Behavior Analysis of Real–Valued Evolutionary Algorithms for Independent Loci in an Infinite Population

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Abstract

Our purpose is theoretical analysis of behavior of Evolutionary Algorithms using real–valued chromosomes by focusing on the change of probability distribution of chromosomes in an infinite population. This paper deals with cases that some loci and the others are stochastically independent each other, and provide some conditions for EAs to maintain the independence. Moreover, we apply these results to special cases of Gaussian fitness function and population, and provide concrete equations of the change of mean values and variances through generations.

1 Introduction

A lot of experimental and theoretical researches on behavior of Evolutionary Algorithms (EAs) through generations have been recently reported. In the theoretical results, most of them are ones for EAs using discrete variables as chromosomes including the Simple Genetic Algorithms (Fogel, 1992, 1994; Booker, 1992; Nix and Vose, 1992; Davis and Principe, 1993; Suzuki, 1993; Dawid, 1994; Rudolph, 1994). On the other hand, some researchers have focused their attention on EAs that use real–valued chromosomes. For example, Qi and Palmieri derived the properties of the genetic operations including a uniform crossover in EAs with an infinite population size (Qi and Palmieri, 1994a, 1994b). In their results, the changes of the population density function (pdf) of chromosomes in the infinite population size through the genetic operations are the main object. Moreover, Rudolph derived the conditions for the convergence in EAs with general state spaces and a finite population size using the concept of Markov Kernel (Rudolph, 1996).

We have also focused our attention on EAs with real–valued chromosomes. In particular, we obtained some results for recombination operators from the perspective of change of pdf of chromosomes in a infinite population size (Nomura, 1997a, 1997b; Nomura and Shimohara, 2001). In this paper, we provide results on behavior of EAs with real valued chromosomes for independent loci, that is, cases where stochastic variables on some loci of chromosomes and them on the others are independent each other, by combining our previous results (Nomura, 1997b; Nomura and Shimohara, 2001) with them of Qi and Palmieri (1994a, 1994b).

2 Formalization

In this section, we prepare our formalization of EAs based on the results of Qi and Palmieri (1994a) for selection and mutation, and our results (1997b, 2001) for recombination.

Each individual in real–valued EAs is represented as a stochastic variable $X = (X_1, \ldots, X_m)$ in the Euclidean space R^m. Now, let $p^{(k)} : R^m \to R$ be the pdf of the chromosomes in the k–th generation of EAs, $q^{(k)}$ be the pdf after roulette selection on $p^{(k)}$, and $v^{(k)}$ be the pdf after recombination on $q^{(k)}$. In this formalization, we assume that $p^{(k+1)}$ is the result of mutation on $v^{(k)}$.

In this paper, we consider only two–parent recombinations formalized in the following form (Nomura, 1997b; Nomura and Shimohara, 2001):

$$\begin{aligned} X &= (X_1, X_2, \ldots, X_m) \in R^m, \\ Y &= (Y_1, Y_2, \ldots, Y_m) \in R^m, \\ X_i' &= a_i X_i + (1 - a_i) Y_i, \\ Y_i' &= (1 - b_i) X_i + b_i Y_i \quad (i = 1, \ldots, m), \\ X' &= (X_1', X_2', \ldots, X_m') \in R^m, \\ Y' &= (Y_1', Y_2', \ldots, Y_m') \in R^m. \end{aligned} \tag{1}$$

Here, X and Y are parents, and X' and Y' are off-

spring. The recombination parameter $(a,b) = (a_1, \ldots, a_m, b_1, \ldots, b_m)$ is a stochastic variable of R^{2m} with pdf $s(a,b)$, and we assume that (a,b) and (X,Y) are statistically independent. Moreover, we assume the following conditions for $s(a,b)$:

$$\begin{aligned} s(a,b) &= s(b,a) \ {}^{\forall}(a,b) \in R^{2m}, && (2)\\ \det C(a_i,b_i) &= a_i + b_i - 1 \neq 0 \ (i = 1, \ldots, m) && (3)\\ & \quad {}^{\forall}(a,b) \ s.t., \ s(a,b) \neq 0 \\ & \quad \left(C(x,y) = \begin{pmatrix} x & 1-y \\ 1-x & y \end{pmatrix} \right. \\ & \quad \left. \text{for } (x,y) \in R^2 \right). \end{aligned}$$

We showed that several recombination operators including one–point, multi–point, uniform, average, linear crossovers (Wright, 1991), and R^3 operator (Radcliffe, 1991) are represented in this form (The authors, 1997b, 2001).

