# 遺伝的アルゴリズムにおける交叉作用素の有効性と遺伝子座変換 竹内 勝

# 株式会社 日立製作所 基礎研究所

あらまし 遺伝的アルコリズムにおけるビルディングブロック仮説を支持する実験結果を示す。実験で取り上げた課題は2次関数の最大値探索問題である。この課題では突然変異より交叉作用素が最適化に有効である。また、実験結果は進化の初期段階では交叉作用素より突然変異が有効に働き、ビルディングブロックが形成されたと考えられる後期段階では交叉作用素が有効に働くことを示す。さらに、遺伝子座変換法というビルディングブロックの形成を促す手法を提案する。これは、適応過程において自動的に遺伝子座を並べ変える手法である。遺伝子座変換法は計算量が大きいという欠点を持つが、前もって最適な遺伝子座を決定する必要がないという利点を持つ。

# Benefits of Crossover and the Locus Transformation Masaru Takeuchi

Advanced Research Laboratory, Hitachi, Ltd. Hatoyama, Saitama 350-03, Japan

Abstract Experimental evidence to support the building block hypothesis is presented. The experiments is aimed at finding the optimal point which gives the maximum value of a quadratic form. Crossovers are more beneficial than mutations in this regard. The results show that crossover is less advantageous at the initial stage of evolution but becomes superior after a number of generations, when it seems that some of the building blocks have been constructed. A new method called the locus transformation method is proposed. This is a procedure which rearranges loci automatically during the adaptive process. It promotes self-organization of building blocks if the building block hypothesis is true. The method is costly in terms of computation, but adopting the method obviates the need to determine rational loci in advance.

#### 1 Introduction

Genetic algorithms (GAs) construct systematic data, called building blocks, describing the relevant part of the information structure of an environment during the adaptive process. It is important to investigate procedures to accelerate the growth of systematic data in self-organizing systems. It has been stated that sophisticated genetic operators are required for self-organization of building blocks [1]. However, Fogel and Atmar [2] have suggested that only selection and mutation are needed to reach the optimal solution. Their experimental evidence concerning linear equation systems shows clearly that sophisticated genetic operators are not required. They suggest that it would be interesting to quantify the benefits, if any, of using sophisticated genetic operators in a variety of environments. This paper shows that there exists an environment in which sophisticated genetic operators are more useful than mutations.

# 2 Method

The problem is to find the optimal point which gives the maximum value of a quadratic form defined in a bounded domain. Consider an *n*-dimensional quadratic form

$$f(x) = \sum_{j,j'=1}^{n} a_{jj'} x_j x_j', \tag{1}$$

which is defined in the n-dimensional bounded domain

$$x = (x_1, x_2, ..., x_n) \in [0, 1]^n.$$
 (2)

To apply a GA to this environment, consider a population P of size m

$$P = \{c_i | i = 1, ...m\}. \tag{3}$$

Each chromosome  $c_i$  is identified by an *n*-dimensional vector defined in the domain

$$c_i = (g_{i1}, g_{i2}, ..., g_{in}) \in [0, 1]^n,$$
 (4)

and the fitness criterion is the quadratic form

$$f(c_i) = \sum_{j,j'=1}^{n} a_{jj'} g_{ij} g_{ij'}.$$
 (5)

The adaptive process using a GA was simulated with randomly chosen coefficients  $a_{jj'}$ s. Coefficients were restricted to within [0,1] in this experiment (Fig.1,(1)). Two populations of different types

P<sub>1</sub> and P<sub>2</sub> were used to compare crossover and mutation: one generates offspring using mutation and the other generates them using crossover. The chromosome length was 10 and initial components of chromosomes in each population were determined randomly with uniform distribution between 0 and 1. Cardinalities of initial populations were equal and the sum of cardinalities was 200 (Fig.1,(2)). Each chromosome in each population was assigned a fitness value according to the fitness criterion of equation (5) (Fig.1,(3-1)). New populations were constructed using a single roulette wheel with slots weighted in proportion to fitness values. In this process, it is expected that the cardinality of the population which adapts better than the others to the environment will increase (Fig.1,(3-2)). The chromosomes in each population were modified separately. The chromosomes in P1 were modified using simple random mutation (100% chance per component). Each component was altered by adding the previous value to the random value with a normal distribution of zero mean and unit variance. The chromosomes in  $P_2$  were modified using one point crossover (60% chance per chromosome) and simple random mutation (1% chance per component) (Fig.1,(3-3)). The two populations competed in the same environment. The population that adapted better is expected to survive after a number of generations (Fig.1,(3)), so the superior operator for the environment was decided by summing the number of wins over a number of different trials (Fig.1,(4)).

```
Repeat Given Times
(1) Generate a Trial.
(2) Initialize Two Populations.
(3) Repeat until the Size of Either of the Populations is Zero.
(3-1) Calculate Fitness Values.
(3-2) Selection (Common).
(3-3) Modify Chromosomes (for Each Population).
(4) Record the Winner.
```

Fig.1. Algorithm 1: Comparison Using Competition.

# 3 Experimental Findings

The results of 1000 trials are presented in Table 1. They suggest that crossover has advantage over mutation in the present environment.

