

# Tuning Genetic Algorithms for Problems Including Neutral Networks - The Simplest Case: The Balance Beam Function -

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## Abstract

Neutral networks, which occur in fitness landscapes containing neighboring points of equal fitness, have attracted much research interest in recent years. In this work, we applied a standard GA and an extended GA with a variable mutation rate strategy to an abstract model of neutral networks in order to investigate the effects of selection pressure and mutation rate on the speed of population movement. Our results demonstrate that speed has an optimal mutation rate and an error threshold since plotting speed against mutation rate results in a concave curve. Increasing selection pressure increased the speed of a population's movement on a neutral network. The variable mutation rate strategy of the extended GA improved the efficiency of the search. For both GAs, we found that high selection pressure was preferable, both for increasing the speed of population movement and for avoiding the effects of an error threshold on a neutral network.

## 1 Introduction

*Selective neutrality* has been found in many real-world applications of artificial evolution, such as the evolution of neural network controllers in robotics [1], and on-chip electronic circuit evolution [2]. This characteristic, caused by highly redundant mappings from genotype to phenotype, is also found in natural systems, and has been of particular interest to evolutionary theorists and molecular biologists [3]. Landscapes which include neutrality have been conceptualized as containing *neutral networks*.

Harvey [4] first introduced the concept of *neutral networks* into the GA community. His definition is 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 fit-

ness."

It has been shown that there is a clear transition in evolutionary dynamics for populations on neutral networks over the mutation rate range. At a very low mutation rate, the population is maintained in a cluster on the neutral network, analogously to *quasi-species* [5]. As the mutation rate increases, the population gradually loses the current network. That is, some individuals fall to lower neutral networks. At a certain critical mutation rate, the whole population will have fallen to lower neutral networks. This mutation rate is called the *phenotypic error threshold*<sup>1</sup> [7][8]. Generally, the error threshold sets the upper limit for a mutation rate that will enable efficient search. This implies that if we adopt a constant mutation rate strategy, we should set a low mutation rate so as to avoid any error threshold effects during the process of evolution. From a practical point of view, however, it would be efficient to shorten the equilibrium period<sup>2</sup> which dominates the whole computation (Fig. 1). One approach would be to employ *variable mutation rate strategies*, which change the effective mutation rate adaptively during the process of evolution. Another would be to investigate the effects of the constant (base) mutation rate, selection pressure and population size on search efficiency.

In this paper, we employ a standard GA, which employs a constant mutation rate, and an extended GA, which can change its mutation rate strategy, in order to investigate the effect of the selection pressure and mutation rate on the speed of population movement. Section 2 describes an abstract model of very simple neutral networks, called the *Balance Beam Function*, which is used as a test problem in this work. Section 3 gives the results of our computer simulations. Section 4 discusses the effect of selection pressure and the variable mutation rate strategy

<sup>1</sup>These concepts originate from molecular evolution [6].

<sup>2</sup>An equilibrium period is a period during which mean fitness of the population does not change [8].

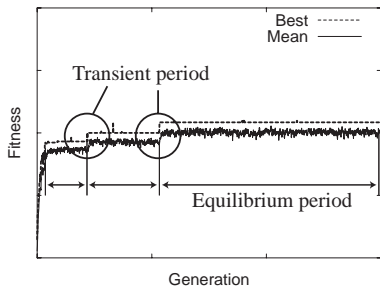


Figure 1: Typical evolutionary dynamics on a fitness landscape featuring neutral networks, which can be classified into transient periods and equilibrium periods [8]: Instead of being stuck in a local optimum, populations may be exploring in the genotype space.

on the evolutionary dynamics on the simple neutral networks. Conclusions are given in the last section.

## 2 Abstract Model of Simple Neutral Networks

The Balance Beam Function, proposed by Yasuda *et al.* [9], was employed as the test function in our computer simulations. It is relatively easy to investigate evolutionary dynamics with this function, because it has a landscape composed of only two neutral networks, each of a different fitness—one of which has the shape of a “balance beam”. The Balance Beam Function (*BBF*) is formulated as follows:  $F = 1.0$ , if  $(A \leq \sum_{i=1}^l s_i \leq B)$  and  $F = 0.0$ , otherwise, where  $F$ ,  $l$  and  $s_i \in \{0, 1\}$  are the fitness value, the length of the genotype and the value of the  $i$ -th locus, respectively.  $A$  and  $B$  ( $0 < A < B \leq l$ ) are constant integers. The neutrality is tunable by changing  $A$  and  $B$ . The abstract width,  $w$ , of a neutral pathway is calculated as  $B - A$ . We focus on the *moving speed* of the individuals which keep remaining on the higher neutral network ( $F = 1.0$ ).

