

# The Nei's Standard Genetic Distance in Artificial Evolution

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**Abstract**—In recent years, not only ruggedness but also neutrality has been recognized as an important feature of a fitness landscape for genetic search. Following that the concept of neutrality in artificial evolution originates from Kimura's neutral theory in natural evolution, it is expected that the dynamics of artificial evolution in the landscapes including neutrality would be described by using techniques in population genetics. Furthermore, new theoretical guidelines might be developed for effective genetic search. In a recent paper [25], we have discussed the use of the *Nei's standard genetic distance*, which originates from population genetics, for measuring neutrality of fitness landscapes. In our results, several consistencies with the population genetics have been found by applying the Nei's standard genetic distance to a tunably neutral NK landscape. In this paper, computer simulations are systematically conducted by using a standard genetic algorithm in order to clarify the characteristics of the Nei's standard genetic distance. The terraced NK landscape is adopted as a test function.

## I. INTRODUCTION

Many EA researchers have been inspired by natural evolution and trying to model the process of natural evolution in order to develop powerful optimization methods [1][2][3]. Therefore, the dynamics in artificial evolution would be explained by the theory of natural evolution. But until recently, few theories which are applicable to artificial evolution have been found. Since the concept of neutrality was introduced into the EA community, EA researchers have expected that the dynamics of artificial evolution would be described by using techniques in population genetics. This is because the concept of neutrality in artificial evolution originates from Kimura's neutral theory in population genetics.

Therefore, neutrality has attracted much research interest in recent years [4][5]. This feature, due to highly redundant mappings from genotype to phenotype or from phenotype to fitness, is also found in natural systems. From this point of view, evolutionary theorists [6] and molecular biologists [7][8] also have investigated it.

Neutrality has been found in many real-world applications of artificial evolution, such as evolution of neural network controllers in robotics [9][10][11][12], on-chip electronic circuit evolution [13][14][15]. Landscapes which include neutrality have been conceptualized as containing *neutral networks* [16][17][18]. Harvey first introduced the concept of *neutral*

*networks* into the EA community [16]. He defined it as follows: "A neutral network of a fitness landscape is defined as a set of connected points of equivalent fitness, each representing a separate genotype: here connected means that there exists a path of single (neutral) mutations which can traverse the network between any two points on it without affecting fitness." For these years, several papers [19][20][17][18] have been published for investigating the evolutionary dynamics.

Population geneticists have been trying to explain evolutionary change quantitatively, that is, the change of gene frequency in the population. Statistical methods for estimating the number of gene differences and the divergence time between related species have been developed. These methods use electrophoretic data for investigating protein variation. The results are compared with the divergence time derived from the fossil records. However, population geneticists cannot get complete information about the genetic material through electrophoresis. In artificial evolution, EA researchers can get all the genetic information of a population. Furthermore they can define genetic operators. Therefore, the introduction of such statistical methods for estimating the number of gene substitutions would be helpful to understand the mechanism of EAs for solving difficult optimization problems.

From a theoretical point of view, it would be beneficial to investigate whether the number of substitutions estimated in EAs can be understood by the theory of natural evolution. According to Kimura's neutral theory [6] and Ohta's nearly neutral theory [21][22], the following assertions have been made [23]:

- 1) For each protein, the rate of evolution in terms of amino acid substitutions is approximately constant per year per site for various lines, as long as the function and tertiary structure of the molecule remain essentially unaltered.
- 2) Functionally less important molecules or parts of a molecule evolve (in terms of mutant substitutions) faster than more important ones.
- 3) Those mutant substitutions that disrupt less the existing structure and function of a molecule (conservative substitutions) occur more frequently in evolution than more disruptive ones.
- 4) Gene duplication must always precede the emergence of

a gene having a new function.

- 5) Selective elimination of definitely deleterious mutants and random fixation of selectively neutral or very slightly deleterious mutants occur far more frequently in evolution than positive Darwinian selection of definitely advantageous mutants.

