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A Proposal of GA Using Symbiotic Evolutionary Viruses and Its Virus Evaluation Techniques

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Abstract– In this paper, we propose a Genetic Algorithm (GA) using symbiotic evolutionary viruses. Our GA is based on both the building block hypothesis and the virus theory of evolution. The proposed GA aims to control a destruction of building blocks by discovering, keeping, and propagating of building blocks based on virus operation. Concretely, we prepare the group of individuals and the group of viruses. In our GA, the group of individuals searches solutions and the group of viruses searches building blocks. These searches done based on the symbiotic relation of both groups. Also, our GA has two types of virus evaluation techniques. One is that each virus is evaluated by the difference of the fitness of an individual between before and after infection of virus. Another is that all viruses are evaluated by the difference of the fitness of an individual between before and after infection of all viruses. Furthermore, we applied the proposed GA to the minimum value search problem of a test function which has some local solutions far from the optimal solution. And, we discuss a difference of behaviors of the proposed GA based on each virus evaluation techniques.

I Introduction

We proposed a Genetic Algorithm (GA) using symbiotic evolutionary viruses[1]. Our GA is based on both the building block hypothesis[2] and the virus theory of evolution[3]. The proposed GA aims to control a destruction of building blocks by discovering, keeping, and propagating of building blocks based on virus operation. Concretely, we prepare the group of individuals and the group of viruses. In our GA, the group of individuals searches solutions and the group of viruses searches building blocks. These searches are based on the symbiotic relation of both groups. Also, our GA has two types of virus evaluation techniques. One is that each virus is evaluated by the difference of the fitness of an individual between before and after infection of virus. Another is that all viruses are evaluated by the difference of the fitness of an individual between before and after infection of all viruses.

On the other hand, various methods which pay attention to building blocks were proposed. As typical method, there is method by Kubota[4]. In Kubota's method, viruses are able to incorporate schemes of individuals. And, viruses are medium that propagate the incorporated schemes to other individuals. Namely, the Kubota's methods aims to keep building blocks exist in the individuals. On the other hand, in our GA, viruses propagates only oneself to individuals. Therefore, comparing with the Kubota's method, it is difficult for our GA to keeping building blocks exist in the individuals directly. But, viruses searches building blocks apart from the individuals. Therefore, when environments should be changed after convergence of the individuals, we will expect that viruses re-searches building blocks efficiently.

In this pepar, we apply the proposed GA to the minimum value search problem of a test function which has some local solutions far from the optimal solution. And, we discuss a difference of behaviors of the proposed GA based on each virus evaluation techniques.

II The Proposed GA

The proposed GA is based on both the building block hypothesis and the virus theory of evolution. Fundamentally, an evolution of our GA is based on a symbiotic relation both an individuals group and viruses group. We would like to explain a difference of the conventional GA and the proposed GA. In the conventional GA, child individuals succeed genes of parent individuals by a selection and a crossover. And, a mutation makes new genes which are not included in parent individuals. They mean a survival of fittest and an environmental adaptation of the Darwin's theory of evolution. On the other hand, in the proposed GA, viruses change genes of individuals. And, this individuals are caused the genetic operations same as the conventional GA. They mean rapid changes of individuals of the virus theory of evolution and the environmental adaptation of the Darwin's theory of evolution. A concrete procedure of the proposed GA is shown in Fig.1. In the proposed GA, the infection operation begins before GA operations such as selection, crossover and mutation. And, GA and the infection operations are repeated until a preset generation.