Moreover, we assume additive noise mutation in the following form (Qi and Palmieri, 1994a):

$$\begin{aligned} \text{For} \quad & X = (X_1, \ldots, X_m) \ \in R^m \\ X_i' &= X_i + W_i^{(k)} \ (i = 1, \ldots, m) && (4)\\ X' &= (X_1', \ldots, X_m') \ \in R^m \end{aligned}$$

where, $W_i^{(k)}$ $(i = 1, \ldots, m)$ are independent stochastic variables with zero mean and a pdf $w^{(k)} : R^m \to R$ with condition $\sup_{x \in R^m} w^{(k)}(x) < \infty$ (here, index k means that mutation in the k-th generation is executed according to $w^{(k)}$).

Furthermore, let $f : R^m \to R$ be a fitness function and assume the following conditions (Qi and Palmieri, 1994a):

1. $f(x)$ has only finite many global maxima;
2. $0 < f(x) < \infty$, $\forall x \in R^m$;
3. $f(x)$ has finitely many discontinuous points;

Then, the change of pdf of chromosomes by the EA process is represented as follows by using the results of Qi and Palmieri (1994a) and us (1997b, 2001):

$$\begin{aligned} q^{(k)}(x) &= \frac{f(x)p^{(k)}(x)}{\int_{R^m} f(x)p^{(k)}(x)dx} && (5)\\ v^{(k)}(x) &= \int_{\Lambda} \frac{s(a,b)}{|\det F(a,b)|} \times && (6)\\ & \quad \left\{ \int_{R^m} q^{(k)}\left(xD(a') + y(I - D(a'))\right) \right. \\ & \quad \left. q^{(k)}\left(x(I - D(b')) + yD(b')\right) dy \right\} da db \end{aligned}$$

$$\begin{aligned} p^{(k+1)}(x) &= (v^{(k)} * w^{(k)})(x) && (7)\\ &= \int_{R^m} v^{(k)}(y) w^{(k)}(x - y) dy \ . \end{aligned}$$

$$\left(\begin{array}{l} I: \ m \times m \text{ unit matrix}, \\ F(x,y) = \begin{pmatrix} D(x) & I - D(y) \\ I - D(x) & D(y) \end{pmatrix} \\ \quad \text{for } (x,y) \in R^{2m} \\ D(x_1, \ldots, x_m) = \begin{pmatrix} x_1 & & \\ & \ddots & \\ & & x_m \end{pmatrix} \\ \quad \text{for } (x_1, \ldots, x_m) \in R^m \\ \Lambda = \{(a,b) \in R^{2m} \ ; \ s(a,b) \neq 0\} \\ a' = (a_1', \ldots, a_m') \ \in R^m \\ b' = (b_1', \ldots, b_m') \ \in R^m \\ a_i' = \frac{b_i}{a_i + b_i - 1}, b_i' = \frac{a_i}{a_i + b_i - 1} \ (i = 1, \ldots, m) \end{array} \right) .$$

Eqn. (5) and eqn. (7) are the result from (Qi and Palmieri, 1994a), and eqn. (6) is the result from (The authors, 1997b, 2001).