Recently, we have discussed the use of the *Nei's standard genetic distance*[24], which is one of such statistical methods for estimating the number of substitutions, for measuring neutrality of fitness landscapes<sup>1</sup> [25]. In our experiments, several consistencies with population genetics have been found by applying the Nei's standard genetic distance to the results of evolution on tunably neutral NK landscapes. These can be summarized as follows:

Under small mutation rate per locus and fixed population size,

- The number of gene substitutions increases with the increase of neutrality.
- The number of gene substitutions decreases with the increase of ruggedness where the landscape includes neutrality.
- The number of gene substitutions is largest when random sampling is applied with mutation.

To clarify whether these results hold for different population sizes and to discuss the consistencies with population genetics, a systematic investigation should be done.

This paper investigates the characteristics of the Nei's standard genetic distance in fitness landscapes including neutrality in various conditions. The next section describes the Nei's standard genetic distance. Section III applies the Nei's genetic distance to one of tunably neutral landscapes called the terraced NK landscape and shows the results. Section IV discusses the *error threshold* on the population size and the mutation rate based on the obtained results. Conclusions are given in the last section.

## II. THE NEI'S STANDARD GENETIC DISTANCE

Genetic distance is a term of population genetics used for estimating gene differences per locus between populations. Although there are several definitions for this, the Nei's standard genetic distance [24] is adopted in this paper.

The Nei's standard genetic distance is defined as follows. Consider two populations,  $X$  and  $Y$ . Let  $x_{ik}$  and  $y_{ik}$  be the frequencies of the  $k$ -th alleles ( $i = 1, \dots, N$ ,  $k \in \{1, 2\}$ ) in a binary coded GA) in  $X$  and  $Y$ , respectively. The probability of identity of two randomly chosen genes is  $j_{xi} = x_{i1}^2 + x_{i2}^2$  in the population  $X$ , while it is  $j_{yi} = y_{i1}^2 + y_{i2}^2$  in the population  $Y$ . The probability of identity of a gene from  $X$  and a gene from  $Y$  is  $j_{xyi} = x_{i1}y_{i1} + x_{i2}y_{i2}$ . The normalized identity of genes between  $X$  and  $Y$  with respect to a locus is defined as

$$I_i = \frac{j_{xyi}}{\sqrt{j_{xi}}\sqrt{j_{yi}}}, \quad (1)$$

<sup>1</sup>Since the assertion 1), 2) and 3) can be interpreted as the number of gene substitutions of each genotype increases with the increase of neutrality, the number of gene substitutions could be an index of neutrality.

where,  $I_i = 1.0$  if the two populations have the same alleles in identical frequencies, and  $I_i = 0.0$  if they have no common alleles. The normalized identity of genes between  $X$  and  $Y$  with respect to the average in all loci is defined as

$$I = \frac{J_{XY}}{\sqrt{J_X}\sqrt{J_Y}}, \quad (2)$$

where,  $J_X = \sum_{i=1}^N j_{xi}/N$ ,  $J_Y = \sum_{i=1}^N j_{yi}/N$  and  $J_{XY} = \sum_{i=1}^N j_{xyi}/N$ . The genetic distance between  $X$  and  $Y$  is defined as

$$D = -\log_e I, \quad (3)$$

under the assumption that the mutation rate per locus is sufficiently small. However, the above definition cannot be applied to the standard GA directly, because it is assumed that a new allele always appears on a locus when a mutation occurs, while "back mutations [21]" frequently occur in the standard GA, due to the binary coding scheme. Therefore, the genetic distance between the population at the initial generation and the one at the last generation is calculated as:

$$D_{final} = \sum_1^{T-1} D_{t,t+1} \quad (4)$$

where  $T$  is the number of the last generation and  $D_{t,t+1}$  is the genetic distance between the population in the  $t$ -th and the  $(t+1)$ -th generation. The rate of gene substitution is defined as the genetic distance per generation.

## III. THE NEI'S STANDARD GENETIC DISTANCE IN A TUNABLY NEUTRAL NK LANDSCAPE

### A. A Terraced NK Landscape

A terraced NK landscape was employed as the test function in our computer simulations. This is the tunably neutral NK landscape proposed by Newman and Engelhardt [26]. A terraced NK landscape has three parameters:  $N$ , the length of the genotype;  $K$ , the number of epistatic linkages between genes; and  $w$ , the contribution of a locus to the fitness of the entire genotype.

