Measurements of Features of Fitness Landscapes on Competitive Co-Evolutionary Robotics

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ABSTRACT– Open-ended evolution is considered to be caused by several factors, one of which would be co-evolution. Competitive co-evolution can give rise to the "Red Queen effect", where the fitness landscape of each population is continuously changed by the competing population. Therefore, if such changes are captured, co-evolutionary progress would be measured. In this paper, we investigated features of competitive co-evolutionary fitness landscapes on a predator-prey problem in computer simulations. The results suggest to us that fitness landscapes on competitive co-evolutionary robotics have no correlation with respect to the genetic data obtained at each generation in the evolutionary runs.

Key Words: Competitive Co-Evolution, Evolutionary Robotics, Fitness Landscapes

1. INTRODUCTION

Open-ended evolution is considered to be caused by several factors, one of which would be co-evolution. In competitive co-evolution, "Red Queen hypothesis" has been discussed where a species must evolve for existence and it becomes extinct if it stops evolving. In the simplest scenario of two competing species, an advantage of one species might lead the disadvantage of the other species, then the other species also responds with counter-adaptive strategies to get its own advantage, which appear "a co-evolutionary arms race".

In competitive co-evolution, the fitness landscapes of competing populations might be continuously changed by such arms races. These changes could prevent populations from being stuck on local areas of the landscape [1] as well as stimulate them to move better regions. Therefore, if such changes could be captured, co-evolutionary progress would be measured.

In the Evolutionary Computation community, the geography of a fitness landscape has been discussed with respect to problem difficulties. These are conceptualized as *isolation*, *deception*, *multimodality* and *flatness*. In recent years, those are measured as the features of a fitness landscape, *ruggedness* (*epistasis*) and *neutrality* [2][3][4].

Recently, we have proposed two methods to estimate features of competitive co-evolutionary fitness landscapes on a predator-prey problem in computer simulations and investigated the Red Queen effect on the fitness landscape [5]. Our results can be summarized as follows:

- In the metric where the features of fitness landscapes are calculated based on the accumulated data from the initial generation to the current one, transition of the features in the fitness landscape almost converged during the process of evolution. Thus, we can not confirm ever-changing fitness landscapes in this metric.
- In the metric where the features of fitness landscapes are calculated based on the accumulated data for certain generations, we confirm the transition of the features over generations.

These were calculated based on the accumulated data for certain generations. We are also interested in whether these are observed through the metric calculated based only on genetic data obtained at each generation. This is because this metric seems natural for competitive co-evolution. In this paper, we investigated features of competitive co-evolutionary fitness landscapes calculated by genetic data

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obtained at each generation. The paper is organized as follows. The next section describes the method to estimate the degree of neutrality and ruggedness in fitness landscapes, which we proposed in [4], and then extends it for competitive co-evolution. Section 3 describes an experimental setup for a predatorprey problem in a robot control problem. Section 4 gives the results of our computer simulations. Section 5 discusses characteristics of the features of the fitness landscapes obtained in the experiments. Conclusions are given in the last section.

2. METHODS FOR MEASUREMENTS OF FEATURES OF FIT-NESS LANDSCAPES

In this section, the procedure for estimating features of a fitness landscape is described. Features to be measured are ruggedness and neutrality. Ruggedness is estimated based on the Smith's measurement[3] and neutrality is based on our measurement, the standard genetic distance[6, 4].

2.1 Measure of Ruggedness

In real-world problems, ruggedness of a fitness landscape is predicted by the fitness correlation [2][3]. In this paper, therefore, the Smith's measurement [3] was employed for the measure of ruggedness because fitness correlation can be expressed as a scalar value in their measurement. In [3], it has been reported that fitness correlation is expressed by the gradient of the expected offspring fitness versus parent fitness graph. The expected offspring fitness for parent fitness k is given by:

$$\bar{f}^k = \frac{\sum_{g \in G^k} f(g)}{|G^k|} \tag{1}$$

where, G^k is the set of offspring from parents with the fitness k over generations, g is an offspring genotype and f(.) is the fitness function. It has been also reported in [4][3] that the gradient, r, increases with the decrease of ruggedness, that this gradient is independent of neutrality and that $r \simeq 1.0$ without any epistatic linkages between genes and $r \simeq 0.0$ with maximum epistatic linkages. In order to measure features of competitive co-evolutionary fitness landscapes from genetic data obtained at each generation, as mentioned in Section 1, we did small modification to the original one as follows:

$$\bar{f}_{t_c}^k = \frac{\sum_{g \in G_{t_c}^k} f(g)}{|G_{t_c}^k|}$$
(2)

where, $G_{t_c}^k$ is the set of offspring from parents with the fitness k at the current generation, t_c . The gradient, r, of $\bar{f}_{t_c}^k$ for k is calculated by using the method of least squares for each generation.