As the initial setting, all individuals in the population are placed on a particular point on the higher neutral network, for instance,  $s_i = 1, i = 1, \dots, d$  and  $s_i = 0, i = d + 1, \dots, l$ , where  $d$  is a constant integer between  $A$  and  $B$ . This would be a situation similar to a population just after a transition period. In the process of evolution, each individual moves along the pathway by flipping the values of loci. Distance is defined as the number of 0s between the 1st locus and the  $d$ -th locus if the individual is on the higher neutral network. Distance is not defined for an individual on the lower neutral network. Therefore, the moving speed of a population can be measured as the number of generations (for generational GAs), or the number of evaluations (for steady state GAs) for one of individuals to reach the furthest distance,  $d$ . For the *BBF*, the optimal mutation rate,  $q_o$ , is identified as the mutation rate which results in the fastest speed over the mutation

rate range. The phenotypic error threshold,  $q_{err}$ , is identified as the mutation rate where the transition mentioned in Section 1 occurs.

## 3 Computer Simulations

### 3.1 Simulation Conditions

Computer simulations were conducted by setting the population size to 50 and the length of the genotype to 200. The extended GA used in this paper is called the operon-GA [10]. The operon-GA uses standard bit mutation and five additional genetic operators: *connection*, *division*, *duplication*, *deletion* and *inversion*. The probabilities for genetic operations were set at 0.3 for *connection* and *division*, 0.1 for *duplication* and 0.05 for *deletion* and *inversion*, as recommended by Ohkura and Ueda [10]. The length of the value list in a locus was 6. The genetic operation for the standard GA was standard bit mutation. For both GAs, the per-bit mutation rate,  $q$ , was set between 0.00001 and 0.1 with step sizes of  $\Delta q = 0.0001$  (if  $q < 0.001$ ), 0.001 (if  $0.001 \leq q \leq 0.01$ ) and 0.01 (if  $0.01 < q \leq 0.1$ ). Crossover was not used for either GA. Tournament selection was adopted. *Elitism*<sup>3</sup> was optionally applied. The tournament size was set at  $s = 2, 4$  and 6. A generational GA was used. Each run lasted 10,000 generations<sup>4</sup>. We conducted 10 independent runs for each problem with the parameters  $(A, B) = (19, 20), (19, 24), (19, 29)$  and  $(19, 39)$ ; that is, with neutral pathways of width  $w = 1, 5, 10$  and 20.  $d$  was set at 19. All results were averaged over 10 runs.

### 3.2 Simulation Results

Fig. 2 and 3 show the average number of generations to reach the furthest distance,  $d$ , with  $s = \{2, 4, 6\}$  and  $w = \{1, 5, 10, 20\}$ , for *non-elitism* and *elitism*, for the standard GA (SGA) and the operon-GA (OGA) respectively. The curves are U-shaped as a function of the mutation rate,  $q$ , and have an optimal mutation rate and an error threshold.

With *non-elitism*, the speed falls sharply when  $q$  exceeds  $q_o$ . Moreover, the optimal mutation rate is just below the error threshold (Fig. 2(a), 2(b) and Fig. 3(a), 3(b)). With *elitism*, both the optimal mutation rate and the error threshold increase, and so does the distance between them (Fig. 2(c), 2(d) and Fig. 3(c), 3(d)).

Increasing the tournament size increases the optimal mutation rate and the error threshold. It also results in improved speeds over the mutation rate range  $q_o < q < q_{err}$  (Fig. 2(a), 2(c) and Fig. 3(a), 3(c)). Due to space restrictions we only show results

<sup>3</sup>An individual, randomly selected from those individuals whose fitness value is 1.0, is passed unmutated to the next generation.