The fitness value is calculated as follows: The fitness contribution of the  $i$ -th locus,  $w_i$ , is an integer generated randomly in the range  $0 \leq w_i < F$ ,  $i = 1, \dots, N$ . To calculate the fitness,  $W$ , of a genotype, the fitness contribution of each locus is averaged, and then divided by  $F - 1$ , normalizing  $W$  to the range 0.0 to 1.0. More formally:

$$W = \frac{1}{N(F-1)} \sum_{i=1}^N w_i. \quad (5)$$

The neutrality of the landscape can be tuned by changing the value of  $F$ . The neutrality of the landscape is maximized when  $F = 2$ , and is effectively non-existent as  $F \rightarrow \infty$ .

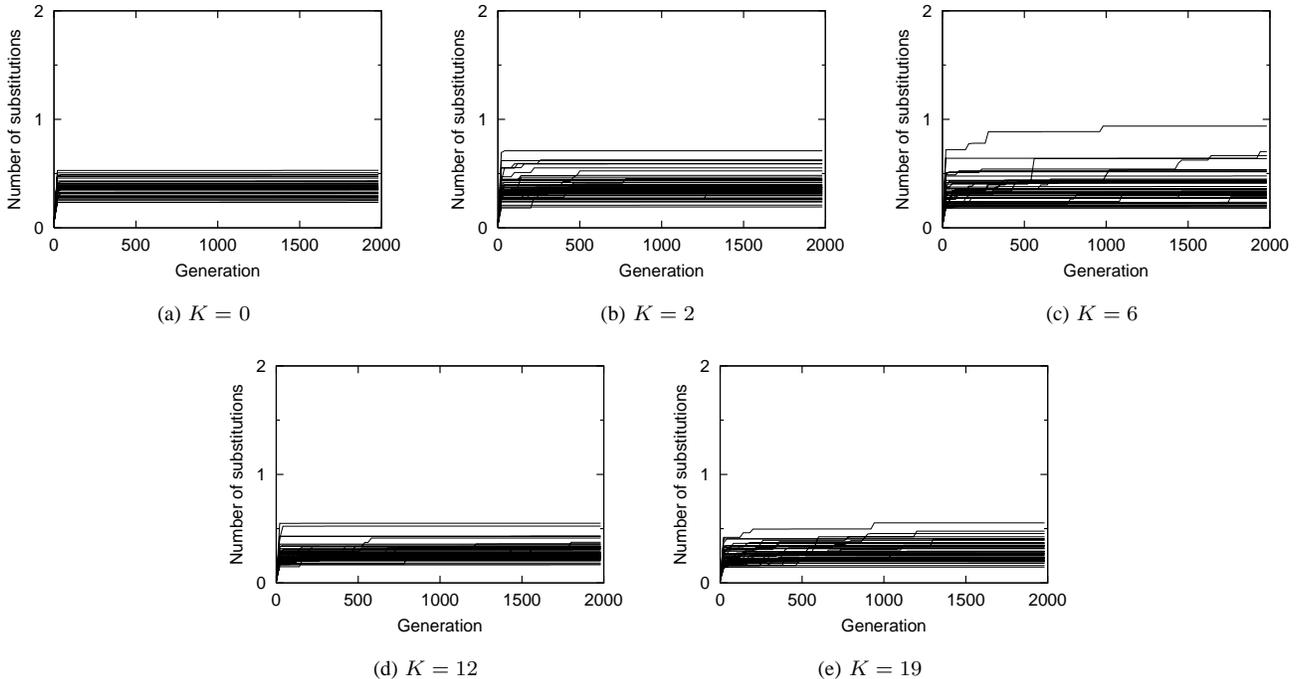


Fig. 1. Number of substitutions at each generation for the SGA with  $q = 0.008$  and  $M = 50$  for  $F = \infty$  in 50 runs

### B. Simulation Conditions

We applied two genetic algorithms: the standard GA (SGA) and the *(random-sampling, q)*-algorithm. The *(random-sampling, q)*-algorithm employs standard bit mutation at the rate of  $q$  as the genetic operation and random sampling as a selection method where  $M$  offsprings are sampled from  $M$  ancestors with replacements. This model was used to investigate the effect of random sampling with mutation on the genetic distance. This is approximately equivalent with Kimura's stochastic genetic models to study random genetic drift and the expected time of fixation of a mutant gene [6].