Here, we describe an composition of viruses. The virus has two types of information. One type is a gene information. Another type is a locus information. The gene information is represented by one bit of binary

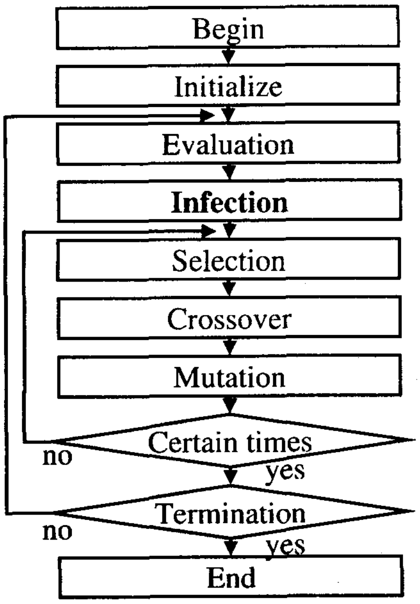

Fig. 1 The procedure of the proposed GA

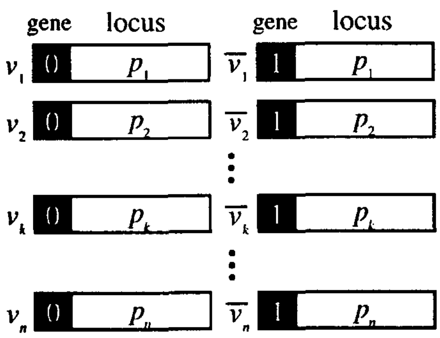

Fig. 2 The set of viruses

cord, and this information is able to become a one of parts of an individual. The locus information is represented by binary cord, and this information means a locus which the virus can infect with. Now, the proposed GA is applied to the problems whose solution candidates are represented by binary cord. Therefore, set of viruses are shown in Fig.2. Here, there are viruses which have the same gene information and the different locus information. These viruses are called the oppositional viruses.

Next, we describe an infection methods for an individual. The infection procedure is shown in Fig.3. Suppose one of the individual which is infected with the viruses were selected at random, the virus fixes the locus based on the locus information, and propagate the gene information to the fixed locus. Such a virus infection is performed to all loci of the selected individual. Also, the viruses are evaluated by the difference of the fitness of an individual before and after infection. This evaluation value of viruses is called $\mathsf{virusvalue}$.

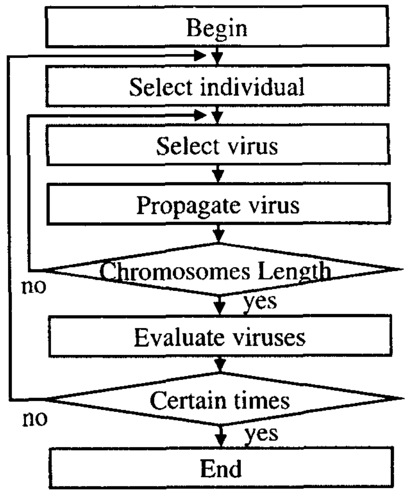

Fig. 3 The procedure of the proposed GA

Then, our GA has two evaluation techniques. One is that each viruses is evaluated by the difference of the fitness of an individual before and after infection of himself. It is called an independent evaluation. Another is that all viruses are evaluated by the difference of a same fitness of an individual before and after infection of all viruses. It is called a same evaluation. Suppose a generation was t, a infecting virus was v_k, a individual which was infected with virus v_k was m, and a group whose this individual belongs is S, each evaluation techniques are defined as Eqs.1 and 2.

$$\mathsf{virusvalue}_{v_k t} = \frac{\sum_{m \in S}(\mathsf{fitness}'_{v_k m} - \mathsf{fitness}_{v_k m})}{\#\{S\}} \quad (1)$$

$$\mathsf{virusvalue}_{v_k t} = \frac{\sum_{m \in S}(\mathsf{fitness}'_{mt} - \mathsf{fitness}_{mt})}{\#\{S\}} \quad (2)$$

where, $\mathsf{fitness}_{v_k m}$ and $\mathsf{fitness}'_{v_k m}$ are the fitness of individual m before and after the infection by virus v_k, and $\mathsf{fitness}_{mt}$ and $\mathsf{fitness}'_{mt}$ are the fitness of individual m before and after the infection by all viruses which include virus v_k. In the independent evauluation, we can evaluate each viruses strictly. But, it is difficult to evaluate a combination of viruses directly. And, In the same evaluation, we can evaluate a combination of viruses directly. But, it is difficult to evaluate each viruses strictly. Then, these infecting viruses are selected on each oppositional viruses. Suppose a generation was t, the selection probability of virus v_k is defined as Eq.3.

