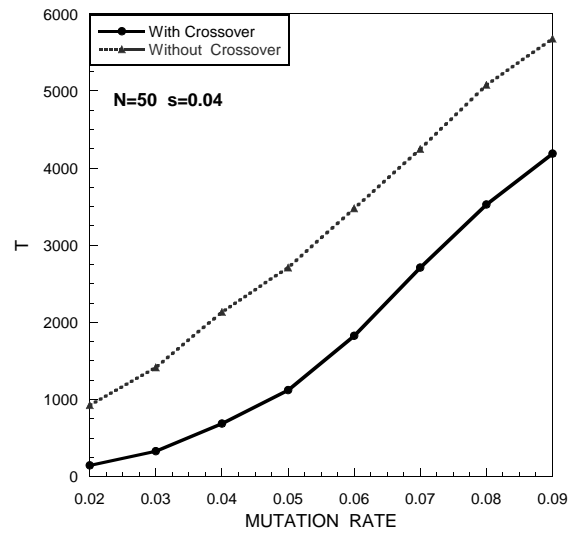


Figure 4:  $p_m$ -dependence of  $T$  with  $N = 50$  and  $s = 0.04$ . Crossover rate are  $p_c = 1, 0$ . The horizontal axis represents mutation rate  $p_m$ .

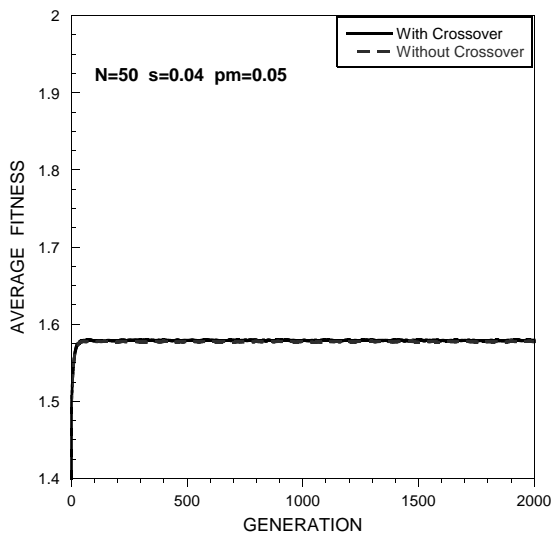


Figure 5: Average fitness  $\bar{f}(t)$  with  $N = 50$  and  $s = 0.04$ . Mutation rate  $p_m = 0.05$  and crossover rate are  $p_c = 1, 0$ . The horizontal axis represents generation.

Figure 2 shows the distribution of generations finding optimum solution without crossover by using the same parameter with Fig(1). By comparing Figs.1 and 2, we can obtain that the convergence of optimum solution distribution with crossover is earlier than that of without crossover.

Figure 3 shows  $p_m$ -dependence of success probability  $S$  with  $N = 50$  and  $s = 0.04$ . (●) is theoretical value from equation (12). As show in this figure, the effect of crossover on success probability is small when mutation rate is larger.

Figure 4 shows  $p_m$ -dependence of  $T$ .  $T$  without crossover is larger than that of with crossover. Figs.3 and 4 also shows the relation of  $T$  and  $1/S$  with and without crossover. Where  $p_m = 0.05$ , when  $p_c = 1$ ,  $S = 0.0008$  and  $T = 1121$ , when  $p_c = 0$ ,  $S = 0.0007$  and  $T = 2710$ . From these date, we can obtain the conclusion as follows. With crossover,  $T = 1/S$ . Without crossover,  $T > 1/S$ .

Figure 5 shows the convergence of average fitness is almost equal with and without crossover when  $p_m$  is large.

## 4 Summary

In numerical calculation, we found that our method reproduces the distribution of the first order schema, and our predicted success probabilities agree quite well with calculated ones. We also found that in the case

of crossover rate  $p_c = 1$ , the proposed estimator shows the good agreement with calculated  $T$ . In the case of no crossover, though the calculated success probabilities are almost the same as those calculated with crossover, the calculated  $T$  is larger than  $1/S$ . For example at string length  $L = 20$ ,  $T$  without crossover is about two times larger than  $T$ , which means crossover accelerates the speed of evolution in GA.

## References

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