Computer simulations were conducted by varying the landscape parameters, the population size,  $M$ , and the mutation rate,  $q$ . The SGA used standard bit mutation as the genetic operation. Crossover was not employed. Tournament selection was adopted for the SGA. The tournament size was set at 2 for the SGA. Each run lasted 2,000 generations. We conducted 50 independent runs for each problem under the landscape parameters,  $N = 20$ ,  $K \in \{0, 2, 6, 12, 19\}$ ,  $F \in \{2, 3, 4, 6, \infty\}$ . The results were averaged over 50 runs.

### C. Existence And Non-existence of Neutrality

The first experiments were conducted to investigate the effect of the existence of neutrality on the transition of the genetic distance and the number of substitutions. Fig. 1 shows the number of substitutions of the SGA for  $F = \infty$ , where  $q$  was set at 0.008 based on the assumption of eq.(3). They

<sup>2</sup>For  $F = \infty$ , the NK fitness landscape[27] was employed instead of the terraced NK landscape as [5], which results in practically non-existence of neutrality.

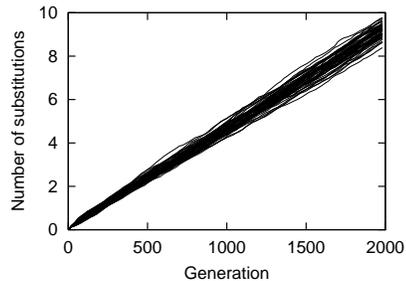


Fig. 2. Number of substitutions at each generation for the *(random-sampling, q)*-algorithm with  $q = 0.008$  and  $M = 50$  in 50 runs

leveled off in the very early generations. This means that the population converged to a certain point in the genotype space then the genetic distance between the generations ( $D_{t,t+1}$  in eq.(4)) became zero. In contrast, the number of substitutions of the *(random-sampling, q)*-algorithm (Fig. 2) and the SGA for  $F \neq \infty$  (for instance, the results for  $F = 2$  are shown in Fig. 3.) with  $q = 0.008$  increased approximately linearly over generations in all runs. This differentiates between the existence and the non-existence of neutrality in the fitness landscape. That is, the increase of the number of substitutions over generations indicates the presence of neutrality in the fitness landscape.

In the remainder of this paper, the rates of substitution for the *(random-sampling, q)*-algorithm and the SGA for  $F \neq \infty$  are shown by using the method of least squares on the results of all the runs because the rate of substitution is equivalent to the gradient of the number of substitutions over generations.