Operator	Number of Wins
Mutation	274
Crossover	$\bf 726$

Table 1. Comparison between Mutation and Crossover.

An example how the competition developed is presented in Fig.2. At first the cardinality of  $P_1$  increased, but it then decreased after seven generations.

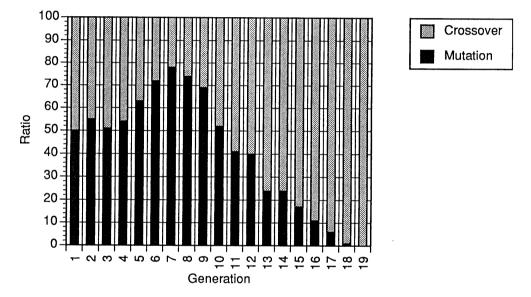


Fig.2. Evolution in Competition.

The development processes after smoothing can be classified into three types. In the first type, the cardinality of the mutation population increases monotonically, and the mutation population wins. In the second type, the cardinality increases at first and then decreases (i.e. is unimodal as shown in Fig.2), and the crossover population wins. In the third type, the cardinality decrease monotonically, and the crossover population wins. The results of 100 trials are presented in Table 2. It seems that mutation has the advantage in the first stage of the adaptive process, but that once the building blocks are self-organized, crossover becomes advantageous.

Type	1st	2nd	3rd
Frequency	37	51	22

Table 2. Classification of Development Processes.

If the building block hypothesis is true, it is assumed, that building blocks are constructed in the early stages of the second type of development process and crossover gains the advantage in the later stages. In the third type of process, it may be speculated that building blocks are formed during the very first stages and crossover wins from the early stages. These results suggest that crossover has advantage over mutation.

# 4 Locus Transformation

GAs are required to construct building blocks. A new method called the locus transformation (LT) method is therefore proposed to accelerate the growth of building blocks. A locus transformation  $\sigma$  is an element of a permutation group of size n and is applied to the loci of chromosomes. The schemata theorem shows that schemata with short defining lengths and high fitness values have a high probability of surviving during the adaptive process. The purpose of the transformation method is to promote the generation of schemata with such properties if the building block hypothesis is true.

The LT to be applied is determined according to the following criterion in the adaptive process. For all loci, calculate covariance  $\gamma_{jj'}$  of locus j and locus j' as

$$\gamma_{jj'} = \frac{1}{m} \sum_{i=1}^{m} (g_{ij} - \mu_j)(g_{ij'} - \mu_{j'})$$
 (6)

where

$$\mu_j = \frac{1}{m} \sum_{i=1}^m a_{ij} \tag{7}$$

and choose a LT  $\sigma$  from a permutation group of size n such that

$$\max_{\sigma} \sum_{j=1}^{n-1} \gamma_{\sigma(j)\sigma(j+1)}. \tag{8}$$

This rearrangement criterion is designed to maximize the sum of the covariances of incident loci. The fitness criterion is

$$f(c_i) = \sum_{j,j'} a_{jj'} g_{i\sigma(j)} g_{i\sigma(j')}.$$
 (9)

Part of algorithm 1 can be modified to adopt the LT method as shown in Fig.3.

- (3) Repeat until the Cardinality of Either of the Populations is Zero.
  - (3-1) Calculate Fitness Values.
  - (3-2) Selection (Common).
  - (3-3) Modify Chromosomes (for Each Population).
  - (3-4) Calculate Covariance (in  $P_2$ ).
  - (3-5) Rearrange Loci (in P<sub>2</sub>).

Fig.3. Algorithm 2: Locus Transformation.

The results of competition between crossover with LT and crossover without LT are presented in Table 3 for various probabilities of crossover and mutation. For each combination of probabilities, 100 trials were done. The results suggest that the LT method has advantages in this environment except when the probability of crossover is 0.0 (i.e. using mutation only).

#### Probability of Mutation = 0.01.

Probability of Crossover	0.0	0.2	0.4	0.6	0.8	1.0
without LT	53	30	28	24	23	33
with LT	47	70	72	76	77	67

#### Probability of Crossover = 0.6

Probability of Mutation	0.00	0.01	0.10	1.00
without LT	24	24	24	28
with LT	76	76	76	72

Table 3. Comparing Crossover without LT and with LT.

The results of 1000 trials comparing mutation against crossover with LT are presented in Table 4. Crossover with LT has the advantage over mutation in the present environment. The proportion of cases in which the population using the LT method wins is higher than that without the LT method in table 1.

Operator	Number of Wins		
Mutation	117		
Crossover with LT	883		

Table 4. Comparing Mutation against Crossover with Locus
Transformation.

The resulting classification of development process types is presented in Table 5. The proportion of the second type in Table 5 is higher than that in Table 2.

Type	1st	2nd	3rd
Frequency	13	72	15

Table 5. Classification of Development Processes.

Schemata with short defining lengths and high fitness values have high possibility of surviving according to the schemata theorem. The fitness values of the schemata within chromosomes in a population after GAs' selection are possibly higher than previously. There is a high probability that schemata constructed using components with high covariances are building blocks. The LT method shortens the defining length of schemata with these high fitness values. Therefore the present results suggest that the LT method is effective when building blocks are created.