2.2 Measure of Neutrality

2.2.1 Standard Genetic Distance and its characteristics

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[6] is adopted in our method [4].

The Nei's standard genetic distance is defined as follows. Consider two populations, X and Y. Let $x_{il} = n_{il}/M$ and $y_{il} = n_{il}/M$ be the frequencies of the *l*-th alleles $(i = 1, \dots, N, N, N)$, the length of the genotype, $l \in \{1, 2\}$ in a binary coded GA, n_{il} , the number of the *l*-th allele, M, the population size) 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 $I_i = j_{xyi}/(\sqrt{j_{xi}}\sqrt{j_{yi}})$ 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 $I = J_{XY}/(\sqrt{J_X}\sqrt{J_Y})$, 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 $D = -\log_e I$. The above definition cannot be applied to the standard GA directly, because it is assumed in population genetics that a new allele always appears on a locus when a mutation occurs while "back mutations [7]" frequently occur in the standard GA due to the binary coding scheme. Therefore, the genetic distance of GAs between the population at the initial generation and the one at the last generation is calculated as:

$$D(T) = \sum_{t=1}^{T-1} D_{t,t+1}$$
(3)

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.

In [8], we investigated the characteristics of the Nei's standard genetic distance mentioned above in the fitness landscapes with neutrality and ruggedness. The characteristics of the Nei's standard genetic distance can be summarized as follows:

When the mutation rate per locus is sufficiently small,

1. The genetic distance increases with the increase of neutrality.

2. The genetic distance decreases with the increase of ruggedness in landscapes with neutrality.

Considering these, we proposed a method for estimate the degree of neutrality in fitness landscapes with single species evolution [4]. That is, we estimate indirectly the degree of neutrality by measuring the gradient of the genetic distance over generations, α , as well as r in Section 2.1.

2.2.2 Estimation of the Degree of Neutrality

In order to measure the degree of neutrality of competitive co-evolutionary fitness landscapes, we calculate the genetic distance from genetic data obtained at each generation as follows:

$$D_{t_c} = D_{t_c-1,t_c},\tag{4}$$

where D_{t_c-1,t_c} is the genetic distance between the population in the current generation, t_c , and the previous generation, $t_c - 1$. Thus, the gradient of the genetic distance over generations, α , is D_{t_c} itself in this metric.

3. CONTROL TASK AND FITNESS FORMULA

The control task used in this paper was a predator-prey problem, and is based on a task originally implemented by Floreano [1]. Following the setting given in [1], this problem was implemented in the context of evolutionary robotics. The simulated environment is shown in Fig. 1(a), where a predator seeks to hit (capture) a prey. Generally, predators and preys are set belonging to different species which have different sensors and motors. Following this setting, two kinds of sensor arrangement were employed, one (the predator) is equipped with linear while the other (the prey) is equipped with omnidirection (Fig. 1(b)). Both agents were equipped with 18 infrared proximity sensors for detecting the opponent agent and walls. The agent's behavior is controlled by an ANN.

Employing a mathematical model of a mobile robot, the displacement of the agent was computed as follows: $x_{k+1} = x_k + \cos \theta_k (V_R + V_L)/2$, $y_{k+1} = y_k + \sin \theta_k (V_R + V_L)/2$, $\theta_{k+1} = \theta_k + (V_R - V_L)/2R$ where V_R and V_L are the velocities applied to the right and left wheel respectively, R is the radius of an agent, 2R is the interval between the wheels. The maximum speed is equally set for both agents. The system error was not implemented due to simple analysis.