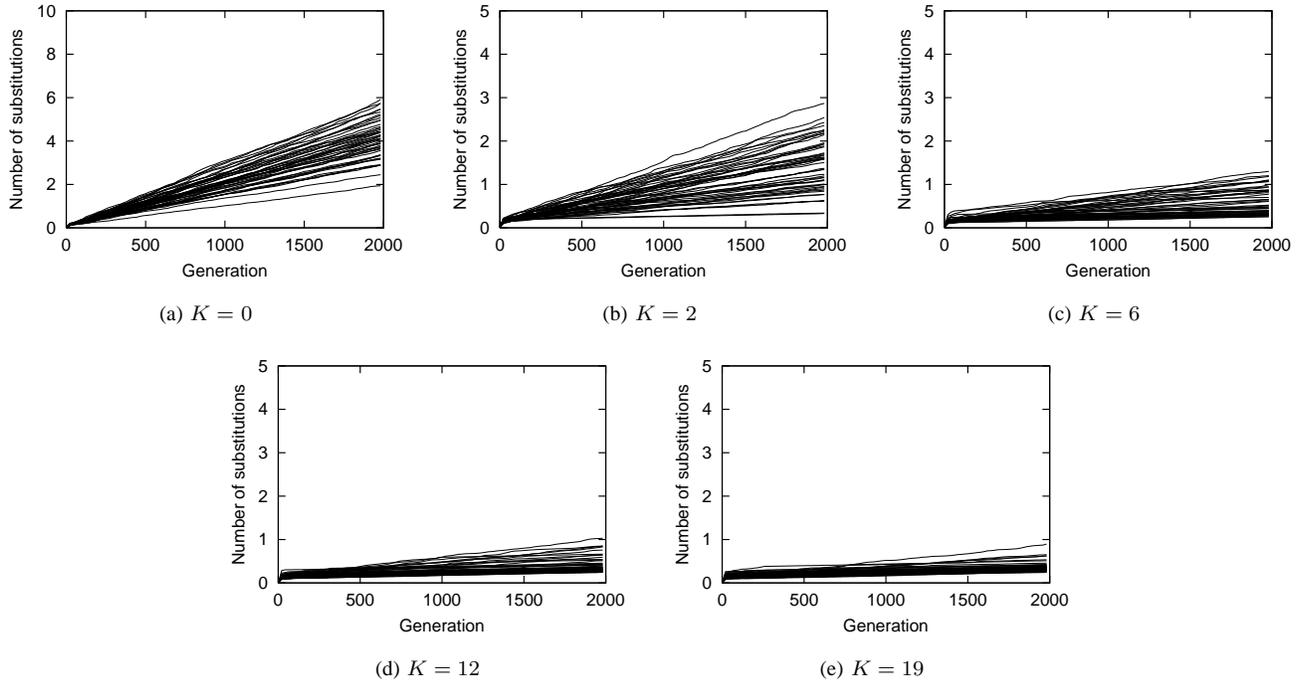


Fig. 3. Number of substitutions at each generation for the SGA with  $q = 0.008$  and  $M = 50$  for  $F = 2$  in 50 runs

TABLE I

THE RATE OF SUBSTITUTION FOR THE SGA WITH  $q = 0.008$  AND  $M = 50$

F \ K	0	2	6	12	19
2	0.002042	0.000666	0.000220	0.000131	0.000106
3	0.001307	0.000421	0.000173	0.000102	0.000104
4	0.001063	0.000318	0.000130	0.000099	0.000087
6	0.000738	0.000235	0.000128	0.000090	0.000087

TABLE II

THE RATE OF SUBSTITUTION FOR THE SGA WITH  $q = 0.008$  AND  $M = 100$

F \ K	0	2	6	12	19
2	0.001370	0.000401	0.000148	0.000079	0.000068
3	0.000843	0.000255	0.000096	0.000051	0.000050
4	0.000607	0.000164	0.000073	0.000057	0.000050
6	0.000405	0.000128	0.000056	0.000048	0.000044

TABLE III

THE RATE OF SUBSTITUTION FOR THE SGA WITH  $q = 0.008$  AND  $M = 200$

F \ K	0	2	6	12	19
2	0.000781	0.000263	0.000086	0.000040	0.000026
3	0.000486	0.000161	0.000051	0.000039	0.000028
4	0.000359	0.000119	0.000041	0.000029	0.000027
6	0.000238	0.000067	0.000031	0.000025	0.000026

TABLE IV

THE RATE OF SUBSTITUTION FOR THE SGA WITH  $q = 0.008$  AND  $M = 400$

F \ K	0	2	6	12	19
2	0.000434	0.000146	0.000043	0.000032	0.000024
3	0.000261	0.000087	0.000032	0.000025	0.000013
4	0.000193	0.000062	0.000019	0.000014	0.000019
6	0.000127	0.000050	0.000017	0.000017	0.000015

#### D. Neutrality And Selective Constraint

With respect to the assertions 1), 2) and 3) in Section I, Kimura has suggested that the rate of gene substitution is largest when the selective advantage of a new mutation over the original allele is zero except that the new mutation is deleterious in a small population [6]. Thus, it seems likely that the number of substitutions increases with the increase of neutrality and that for the (*random-sampling*,  $q$ )-algorithm is largest, because *random-sampling* can be considered completely neutral for selection. In addition to this, according to

Ohta's nearly neutral theory [21][22], the stronger the selective constraint on the molecule is, the lower its rate of evolution becomes. That is, the number of substitutions is likely to decrease with the increase of selective constraint,  $K$ .

Table I and Fig. 4 show the rate of substitution for the SGA with  $q = 0.008$  and  $M = 50$ . Notice first that the rate of substitution increased with the decrease of  $F$  for all  $K$ s. This means that the rate of substitution increases with the increase of neutrality as predicted. Secondly, the rate of substitution decreased with the increase of  $K$  for all  $F$ s.