<sup>4</sup>If no individual reaches the furthest distance by the final generation, the number of generations to reach the furthest distance is taken to be 10,000.

for  $w = 1$ . However, increasing tournament size had the same effect for all widths.

The OGA produced higher speeds than the SGA when  $q$  was below  $q_o$  both with *non-elitism* and *elitism* (Fig. 4). Fig. 5 shows the average *effective mutation rate* in an OGA population for *non-elitism* and *elitism*, with  $s = 6$ ,  $w = 1$  and a per-bit mutation rate  $q = 0.001$ . (The evolutionary dynamics shown are representative of all OGA runs in this study.) The effective mutation rate is calculated as the number of flipped bits per genotype after the genetic operators have been applied. It is distributed around the optimal mutation rate  $q_o = 0.006$  (for *non-elitism*) and  $q_o = 0.01$  (for *elitism*).

## 4 Discussion

Our results suggest that optimal mutation rates and error thresholds are strongly correlated with selection pressure. With *non-elitism*, the optimal mutation rate will be just below the error threshold. If the mutation rate is set by estimating the optimal mutation rate, a misjudgement could result in the error threshold being exceeded, and thus lead to poor performance. With higher selection pressure, the optimal mutation rate and error threshold both increase. *Elitism* improves the moving speed when  $q$  is larger than  $q_o$ . Note that extreme elitism (e.g. 50% of offspring are identical to their parents) will reduce the moving speed, since the population will tend to repeatedly sample the same genotypes [11]. This may be related to the effects of sampling fluctuation. Nimwegen *et al.* [8] have suggested that there is an appreciable chance that all individuals on higher neutral networks will be lost through sampling fluctuations<sup>5</sup>. From these results, we can say that high selection pressure decreases the probability with which the individuals are lost through sampling fluctuation, with the result that the optimal mutation rate and error threshold are shifted to higher mutation rates. This would explain why, when  $q$  exceeds  $q_o$ , the moving speed improves if (relatively) high selection pressure is applied.

We have also shown that, for the BBF, the variable mutation rate strategy of the OGA improves the efficiency of the search when  $q$  is less than  $q_o$ , as a result of adaptively varying the effective mutation rate.

## 5 Conclusions

We have investigated the effect of the selection pressure and the mutation rate on the speed of population movement on landscapes with different levels of neutrality, using a standard GA and the operon-GA. Our results can be summarized as follows: (1) For a given population size, the speed of a population plotted as a function of the mutation rate

yields a concave curve with an optimal mutation rate and an error threshold. (2) When *non-elitism* is employed, the optimal mutation rate will be just below the error threshold. (3) If the mutation rate exceeds the optimal mutation rate, increasing the selection pressure will improve the speed at which a population moves on a neutral network. (4) The variable mutation rate strategy in the operon-GA improves search efficiency when the constant mutation rate is less than the optimal constant mutation rate.

Establishing the generality of these results will require investigating the performance of the standard GA and the operon-GA on more complex problems. However, our recent experiments with a more complex problem, terraced NK landscapes, suggest that these results may generalize well [12].

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<sup>5</sup>Higher neutral networks will tend to have narrower neutral pathways, with more bits on the genotype being subject to *selective constraints*.

