

組み合わせ問題のためのウイルス進化論を用いた 遺伝的アルゴリズム

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概要 ウイルス進化論を模した遺伝的アルゴリズムが開発され、組み合わせ問題に適用された。この研究におけるアルゴリズムはひとつの個体とたくさんのウイルスを用いる。個体はウイルスにより攻撃され、感染され、改良される。ウイルスは二つの遺伝子(トップ遺伝子とテイル遺伝子)からなる。もし個体が攻撃によって改善されれば、感染が起こる。局所解を抜け出すために、感染に余裕率を設けている。感染後、ウイルスのテイル遺伝子は突然変異される。もし同じウイルスが数回攻撃し、感染しなかったならば、トップ遺伝子が突然変異される。個体はこの突然変異により、効率的に改善される。最適解を得るために、部分攻撃がまた有効である。

A Genetic Algorithm by Use of Virus Evolutionary Theory for Combinatorial Problems

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Abstract *A genetic algorithm that simulates the virus evolutionary theory has been developed and applied to combinatorial optimization problems. The algorithm in this study uses only one individual and a population of viruses. The individual is attacked, infected and improved by the viruses. The viruses are composed of two genes (a top gene and a tail gene). If the individual is improved by the attack, infection occurs. To escape from local minima, an infection allowance is set. After the infection, the tail genes are mutated. If the same virus attacks several times and fails to infect, the top genes of the virus are mutated. The individual can be improved effectively using this mutation. To obtain the optimal solution, "sub-attack" is also useful.*

1 Introduction

Recently, several evolutionary theories such as the virus evolutionary theory [1] have been proposed in biology. In this study a genetic algorithm (GA) that simulates the evolutionary theory by virus infection (GAV) has been developed and reported [2][3][4].

A standard GA is a simulation based on the mechanism of natural selection also known as the evolutionary theory of Darwin. The standard GA is carried out by generating a number of individuals and performing selection, crossover and mutation on them.

On the other hand, GAV developed in this study uses only one individual and a population of viruses. The individual is attacked and infected by the viruses and the individual is improved without using the selection and the crossover and so on.

2 The Virus Evolutionary Theory

Imanishi's evolutionary theory [5] posits that the evolution of species occurs drastically in a short period (horizontal evolution) after keeping its characteristics stable for a relatively long period. It is also presumed that the mechanism of Imanishi's

evolutionary theory can be explained by the virus evolutionary theory.

The virus evolutionary theory in biology assumes that the genes of a virus or transposons of another individual are buried on the chromosome of an individual by the virus and bacillus.

Table 1: A chromosome for way

Route	3	18	5	4	21	...
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3 Algorithm of GAV

3.1 The chromosome

The chromosome is expressed by the string of the genes as shown in Table 1. The GAV developed in this study uses a single individual. The chromosome of Table 1 shows the route that is described by the sequence of the numerals.

3.2 The genes of the virus

The virus is composed of two genes, the top gene and the tail gene (Figure 1). Although there is only a single chromosome, a population of viruses is generated in this algorithm. These viruses are mutated after the attack on the chromosome.

3.3 The virus attack

If one of the viruses attacks the individual, the genes of the chromosome are attacked (Figure 1). The virus attacks the gene of the individual that is same to the top gene.

If the individual is improved by the attack, the infection occurs by reversing the segment of the chromosome between the next gene after the top gene and the tail gene. After the infection, the tail genes are mutated. If the same virus attacks several times and fails to infect, the top genes of the virus are mutated. The mutation of viruses is very important for the improvement of the individual.

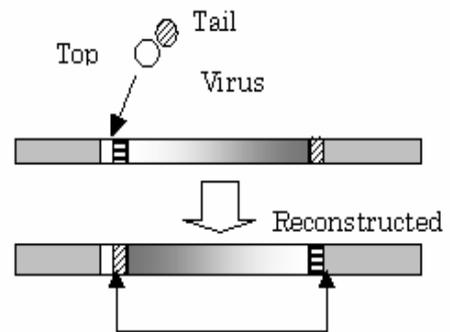


Figure 1: The virus attack

3.4 Escape from the local minimum

Solutions determined by the procedure stated above fall easily into local minima as in other search methods. To escape from the local minima, two methods are proposed. One method introduces an allowance into the infection process. This allowance allows an infection to occur even if it worsens the evaluation value at a small rate. In this report, the value of the allowance is modified according to whether it is infected by the attack. Therefore, the proper value of the allowance is set automatically.

Another method is to allow multiple partial attacks as described later in section 4.2. This method is very useful for escaping from local minima. This attack is referred to as "sub-attack" in this paper.

3.5 The flow of the basic GAV algorithm

The following is the basic GAV algorithm:

- Start;
- Generate the individual;
- Generate a population of the viruses;

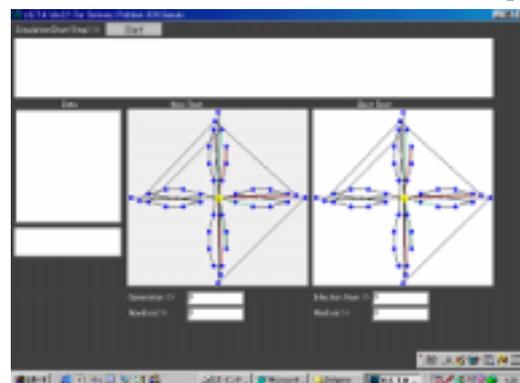


Figure 2: The initial condition of the program

Repeat until a satisfactory solution is reached;

Attack the virus;

Repeat sub-attack of the virus;

Evaluate the objective function;

if objective function increased
{Infect by virus; Decrease AR by 0.01 ;}

else, if the objective function value is less than AR times the previous one

{Infect by virus; AR is decreased by 0.01; }

else, if the objective function value is more than AR times the previous one {Infection is not allowed.; AR is increased by 0.0001;}

Mutate the tail gene of the virus;
if the attack by the same virus fails to infect several times,
{Mutate the top gene; }

End of repeat of sub-attack;

End of repeat;

End.