3 Behavior of EAs for Separable Fitness Functions and Independent Loci

Now, we assume the following conditions:

Assumption 1:
$f(x)$ is separable for $\{x_{i_{11}}, \ldots, x_{i_{1d_1}}\}$, $\{x_{i_{21}}, \ldots, x_{2d_2}\}$, $\ldots$, $\{x_{i_{L1}}, \ldots, x_{i_{Ld_L}}\}$ $(2 \leq L \leq m$, $\sum_{j=1}^{L} d_j = m$, $d_j \geq 1$, $1 \leq i_{j1} < \cdots < i_{jd_j} \leq m \ (j = 1, \ldots, L))$, that is, $f(x_1, \ldots, x_m) = \prod_{j=1}^{L} f_j(x_{i_{j1}}, \ldots, x_{i_{jd_j}})$;

Assumption 2:
For the stochastic variables $X_1, \ldots, X_m$ on loci of chromosomes in the k-th generation, $\{X_{i_{11}}, \ldots, X_{i_{1d_1}}\}$, $\{X_{i_{21}}, \ldots, X_{i_{2d_2}}\}$, $\ldots$, $\{X_{i_{L1}}, \ldots, X_{i_{Ld_L}}\}$ are independent each other, that is, $p^{(k)}(x_1, \ldots, x_m) = \prod_{j=1}^{L} p_j^{(k)}(x_{i_{j1}}, \ldots, x_{i_{jd_j}})$ ($p_j^{(k)}$ is the pdf of $\{X_{i_{j1}}, \ldots, X_{i_{jd_j}}\}$ in the k-th generation).

Under these assumptions, we derive some properties of the EAs formalized in section 2.

3.1 General Case

First, we can obtain the following equations from the assumptions and eqn.(5):

$$q^{(k)}(x_1, \ldots, x_m) = \prod_{j=1}^{L} q_j^{(k)}(x_{i_{j1}}, \ldots, x_{i_{jd_j}}) \quad (8)$$

$$q_j^{(k)}(x_{i_{j1}},\ldots,x_{i_{jd_j}}) = \frac{f_j p_j^{(k)}}{\int f_j p_j^{(k)} dx_{i_{j1}}\cdots x_{i_{jd_j}}}$$

It is trivial that $q_j^{(k)}$ is the pdf of $\{X_{i_{j1}}, \ldots, X_{jd_j}\}$ after selection.

Second, if we assume that for the stochastic variables $X_1, \ldots, X_m$ on loci of chromosomes after recombination in the k-th generation, $\{X_{i_{11}}, \ldots, X_{i_{1d_1}}\}$, $\{X_{i_{21}}, \ldots, X_{2d_2}\}$, $\ldots$, $\{X_{i_{L1}}, \ldots, X_{i_{Ld_L}}\}$ are independent each other, that is, $v^{(k)}(x_1,\ldots,x_m) = \prod_{j=1}^{L} v_j^{(k)}(x_{i_{j1}},\ldots,x_{i_{jd_j}})$ ($v_j^{(k)}$ is the pdf of $\{X_{i_{j1}}, \ldots, X_{i_{jd_L}}\}$ after recombination in the k-th generation), we obtain the following equations from eqn.(7) and the assumption on mutation $w^{(k)}(x_1,\ldots,x_m) = \prod_{i=1}^{m} w_i^{(k)}(x_i)$:

$$\begin{aligned} p^{(k+1)}(x) &= \int \prod_{j=1}^{L} v_j^{(k)}(y_{i_{j1}},\ldots,y_{i_{jd_j}}) \\ &\quad \prod_{i=1}^{m} w_i^{(k)}(x_i - y_i) dy_1 \cdots dy_m \\ &= \prod_{j=1}^{L} p_j^{(k+1)}(x_{i_{j1}},\ldots,x_{i_{jd_j}}) \end{aligned} \tag{9}$$

$$p_j^{(k+1)}(x_{i_{j1}},\ldots,x_{i_{jd_j}}) = \int dy_{i_{j1}}\cdots dy_{i_{jd_j}} \; v_j^{(k)}(y_{i_{j1}},\ldots,y_{i_{jd_j}}) \left(\prod_{l=1}^{d_j} w_{i_{jl}}^{(k)}(x_{i_{jl}} - y_{i_{jl}})\right)$$

Thus, we obtain the following facts:

Fact 1:
Under Assumption 1 and 2, the stochastic variables on loci of chromosomes $\{X_{i_{11}}, \ldots, X_{i_{1d_1}}\}$, $\{X_{i_{21}}, \ldots, X_{2d_2}\}$, $\ldots$, $\{X_{i_{L1}}, \ldots, X_{i_{Ld_L}}\}$ are independent each other after selection in the k-th generation.