$$P_t[v_k] = f(\mathit{diff}_{kt}/T) \quad (3)$$

where, $\mathit{diff}_{kt}$is defined as Eq.4. Then, the selection probability of virus $\overline{v_k}$ $P_t[\overline{v_k}]$ is $P_t[\overline{v_k}] = 1 - P_t[v_k]$.

$$\mathit{diff}_{kt} = \mathsf{virusvalue}_{v_k t} - \mathsf{virusvalue}_{\overline{v_k} t} \quad (4)$$

Also, $f(x)$ is defined as Eq.5. Generally, this function is called the sygmoid function. This will cause that we can use the selection probability based on virus learning. And, $diff_{kt}$ is divided by parameter T. This will give us the selection probability which can deal with a many kinds of problem.

$$f(x) = \frac{1}{1 + \exp(-x^2)} \qquad (5)$$

And, suppose the number of individuals which are infected with viruses turned into a certain number, the infection terminate.

III Simulation

A Simulation Environments

In this paper we apply the proposed GA using each evaluation techniques to the minimum value search problem of a test function which has some local solutions far from the optimal solution. And, we discuss a difference of behaviors of the proposed GA based on each virus evaluation techniques. The test function is defined as Eq.6.

$$F(x) = \sum_{i=1}^{n} -x_i \sin\sqrt{|x_i|} \qquad (6)$$
$$(-512 \leq x_i < 512)$$

Also, we defined $n = 2$ and $\Delta x_i = 1$. Next, we defined simulation parameters as Table1. We determined these parameters by trial and error. We defined a fitness function for GA as Eq.(7).

$$fitness(x) = \frac{f_{max} - f(x)}{f_{max} - f_{min}} \qquad (7)$$

where f_{max} and f_{min} are maximum and mimimun values of the original sphere funcion, respectively. In Eq.(7), if the value of $f(x)$ becomes small, the value of fitness becomes large. And, the maximum value of **fitness** is one, and the minimum value of **fitness** is zero.

Also, in the proposed GA, viruses searches building blocks apart from individuals. Therefore, when environments should be changed after convergence of individuals, we will expect that viruses re-search building blocks efficiently. To confirm our expectation this character, we use the initialized individuals which belong to the solution space without an optimal solution. Concretly, this solution space is $-512 \leq x_i \leq 200$ because the optimal solution of this function is $x_i = 421$. It is called a fixed inidividual group initialization. And, generally, we define the **virusvalue** of all viruses as same value bacause we must set same to the selection probaility of all viruse. Howevere, there are two conditions of **virusvalues** when individuals are converging. One type is that on most of all oppositional viruses, the difference of **virusvalue** is large. we can view this type as the condition that the most of viruses are learning enough. Another type is that on most of all oppositional viruses, the difference of **virusvalues** is small. we can view this type as the condition that the most of viruses need learning more. Therefore, we prepare the two types of **virusvalue**'s initialization. One type is general initialization. Another type is that on the all oppositional viruses, the **virusvalue** of a virus whose gene information is 0 is temperature T, and the **virusvalue** of a virus whose gene information is 1 is zero. It is called a fixed virus initialization. The simulations were carried out 10 times in the above environments. Therefore, all simulation results in the next section are the averages of 10 simulations.

B Results

Fig.4 shows the best fitness transition of the proposed GA using each virus evaluation techniques. In this simulation, we use an initialized individuals group which belong the solution space $-512 \leq x_i \leq 512$, and the genaral virus initialization. Fig.4 says the proposed GA using the same evaluation has slower convergence than the proposed GA using the independent evaluation. Next, Figs.5 and 6 show the error distance from the optimal solution on the fixed inidividuals initialization. In Fig.5, we use the general virus initialization. In Fig.6, we use the fixed virus initialization. Fig.5 says the proposed GA using the independent evaluation searches more near the optimal solution than the proposed GA using the same evaluation.