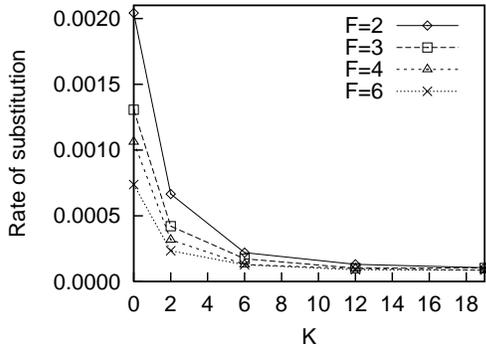


Fig. 4. Rate of substitution for the SGA with  $q = 0.008$  and  $M = 50$

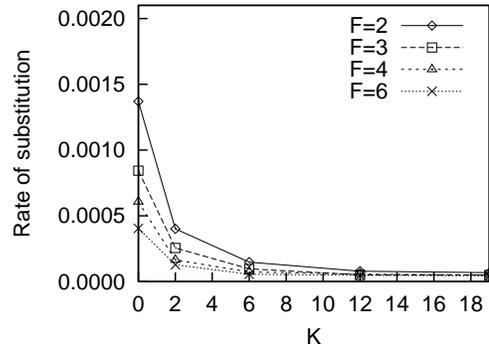


Fig. 5. Rate of substitution for the SGA with  $q = 0.008$  and  $M = 100$

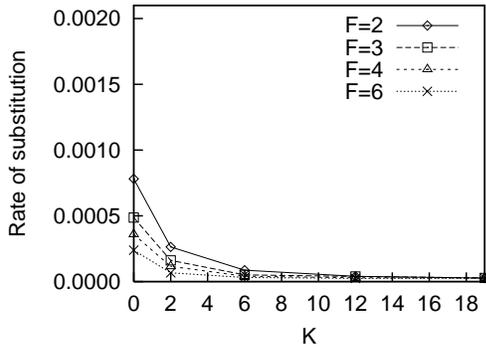


Fig. 6. Rate of substitution for the SGA with  $q = 0.008$  and  $M = 200$

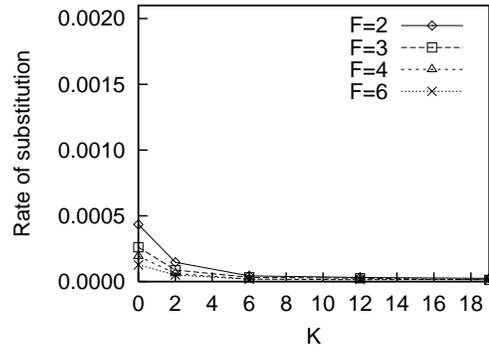


Fig. 7. Rate of substitution for the SGA with  $q = 0.008$  and  $M = 400$

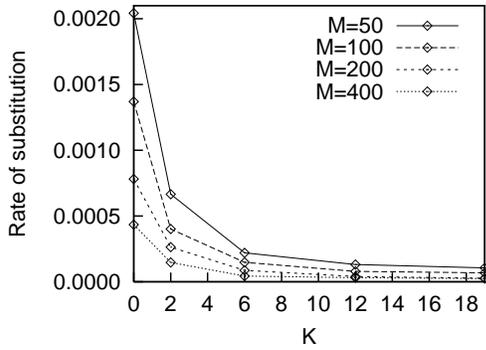


Fig. 8. Rate of substitution for the SGA with  $q = 0.008$  for  $F = 2$

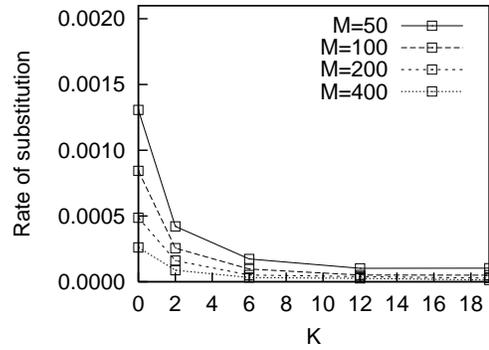


Fig. 9. Rate of substitution for the SGA with  $q = 0.008$  for  $F = 3$

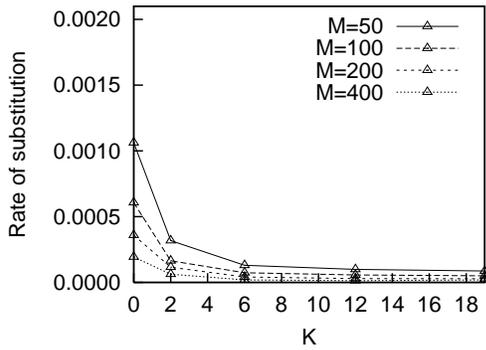


Fig. 10. Rate of substitution for the SGA with  $q = 0.008$  for  $F = 4$

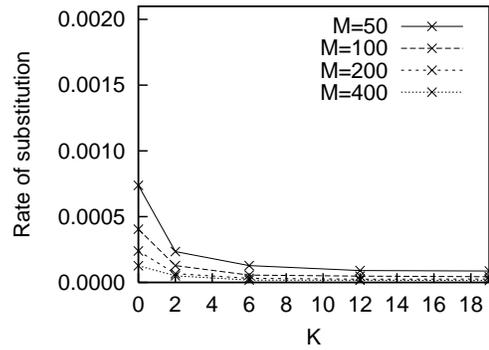


Fig. 11. Rate of substitution for the SGA with  $q = 0.008$  for  $F = 6$

TABLE V

THE RATE OF SUBSTITUTION FOR THE  $(random\text{-}sampling, q)$ -ALGORITHM  
WITH  $q = 0.008$  FOR EACH POPULATION SIZE

$M$	50	100	200	400
rate	0.004576	0.003194	0.001971	0.001120

This means that not only neutrality but also ruggedness has an influence on the rate of substitution. This tendency is consistent with Ohta's results for NK landscapes with weak selection based on the nearly neutral theory, where the number of substitutions decreases with the increase of  $K$  [22][28]. Similar behavior to  $M = 50$  is shown for each population size  $M = \{100, 200, 400\}$  (Table II, III and IV, and Fig. 5, 6 and 7).