Fact 2:
If for the stochastic variables $X_1, \ldots, X_m$ on loci of chromosomes after recombination in the k-th generation, $\{X_{i_{11}}, \ldots, X_{i_{1d_1}}\}$, $\{X_{i_{21}}, \ldots, X_{i_{2d_2}}\}$, $\ldots$, $\{X_{i_{L1}}, \ldots, X_{i_{Ld_L}}\}$ are independent each other, these stochastic variables are also independent each other after mutation, that is, in the $(k+1)$-th generation.

Fact 3:
Under Assumption 1 and 2, if recombination maintains the above independence, the EA process formalized in section 2 maintains the independence through one generation.

However, two–parent recombinations generally do not maintain the independence in Assumption 1 and 2. We can obtain the following equation from the assumptions, eqn. (6), and eqn. (8):

$$\begin{aligned} v^{(k)}(x) &= \int_{\Lambda} da db\, s(a,b) \times \\ &\prod_{j=1}^{L} h_j^{(k)}(x_{i_{j1}},\ldots,x_{i_{jd_j}}, a_{i_{j1}},\ldots,a_{i_{jd_j}}, b_{i_{j1}},\ldots,b_{i_{jd_j}}) \end{aligned} \tag{10}$$

$$\begin{aligned} h_j^{(k)} &= \frac{1}{\prod_{l=1}^{d_j}(a_{i_{jl}} + b_{i_{jl}} - 1)} \int dy_{i_{j1}}\cdots dy_{i_{jd_j}} \\ &\Big\{ q_j^{(k)}(a'_{i_{j1}} x_{i_{j1}} + (1 - a'_{i_{j1}}) y_{i_{j1}}, \\ &\quad \ldots, a'_{i_{jd_j}} x_{i_{jd_j}} + (1 - a'_{i_{jd_j}}) y_{i_{jd_j}}) \times \\ &\quad q_j^{(k)}((1 - b'_{i_{j1}}) x_{i_{j1}} + b'_{i_{j1}} y_{i_{j1}}, \\ &\quad \ldots, (1 - b'_{i_{jd_j}}) x_{i_{jd_j}} + b'_{i_{jd_j}} y_{i_{jd_j}}) \Big\} \end{aligned}$$

Thus, if $\{a_{i_{j1}}, \ldots, a_{i_{jd_j}}, b_{i_{j1}}, \ldots, b_{i_{jd_j}}\}$ $(j = 1,\ldots,L)$ are stochastically independent each other, $v^{(k)}$ can be the product of the pdfs of $\{X_{i_{j1}}, \ldots, X_{i_{jd_j}}\}$ $(j = 1,\ldots,L)$ and the recombination maintains the independence. However, they are generally dependent and we cannot determine from eqn. (10) whether recombination maintains the independence.

3.2 Special Cases: One–Point, Multi–Point, and Uniform Crossovers

In this section, we derive some properties of the EAs formalized in section 2 by adding stronger conditions to Assumption 1 and 2.

First, we assume $L = m$ in Assumption 1 and 2, that is:

Assumption 3:
$f(x)$ is separable for $x_1, \ldots, x_m$, that is, $f(x_1,\ldots,x_m) = \prod_{i=1}^{m} f_i(x_i)$;

Assumption 4:
In the k-th generation, the stochastic variables on all the loci of chromosomes are independent each other, that is, $p^{(k)}(x_1,\ldots,x_m) = \prod_{i=1}^{m} p_i^{(k)}(x_i)$ ($p_i^{(k)}$ is the pdf of X_i).