# 5 Discussion

First we discuss reasons why the building block hypothesis holds in the present environment. Let

$$f(c_i) = a_{jj}g_{ij}^2 + a_{jj'}g_{ij}g_{ij'} + a_{j'j'}g_{ij'}^2 + f'(c_i)$$
(10)

for some j and j' where  $f'(c_i)$  represents other terms which are supposed to remain constant for the moment. If  $a_{jj'}$  is high, schemata which take values near to 1.0 on both loci j and j' get high fitness values (Table 6-(1)). The schemata also get high values in cases where both  $a_{jj}$  and  $a_{j'j'}$  take high values (Table 6-(2)). In these cases, schemata which take values near 1.0 only on locus j get lower fitness values (Table 6-(3)), although the schemata do not get high values when  $a_{jj'}$  has a high value (Table 6-(4)). An environment with high  $a_{jj'}$  distinguishes more exactly between the case where both  $g_{ij}$ 

and  $g_{ij'}$  are high value, and the case where only  $g_{ij}$  is high value than does an environment where both  $a_{jj}$  and  $a_{j'j'}$  are high. This may give crossover an advantage over mutation.

id.	$a_{jj}$	$a_{jj'}$	$a_{j'j'}$	$g_{ij}$	$g_{ij'}$	$f(c_i)$
1	Low	High	Low	1.0	1.0	High
2	High	$\mathbf{Low}$	High	1.0	1.0	High
3	High	$\mathbf{Low}$	High	1.0	0.0	Less Higher
4	Low	High	Low	1.0	0.0	Low

Table 6. Relation between Chromosome Components and Coefficients.

The LT method has several problems for example its high computational cost.

The LT method uses  $n^2$  covariances  $\gamma_{jj'}$  of loci j and j' to determine the optimal transformation for all loci at each generation. To reduce the computational cost, algorithm 3 in Fig.4 can be used instead of the algorithm 2 in Fig.3. In algorithm 3, the first part refer to  $\sigma(1)$ ,  $\sigma(2)$ , ...,  $\sigma(j)$ , the second part refer to  $\sigma(j+1)$ ,  $\sigma(j+2)$ , ...,  $\sigma(n)$ , and to inverse a part means to change the values  $\sigma(k)$ ,  $\sigma(k+1)$ , ...,  $\sigma(l)$  to  $\sigma(l)$ ,  $\sigma(l-1)$ , ...,  $\sigma(k)$ . The computational cost will be reduced by a factor of  $4/n^2$ .

- (3) Repeat until the Cardinality of Either of the Populations is Zero. (3-1) Calculate Fitness Values.
  - (3-2) Selection (Common).
  - (3-3) Modify Chromosomes (for Each Population).
  - (3-4) Randomly choose a locus j.
  - (3-5) Calculate  $\gamma_{1,j+1}$ ,  $\gamma_{1n}$ ,  $\gamma_{j,j+1}$  and  $\gamma_{jn}$ .
  - (3-6) if  $\gamma_{i,j+1}$  is max then inverse first part.
  - else if  $\gamma_{jn}$  is max then inverse second part.
  - else if  $\gamma_{1n}$  is max then inverse both part.

Fig.4. Algorithm 3: Modified Locus Transformation.

There is another merit to the LT method: it promotes selforganization of building blocks, and so the optimal locus arrangement is determined spontaneously for each environment. Therefore it is not necessary when using GAs with LT to investigate each environment in advance to determine a good locus arrangement with respect to the principle of meaningful building blocks. According to this investigation, genetic operators should be applied as follows. Crossover should be used after some useful structure has been created, because the experimental results show that, in the initial stage of the evolutionary process, crossover is less beneficial than random mutation. Another self-organizing mechanism such as GAs with mutation is better at the initial stage of the adaptive process. The LT method should not be used in the last stage of the process because rearrangement of loci will no longer occur when the searching points approach the optimal point, and also because the LT method has a high computational cost as stated above.

### 6 Conclusion

This paper has compared crossover with mutation in seeking the optimal point which gives the maximum value of a quadratic form defined on a bounded domain. The locus transformation method is proposed to determine automatically the optimal loci in the adaptive process.

The experimental results of this comparison suggest that crossover has the advantage in this environment. Analysis of development processes suggests that mutation has the advantage in the initial stage of the adaptive process, and crossover is better once some building blocks are self-organized. This result supports the building block hypothesis.

The experimental results for the locus transformation method suggest that it promotes self-organization of building blocks, as the building block hypothesis dictates. When using GAs with the locus transformation, it is not necessary to find loci reflecting the information structure of the environment in advance.

# References

- [1] D.E.Goldberg: Genetic Algorithms in Search, Optimization and Machine Learning, Addison-Wesley(1989).
- [2] D.B.Fogel and J.W.Atmar: Comparing Genetic Operators with Gaussian Mutations in Simulated Evolutionary Processes Using Linear Systems, Biol.Cybern.63, pp111-114(1990).