The rate of substitution for the  $(random\text{-}sampling, q)$ -algorithm with each  $M$  is shown in Table V. It is confirmed that for each  $M$ , the rate of substitution for the  $(random\text{-}sampling, q)$ -algorithm was always larger than any others for the SGA with  $K$  and  $F$  (from Table I to IV). This agrees with our expectation.

#### E. Varying The Population Size

In the next experiments, the analysis was extended by varying the population size. According to Ohta's nearly neutral theory [21][22], population movement depends on the population size. That is, mutant dynamics becomes slower by increasing the population size. This is demonstrated from Fig. 8 to 11 and Table V. With the increase of the population size, the rate of substitution decreased for each  $K$  and  $F$ . Therefore, the larger the population size becomes, the slower the population moves. This tendency is also consistent with Ohta's results for NK landscapes with weak selection based on the nearly neutral theory, where the number of substitutions decreases with the increase of the population size [22][28].

Table V shows the rate of substitution for the  $(random\text{-}sampling, q)$ -algorithm with each  $M$ . The rate of substitution also decreased with the increase of the population size.

#### F. Varying The Mutation Rate

In population genetics, it is assumed that the mutation rate per locus is sufficiently small as mentioned in Section II. In the last series of experiments, the transition of the Nei's genetic distance were observed by varying the mutation rate from  $q = 0.005$  to  $0.010$  and  $0.1$  for the SGA with  $M = 50$ .