It is easily shown from the results in section 3.1 that selection maintains this independence,that is:

$$\begin{aligned} q^{(k)}(x) &= \prod_{i=1}^{m} q_i^{(k)}(x_i) \\ q_i^{(k)}(x_i) &= \frac{f_i(x_i) p_i(x_i)}{\int_R f_i(x_i) p_i(x_i) dx_i} \end{aligned} \tag{11}$$

Now, we consider cases that recombination is one–point, multi–point, or uniform crossover. The change of the pdf by these crossovers is formalized as follows (Nomura, 1997b; Nomura and Shimohara, 2001):

One–Point Crossover

$$\begin{aligned} v^{(k)}(x) &= \frac{r}{m-1}\sum_{k=1}^{m-1}\left\{q^{(k)}_{(12\cdots k)}(x_1,\ldots,x_k)\right. \\ &\quad \left. q^{(k)}_{(k+1\cdots m)}(x_{k+1},\ldots,x_m)\right\} \\ &\quad +(1-r)q^{(k)}(x) \end{aligned} \tag{12}$$

c–Point Crossover ($c \geq 2$)

$$\begin{aligned} v^{(k)}(x) &= \frac{r}{C_m} \times \sum_{1\leq i_1<i_2,<\cdots<i_c<m} \\ &\left\{q^{(k)}_{(1\cdots i_1 i_2+1\cdots i_3 i_4+1\cdots)}(x_1,\ldots,x_{i_1}, \right. \\ &\quad x_{i_2+1},\ldots,x_{i_3},x_{i_4+1},\ldots) \\ &\quad \times q^{(k)}_{(i_1+1\cdots i_2 i_3+1\cdots i_4 i_5+1\cdots)}(x_{i_1+1},\ldots,x_{i_2}, \\ &\quad \left. x_{i_3+1},\ldots,x_{i_4},x_{i_5+1},\ldots)\right\} \\ &+(1-r)q^{(k)}(x) \\ &\left(C_m = \begin{pmatrix} m-1 \\ c \end{pmatrix}\right) \end{aligned} \tag{13}$$

Uniform Crossover

$$\begin{aligned} v^{(k)}(x) &= \sum_{k=0}^{m} r^k(1-r)^{m-k} \times \\ &\quad \sum_{1\leq i_1<i_2,<\cdots<i_k\leq m} \left\{q^{(k)}_{(i_1\cdots i_k)}(x_{i_1},\ldots,x_{i_k})\times \right. \\ &\quad \left. q^{(k)}_{(i_{k+1}\cdots i_m)}(x_{i_{k+1}},\ldots,x_{i_m})\right\} \\ &= \sum_{k=0}^{d}\left[r^k(1-r)^{m-k}+r^{m-k}(1-r)^k\right] \times \\ &\quad \sum_{1\leq i_1<i_2,<\cdots<i_k\leq m} \left\{q^{(k)}_{(i_1\cdots i_k)}(x_{i_1},\ldots,x_{i_k})\times \right. \\ &\quad \left. q^{(k)}_{(i_{k+1}\cdots i_m)}(x_{i_{k+1}},\ldots,x_{i_m})\right\} \\ &\left(\begin{array}{l} d = \left\{ \begin{array}{ll} \frac{m}{2} & \text{if } m \text{ is even} \\ \frac{m-1}{2} & \text{if } m \text{ is odd} \end{array}\right. \\ \{i_{k+1},\ldots,i_m\} = \\ \quad \{1,\ldots,m\}-\{i_1,\ldots,i_k\}, \\ 1\leq i_{k+1}<i_{k+2}<\cdots i_m\leq m \end{array}\right) \end{aligned} \tag{14}$$

Here, r is the crossover rate. $q^{(k)}_{i_1,\ldots,i_d}(x_{i_1},\ldots,x_{i_d})$ is the pdf of the stochastic variables on the i_1, ..., i_d-th loci of chromosomes after selection in the k-th generation:

$$\begin{aligned} q^{(k)}_{(i_1\ldots i_k)}(x_{i_1},\ldots,x_{i_d}) &= \int q^{(k)}(x)dx_{i_{d+1}}\cdots dx_m \\ &\left(\begin{array}{l} \{i_{d+1},\ldots,i_m\} = \\ \quad \{1,\ldots,m\}-\{i_1,\ldots,i_d\}, \\ 1\leq i_{d+1}<i_{d+2}<\cdots i_m\leq m \end{array}\right) \end{aligned} \tag{15}$$