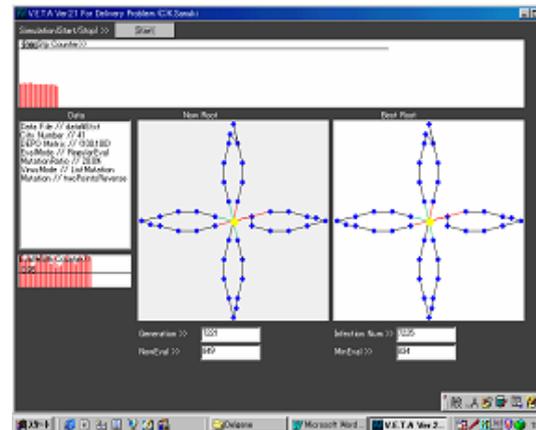


Figure 3: The optimal solution

Table 2: Average attack frequency

A1	5	10	20	30	40
AAF	7062	6621	7197	7825	9369

AR is the allowance rate. If the evaluation value multiplied by AR is lower than the previous evaluation value, the infection is admitted.

4 Results of GAV

Figure 2 shows the initial condition of the execution for the vehicle routing program. The optimal value of the solution is 800.

Figure 3 shows the optimum solution is obtained.

It looks easy to obtain the optimal condition. But this problem is easily trapped in local minima and it is difficult to obtain the optimal solution.

Two models (the first and the second model) are tried in this algorithm.

4.1 The First Model

The value of AR is adjusted according to the infection or non-infection of the viruses in the first model. Therefore the proper value of the AR is set automatically.

(1) If the infection is allowed, AR is decreased by 0.01.

(2) If the infection is not admitted, AR is increased by 0.0001, 0.0002 or 0.0005.

(3) The former value of the evaluation is multiplied by AR once every 100 attacks.

If the evaluation value becomes small compared with the multiplier, the infection is also allowed and the AR is decreased by 0.01.

(4) The previous value is multiplied by 1.3 once every 500, 1000 or 2000 attacks, and then if the evaluation value becomes small compared with the multiplier, the infection is also allowed and the AR is decreased by 0.01.

4.2 The second model

The second model is an improvement of the first model.

(1) The second model allows multiple partial virus attacks. This attack is called a “sub-attack” in this report. The number of multiple sub-attacks is denoted by A1 in Table 2. This sub-attack is repeated at a certain frequency A1 (5,10,,,,,) as described in Table 2.

(2) It increases the AR by 0.0001 when the infection fails at a frequency greater than B1 (Table3) and by 0.00005 at attack number of over a certain number B2 (Table 3). This is in order to decrease the rate of infection that makes the objective function value worse as the attack frequency increases.

By implementing these improvements, an optimal solution is obtained at almost every trial.

Table 2 shows the results of the second model where AAF in Table 2 is the Average Attack Frequency for each A1.

In this case, A1=10 shows the best result.

4.3 The comparison between the first and second model

Figure 4 show the time series of the objective function value of the second model. The dotted lines in Figure 4 indicate the optimal value of evaluation.

The first model shows that there are a lot of useless attacks. On the other hand, for the second model, the evaluation value changes significantly at attack frequencies less than 3000 (see Figure 4) and it is recognized that the useless attacks are reduced at attack frequencies higher than 3000.

Table 3: The influence of B1 and B2

B1	5000	3000	2000	1000
B2	10000	8000	5000	3000
AAF	6621	5875	6071	3091

5 Conclusions

An algorithm that expresses the combinatorial problems by chromosomes and solves them by improving the chromosome by attacking it with many viruses has been developed. The validity of the algorithm has been recognized through application to the vehicle routing problem.

This method (GAV) has one defect; it falls into local minima like in other search methods. Some means are pursued to escape from these local minima. The improvements are carried out by allowing infections that worsen the objective function’s value by setting an allowance rate (AR) at a small probability. In this case, the value of AR is set automatically according to the virus infection or the failure of the infection. The sub-attack is also useful for escaping from the local minima and for obtaining an optimal solution.

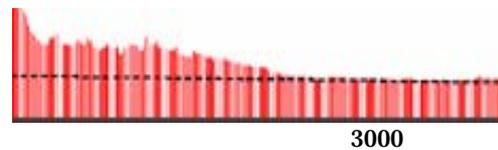


Figure4: The time series of the second attack, A1=10, B1=1000, B2=3000

References

- [1]Anderson,N., Evolutionary Significance of Virus Infection, Nature, Vol227, 1347, (1970)
- [2] Saito,S., A Genetic Algorithm by Use of Virus Evolutionary Theory, Proc. of 2nd Asia-Pacific Conf. on Industrial Engineering and Management System, 335-338(1998)
- [3] Saito,S., A Genetic Algorithm by Use of Virus Evolutionary Theory for Combinatorial Problem, Proc. of APORS (CD-ROM)(2000)
- [4] Saito,S., A Genetic Algorithm by Use of Virus Evolutionary Theory for Scheduling, Proc. of SeoulSim2001, 365-369(2001)
- [5] Harstead,B,. Anti-Darwinian Theory in Japan Nature, Vol.317, 587(1985)