At the beginning of each trial, the predator and prey were always positioned on a horizontal line at the four random orientations for each in the middle of the environment at a distance corresponding to half the environment width (Fig. 1(a)). One trial ended either when the predator hits the prey or when 400 steps are performed without the hit. Based on the fitness function used by [1], the performance



Fig. 1. Experimental setup for a predator-prey problem.

measure to be maximized for the predator, pr, and the prey, py, were as follows: $F_{pr} = \sum_{i=1}^{NumTrials} \{1 - Step_i/MaxStep\}/NumTrials, F_{py} = \sum_{i=1}^{NumTrials} \{Step_i/MaxStep\}/NumTrials$ where NumTrials is the number of trials for an individual (16 trials for each individual) and MaxStep is set at 400. The fitness function increases as the predator catches the prey more quickly while the prey escapes longer before being caught by the predator.

4. COMPUTER SIMULATIONS

4.1 Simulation Conditions

In this work, the agent controller was constructed by the ANN with 18 sensory neurons, 2 fully interconnected motor neurons and 3 fully interconnected hidden neurons. The connection weights among neurons were genetically encoded and evolved. The total number of parameters is equal to 115. The parameters were mapped linearly with the range, $\omega \in [-1.0, 1.0]$. The output of neurons is given by the sigmoid function, f(x) = 1/(1 + exp(-x)).

In the general settings of competitive co-evolution, an individual I from generation g is evaluated against representatives of I's opponent population from each previous generation [10]. In this experiment, however, each individual was evaluated only against an individual selected randomly from the same generation of the opponent population. This is because features of fitness landscapes are measured through genetic data obtained at each generation.

Computer simulations were conducted by setting the population size 50 for each species. Each individual was encoded as binary strings with 10 bits for each parameter. Therefore, the total length of the genotype is L = 1150. The simple GA (SGA) were adopted to evolve ANN parameters as well as calculate the genetic distance. The genetic operation for the SGA was standard bit mutation according to the setting in our previous results in [4]. Based on the assumption of the genetic distance in Section 2.2.1, the per-bit mutation rate, q, was set at 10/L. Tournament selection was adopted. Elitism was applied. The tournament size was set at 2. A generational model was used. Each run lasted 5,000 generations. We conducted 10 independent runs. We did not notice significant differences among these runs with respect to all the measures and analyses reported here. Therefore, for clarity of explanation, we give data for a single run, which will be described below.



Fig. 2. Maximum fitness at each generation



Fig. 3. Genetic distance α as a function of the correlation r

4.2 Simulation Results

Figure 2(a) and 2(b) show the maximum fitness at each generation for pr and py, respectively. We observed dominance of pr against py in almost every generation although a set of oscillations in fitness of py emerged.

Figure 3(a) and 3(b) show r and α at each generation for pr and py, respectively. The data were scattered widely around the value, r = 0, for each species. This seems less likely that there are correlation in their fitness landscapes. On the other hand, the genetic distances, α , were large. This means that those fitness landscapes include large neutrality.

5. Discussion

The obtained results in the previous section show that their fitness landscapes have no correlation from the view point of the short time period (for each generation). This means that evolutionary search became random. This would be explained as follows:

- In the experiment, each individual was evaluated only against an individual selected randomly from the same generation of the opponent population. Therefore, representatives of opponent population were substituted so frequently that fitness landscapes changed radically at each generation. As a result, both species could not adapt enough to each other.
- The features of the fitness landscapes were calculated only from the genetic data obtained at each generation. This seems likely that the amount of sampling data collected for each generation were too small to estimate features of the fitness landscapes adequately.
- The mutation rate set in the experiment was 10/L. Due to this rate, the effective mutation rate was likely to exceed a certain critical mutation rate[9] although we have confirm the characteristics mentioned in Section 2 at this mutation rate in our preliminary experiments using test functions.

6. Conclusions

In this work, we investigated features of competitive co-evolutionary fitness landscapes calculated by genetic data obtained at each generation. Our results can be summarized as follows:

- We confirmed the radical transition of the features of fitness landscapes but did not find any trends of them.
- The degree of ruggedness was so large that there were no correlation in their fitness landscapes.
- Fitness landscapes include large neutrality.

In this work, we also cannot confirm ideal co-evolutionary progress[10], where there is continuous progress in both competing populations. On the other hand, the obtained knowledges in this paper can help us understand the results obtained in the same kinds of experiments where fitness landscapes are changed so frequently such as evolution in dynamical environments.

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