We can formalize the change of pfd by these crossovers in the following abstract form:

$$\begin{aligned} v^{(k)}(x) &= \sum_{h=1}^{m} \sum_{\substack{j_1<\cdots<j_h \\ \{j_1,\ldots,j_h\}\cup\{j_{h+1},\ldots,j_m\}=\{1,\ldots,m\}}} \\ &\left\{r_{j_1,\ldots,j_h} q^{(k)}_{(j_1\cdots,j_h)}(x_{j_1},\ldots,x_{j_h})\right. \\ &\quad \left. q^{(k)}_{(j_{h+1}\cdots,j_m)}(x_{j_{h+1}},\ldots,x_{j_m})\right\} \end{aligned} \tag{16}$$

$$\left(\sum_{h=1}^{m-1} \sum_{\substack{j_1<\cdots<j_h \\ \{j_1,\ldots,j_h\}\cup\{j_{h+1},\ldots,j_m\}=\{1,\ldots,m\}}} r_{j_1,\ldots,j_h} = 1\right)$$

Moreover, we obtain the following equation from eqn.(11) and (15):

$$\begin{aligned} & q^{(k)}_{(j_1\cdots,j_h)}(x_{j_1},\ldots,x_{j_h}) q^{(k)}_{(j_{h+1}\cdots,j_m)}(x_{j_{h+1}},\ldots,x_{j_m}) \\ &= \prod_{l=1}^{h} q^{(k)}_{j_l}(x_{j_l}) \times \prod_{l=h+1}^{m} q^{(k)}_{j_l}(x_{j_l}) \\ &= \prod_{i=1}^{m} q_i(k)(x_i) = q^{(k)}(x) \end{aligned} \tag{17}$$

Thus, we obtain $v^{(k)} = q^{(k)}$ from eqn.(16) and (17). In other words, one–point, multi–point, and uniform crossovers do not change the pdf of chromosomes if the stochastic variables on all the loci are independent each other (note that the proof of this proposition does not refer the assumption on the fitness function).

Furthermore, it is easily shown from the results in section 3.1 that mutation maintains this independence,that is:

$$\begin{aligned} p^{(k+1)}(x) &= \prod_{i=1}^{m} p_i^{(k+1)}(x_i) \\ p_i^{(k+1)}(x_i) &= \int v_i^{(k)}(x_i) w_i(x_i-y_i)dy_i \\ v_i^{(k)}(x_i) &= q_i^{(k)}(x_i) \end{aligned} \tag{18}$$

Thus, we obtain the following facts:

Fact 4:

If the stochastic variables on all the loci of chromosomes are independent each other, one–point, multi–point, and uniform crossovers do not change the pdf.

Fact 5:

Under Assumption 3 and 4, if EAs formalized in section 2 adopt one–point, multi–point, and uniform crossovers as recombination, they maintain the independence between the loci in the $k+1$ generation.

4 Behavior of EAs for Gaussian Population and Fitness Function

In this section, we assume the following conditions:

Assumption 5:

The fitness function f is Gaussian, that is:

$$\begin{aligned} f(x) &= \exp\left[-\frac{1}{2}(x-x^*)Q(x-x^*)^T\right] \quad (19)\\ x^* &= (x_1^*,\ldots,x_m^*) \in R^m \\ &\quad : \text{the unique maximum point} \\ Q &: \text{a } m\times m \text{ positive definite} \\ &\quad \text{symmetric matrix} \\ &\quad \left({}^T : \text{transpose operator for vectors}\right) \end{aligned}$$

Assumption 6:

The pdf of chromosomes in the 0-th generation is Gaussian, that is:

$$\begin{aligned} p^{(0)}(x) &= \frac{1}{(2\pi)^{m/2}|\Sigma^{(0)}|^{1/2}} \quad (20)\\ &\quad \exp\left[-\frac{1}{2}(x-\mu^{(0)}){\Sigma^{(0)}}^{-1}(x-\mu^{(0)})^T\right] \\ \mu^{(0)} &= \left(\mu_1^{(0)},\ldots,\mu_m^{(0)}\right) \\ &\quad : \text{the mean value vector} \\ \Sigma^{(0)} &= \left(\left(\Sigma^{(0)}\right)_{ij}\right) \\ &\quad : \text{the covariance matrix} \end{aligned}$$

Assumption 7:

The mutation in section 2 is indpendent Gaussian with covariances $\sigma_w^{(k)} = (\sigma_{w1}^{(k)},\ldots,\sigma_{wm}^{(k)})$ in any k-th generation.