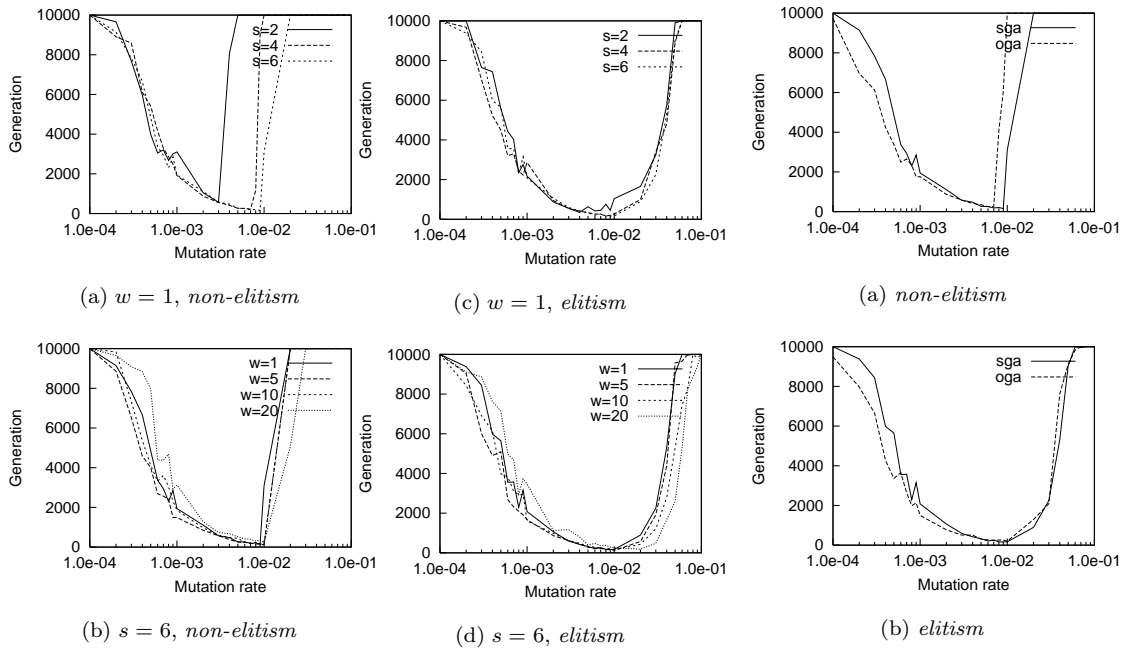


Figure 2: Average generations to reach the furthest distance in ten runs by the SGA

Figure 4: Comparison between the SGA and the OGA ( $w = 1, s = 6$ )

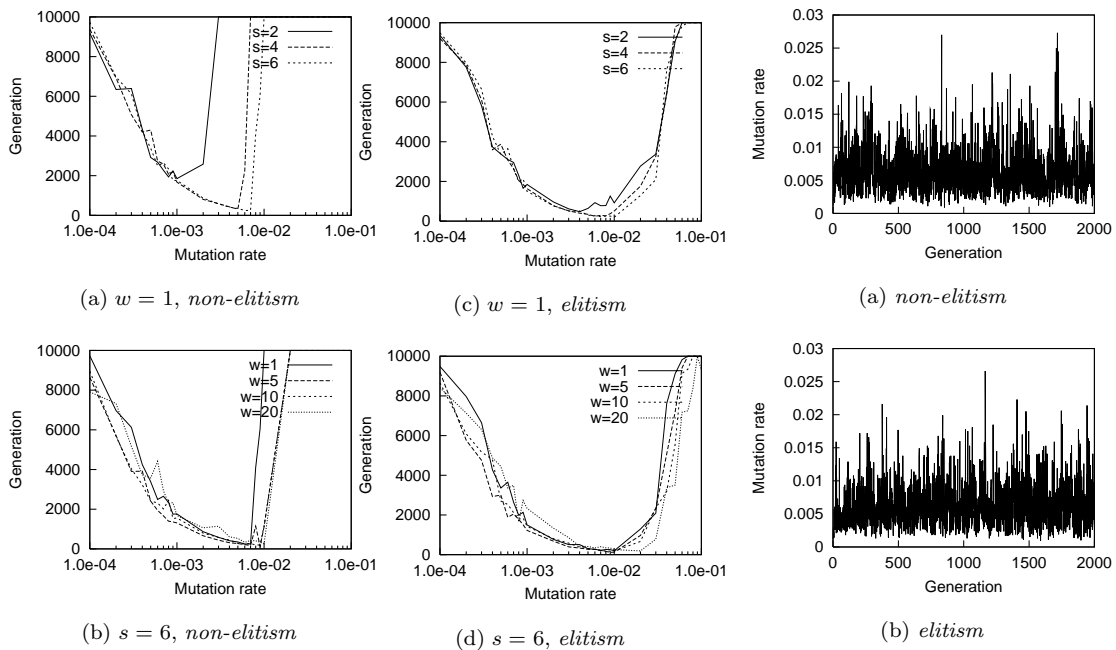


Figure 3: Average generations to reach the furthest distance in ten runs by the OGA

Figure 5: Effective mutation rate by the OGA ( $w = 1, s = 6, q = 0.001$ )