Table 1 Simulation parameters

Population size	50
Gene length	20
Cording	Gray cording
Selection method	Roulette selection
Crossover method	Two point crossover
Crossover rate	0.9
Mutation method	Bit reverse
Mutation rate	0.025
Termination condition	1000 generations
Number of infection times	1
Temperature T	0.025

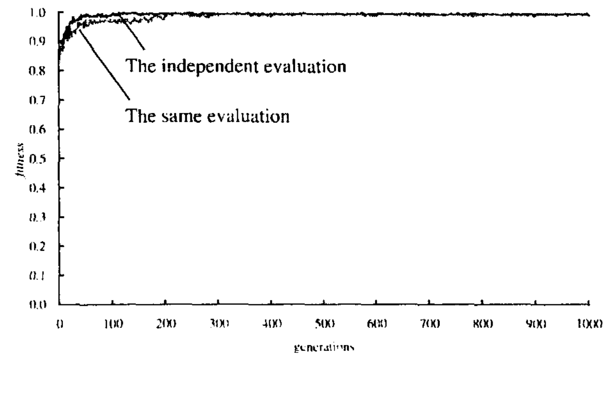

Fig. 4 The best fitness transition

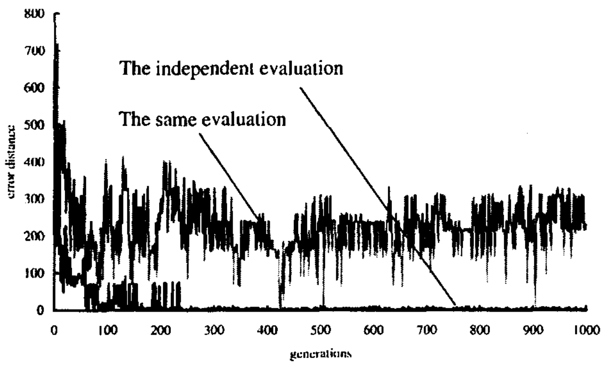

Fig. 5 The distance between best solution and the optimal solution (fixing viruses)

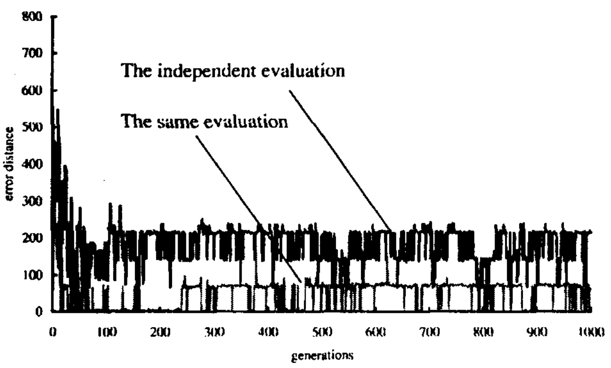

Fig. 6 The distance between best solution and the optimal solution

Because only viruses which must re-learn in enough learning viruses rel-earned effectively by strict evaluation to each viruses. On the other hand, Fig.6 says that proposed GA using the same evaluation searches more near the optimal solution than the proposed GA using the independent evaluation. In this environment, the learn degree of viruses is low. Therefore, the individual group moved near the optimal solution effectively by using a combination evaluation. And this conbination evaluation is based on the same evaluation.

IV Conclusions

In this paper, we proposed the GA using symbiotic evolutionary viruses. And, we discusses the difference of behaviors of the proposed GA based on each virus evaluation techniques. As the results, In the proposed GA using the independent evaluation, only viruses which must re-learn in enough learning viruses rel-earned effectively by strict evaluation to each viruses. And, In the proposed GA using the same evaluation, the individual group moved near the optimal solution effectively by using a combination evaluation. As future works, we need to apply the proposed GA to the cheat problem. And, we must discuss the behavior and usefulness of our GA.

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