4.1 General Case

Qi and Palmieri (1994a) proved that under Assumption 5, 6 and 7 selection and mutation maintain Gaussian property in the distribution of chromosomes through any generation, and derived equations of the change of mean values and covariance matrix. Moreover, we derived equations of the change of mean values and covariances for two–parent recombination formalized in section 2. By combining these results, we obtain the following fact:

Fact 6:

Under Assumption 5, 6 and 7, if recombination maintains Gaussian property of the distribution of chromosomes, the distribution of chromosomes in the k-th generation by the EA formalized in section 2 is also Gaussian with mean $\mu^{(k)}$ and covariance $\Sigma^{(k)}$ for any k (≥ 0). Moreover, the change of mean values and covariances are formalized as follows:

$$\begin{aligned} \mu^{\prime(k)} &= \left[x^*Q + \mu^{(k)}{\Sigma^{(k)}}^{-1}\right]\Sigma^{\prime(k)} \quad (21)\\ \Sigma^{\prime(k)} &= \left(Q + {\Sigma^{(k)}}^{-1}\right)^{-1} \quad (22)\\ \mu^{\prime\prime(k)} &= \mu^{\prime(k)} \quad (23)\\ \Sigma^{\prime\prime(k)} &= MM\left(PC, \Sigma^{\prime(k)}\right) \quad (24)\\ \mu^{(k+1)} &= \mu^{\prime\prime(k)} \quad (25)\\ \Sigma^{(k+1)} &= \Sigma^{\prime\prime(k)} + D(\sigma_w^{(k)}) \quad (26)\\ &\quad (k=0,1,\ldots) \end{aligned}$$

$$\left(\begin{array}{lcl} C & = & MM(A,B) \ : \ m\times m \text{ matrix} \\ (C)_{ij} & = & (A)_{ij}\times(B)_{ij} \\ & & \text{for } m\times m \text{ matrices } A,B \\ PC & : & m\times m \text{ matrix} \\ (PC)_{ij} & = & E(2a_ia_j - a_i - a_j) + 1 \\ & & (E() : \text{expectation value}) \end{array}\right)$$

Here, $\mu^{\prime(k)}$ and $\Sigma^{\prime(k)}$ are the mean value vector and covariance matrix of chromosomes after selection in the k-th generation respectively. Moreover, $\mu^{\prime\prime(k)}$ and $\Sigma^{\prime\prime(k)}$ are the mean value vector and covariance matrix of chromosomes after recombination in the k-th generation respectively.

Eqn.(21), (22), (25), and (26) are the results of Qi and Palmieri (1994a), and eqn.(23) and (24) are our results (Nomura, 1997b; Nomura and Shimohara, 2001). The eqations in Fact 6 are summurized as difference equations of mean values and covariance matrices in the following form:

$$\begin{aligned} \mu^{(k+1)} &= \mu^{(k)} \\ &\quad -\left(\mu^{(k)} - x^*\right) Q \left(Q + {\Sigma^{(k)}}^{-1}\right)^{-1} \quad (27) \end{aligned}$$

$$\Sigma^{(k+1)} = MM\left(PC, \left(Q + \Sigma^{(k)^{-1}}\right)^{-1}\right) + D\left(\sigma_w^{(k)}\right) \quad (k = 0, 1, \ldots) \tag{28}$$

However, two–parent recombination may generally not maintain the Gaussian property of the population after selection. In the next section, thus, we consider more special cases in the same way in section 3.2.

4.2 Special Cases: One–Point, Multi–Point, and Uniform Crossovers

Now, we assume the following stronger conditions:

Assumption 8:
In addition to Assumption 5, $f(x)$ is separable for x_1, ..., x_m, that is, Q is diagonal ($Q = D(Q_1, \ldots, Q_m)$);

Assumption 9:
In addition to Assumption 6, the stochastic variables on all the loci of chromosomes are independent each other, that is, $\Sigma^{(0)}$ is diagonal such that $\Sigma^{(0)} = D\left(\Sigma_1^{(0)}, \ldots, \Sigma_m^{(0)}\right)$ if $\Sigma_i^{(0)}$ is the i-th variance in the 0-th generation ($i = 1, \ldots, m$).