Fig. 12 shows the results with  $q = \{0.005, 0.006, 0.007, 0.008, 0.009, 0.010\}$ . In this range, the rate of substitution increased with the increase of the mutation rate for each  $K$  and  $F$ . For each  $q$ , similar behaviors were observed to the results with  $q = 0.008$  in the previous subsections. In contrast, the results with  $q = 0.1$  show the different behaviors (Fig. 13). Surprisingly, the rate of substitution increased with the increase of  $K$  for all  $F$ s. In addition to this, no significant differences were found between the graphs of different  $F$ s. The rate of substitution for the  $(random\text{-}sampling, q)$ -algorithm with  $q = 0.1$  was

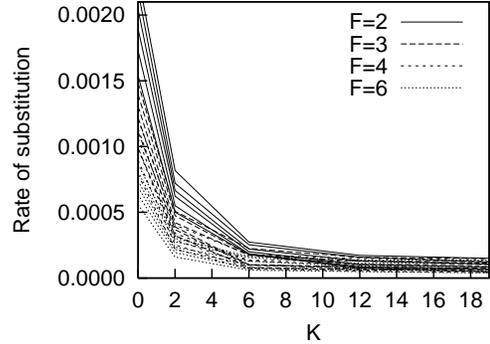


Fig. 12. Rate of substitution for the SGA with  $M = 50$ : The solid lines, from left to right, correspond to the rate of substitution for  $F = 2$  with  $q = \{0.005, 0.006, 0.007, 0.008, 0.009, 0.010\}$ . Similarly, the dashed lines correspond to the rate of substitution for  $F \in \{3, 4, 6\}$ .

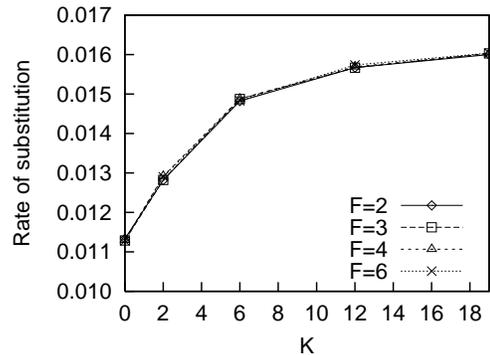


Fig. 13. Rate of substitution for the SGA with  $q = 0.1$  and  $M = 50$

0.0135733. Thus, the rate of substitution for the SGA was higher than that for the  $(random\text{-}sampling, q)$ -algorithm for  $K > 2$  and all  $F$ s. This implies that artificial evolution has changed into random search, caused by the mutation rate which is larger than the *error threshold*[17].

From the above, we confirmed that the Nei's genetic distance depends on the mutation rate, and can be used as long as the mutation rate is sufficiently small compared with the error threshold.

## IV. DISCUSSION

In the previous section, it has been shown that population movement depends on the population size. If the population size is small, the population for the SGA moves quickly. This would have the advantage of flexibility. As pointed out in [22], evolution would become more flexible for a small population size than for a large population size, particularly when the environment is not static, that is, the fitness landscape changes occasionally. On the other hand, it has been reported that as the population size becomes too small, it becomes easier for the population to lose the current best individuals through random sampling or mutation and fall to lower neutral networks [20]. This phenomenon is due to the influence of the error threshold on the population size<sup>3</sup>. This would be more understandable

<sup>3</sup>It has been known that there are two kinds of error threshold: on the mutation rate and on the population size [20][17].

by considering the population movement. Due to the small population size, the population on the neutral networks moves too quickly to keep the current neutral network. This implies that there exists the optimal population size that keeps the fastest speed as well as avoids the influence of the error threshold.

The same discussion can be applied to the error threshold on the mutation rate mentioned in Section III-F [17][18].

## V. CONCLUSIONS

We have investigated the characteristics of the Nei's standard genetic distance by applying it to the Terraced NK landscapes, and shown the consistencies of the results with the neutral theory and the nearly neutral theory in population genetics. Based on the presented results, we discussed the influence of the error threshold on the population size and the mutation rate.

The characteristics of the number of substitutions estimated by the Nei's genetic distance can be summarized as follows:

When the mutation rate per locus is small,

- Random sampling with mutation results in the largest number of substitutions.
- The number of substitutions increases with the increase of neutrality.
- The number of substitutions decreases with the increase of ruggedness where the landscape includes neutrality.
- The number of substitutions decreases with the increase of the population size.

These results can be predicted mainly by the assertion of the neutral theory and the nearly neutral theory, "functionally less important molecules or parts of a molecule evolve faster than more important ones". Consequently, these allow us to understand the evolutionary dynamics of GAs from the viewpoint of population genetics using the Nei's standard genetic distance. Therefore, this method will play a significantly important role that connects artificial evolution and natural evolution.

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