Then, one–point, multi–point, and uniform crossovers maintain the Gaussian property of the population because it is clear from the results in 3.2 that they do not change the pdf, in particular, PC is the unit matrix. Thus, we obtain the following fact:

Fact 7:
Under Assumption 7, 8, and 9, if the EAs formalized in section 2 use one–point, multi–point, or uniform crossover as recombinaion, the distribution of chromosomes in the k-th generation is also independent Gaussian for any k (≥ 1). Moreover, the change of the mean values $\mu_i^{(k)}$ and variances $\Sigma_i^{(k)}$ ($i = 1, \ldots, m$) is formalized as follows:

$$\mu_i^{(k+1)} = \mu_i^{(k)} - \frac{\Sigma_i^{(k)} Q_i}{\Sigma_i^{(k)} Q_i + 1}\left(\mu_i^{(k)} - x_i^*\right) \tag{29}$$

$$\Sigma_i^{(k+1)} = \frac{\Sigma_i^{(k)} Q_i}{\Sigma_i^{(k)} Q_i + 1} + \sigma_{wi}^{(k)} \quad (i = 1, \ldots, m,\ k = 0, 1, \ldots) \tag{30}$$

In addition, if the $\sigma_{wi}^{(k)}$ is a constant σ_{wi} for k,

$$\lim_{k\to\infty} \mu_i^{(k)} = x_i^* \tag{31}$$

$$\Sigma_i = \lim_{k\to\infty} \Sigma_i^{(k)} = \frac{1}{2}\left\{\sigma_{wi} + \sqrt{\sigma_{wi}^2 + \frac{4\sigma_{wi}}{Q_i}}\right\} > \sigma_{wi} \tag{32}$$

The last statement on $\Sigma_i^{(k)}$ is derived from the fact that $g(\Sigma_i) = \Sigma_i$ and $0 < g'(\Sigma_i) < 1$ for $g(x) = \frac{x}{Q_i x + 1} + \sigma_{wi}$ $\left(g'(x) = \frac{1}{(Q_i x + 1)^2}\right)$.

5 Discussions

Although we theoretically derived several facts on EAs in the previous sections, we have some problems for them.

We cannot deny that these facts are satisfied under very special conditions (Assumption 1—9). These results may be trivial from experimental perspective. Thus, we must extend these results to more general cases.

In particular, we have still not obtained general properties of two–parent recombination for maintenance of independence and Gaussian property. It was proved that repeated applications of one–point, multi–point, and uniform crossovers lead to asymptotic independence among the loci of chromosomes (Qi and Palmieri, 1994b; Nomura and Shimohara, 2001). Moreover, it was proved that the EAs can converge to the maximum point even if recombination is not executed (Qi and Palmieri, 1994a). We must investigate other recombination methods including linear and BLX–α to clarify what roles recombination can play in EA processes.

6 Conclusions

In this paper, we analyzed behavior of real–valued EAs formalized in section 2 for cases that some loci and the others are stochastically independent each other and the fitness function is separable for the corresponding variabless. First, we derived the fact that selection and mutation maintain the independence (Fact 1 and Fact 2) and the EAs maintain the independence if recombination maintains the independence (Fact 3). Then, for special cases that all the loci are independent each other and the fitness function is perfectlly separable, we derived that one–point, multi–point, and uniform crossovers do not change the distribution of chromosomes (Fact 4) and the EAs using these crossovers as recombination maintain the independence. Furthermore, for cases that the fitness function, the distribution of chromosomes, and mutation are Gaussian, we

derived the fact that the EAs maintain the Gaussian property if recombination maintains it, and provided equations of the change of mean values and covariances (Fact 6). Finally, for more special cases that the fitness function and the distribution of chromosomes are independent Gaussian, we derived the fact that the EAs using one–point, multi–point, and uniform crossovers as recombination maintain the Gaussian property, and provided equations of the change of mean values and variances, and their limit values (Fact 7).

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