# Schema Analysis of Average Fitness in Multiplicative Landscape 

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#### Abstract

By applying the schema theorem, we study the effects of crossover in Genetic Algorithms with the multiplicative fitness function. On this landscape, the analytical expression of the exact schema theorem can be obtained, and this makes it possible to carry out the mathematical investigation of genetic operators. We consider the average fitness under the action of selection, mutation and crossover. To do this, we give the expressions for the average and variance of fitness in terms of schema frequencies. The theoretical results are compared with numerical experiments.


## 1 Introduction

It is in general very difficult to know the effects of crossover and mutation in Genetic Algorithms (GAs). Even now, we cannot predict the behavior of a population in a given GA calculation under crossover and mutation. In this paper, we consider this problem by applying the method of schema analysis [1].

The schema theorem was proposed by Holland [2], and used in the theoretical analysis of GAs. However, there have been also given many criticisms on its effectiveness. For example, it only takes into account the destructive nature of crossover and mutation on schemata without considering their constructive roles [1].

There are several attempts to make the schema theory more quantitative. Stephens and Waelbroeck obtained exact schema evolution equations for mutation and crossover [34]. Vose has pointed out a close relationship between the schema frequency and the Walsh transform of genotype frequency [5]. Wright derived a version of exact schema theorem by using the Walsh transformation method of Vose 6].

Recently, we have also developed a method to derive a schema theorem from a evolution equation of genotype frequency by applying Walsh transformation [7]. Fortunately, it was found recently that evolution equations for mutation and crossover can be expressed in very simple forms by Walsh transformation [5], 8]. Therefore, it is not difficult to obtain the schema evolution equations for mutation and crossover [1].

Selection is the most important operator in genetics and GA, and plays the role of a driving force in evolution. In this paper, we consider the evolution of
a population on the multiplicative landscape. Though there are many papers on this landscape 91011 , we study this problem again from the viewpoint of schema evolution. Previously, we have shown that the evolution equation for that population can be solved exactly [12]. In this paper, we apply the schema theorem to this problem, and study the roles of genetic operators microscopically. We derive an exact evolution equation of schemata evolving under the action of selection, mutation and crossover. The effect of linkage on the average fitness is studied mathematically. The theoretical results are compared with numerical experiments.

## 2 Mathematical Model

### 2.1 Model

In this paper, we study the action of selection, mutation and crossover in GAs. We use the fitness proportionate selection and uniform crossover. A population is assumed to evolve in discrete and non-overlapping generations, and the process is described by a set of difference equations. We consider GAs of infinite population size, and neglect the effect of random sampling.

An individual is represented by a binary string of length $\ell$, and thus there are $n=2^{\ell}$ possible genotypes, or strings. The $i$ th genotype $B_{i}$ is defined as $B_{i}=<i(\ell), \cdots, i(1)>$. The integer $i$ is sometimes identified with $B_{i}$. We use the notation $|i|$ for the number of bit ones in $i$

$$
\begin{equation*}
|i|=\sum_{k=1}^{\ell} i(k) \tag{1}
\end{equation*}
$$

We use the relative frequency $x_{i}(t)$ of the genotype $B_{i}$ at generation $t$ for the analysis. The relative frequencies satisfy the normalization condition

$$
\begin{equation*}
\sum_{i=0}^{n-1} x_{i}(t)=1 \tag{2}
\end{equation*}
$$

### 2.2 Walsh Transformation

The evolution of a GA system can also be described by the Walsh transform of $x_{j}(t)$

$$
\begin{equation*}
\tilde{x}_{i}(t) \equiv \sum_{j=0}^{n-1} W_{i j} x_{j}(t) \tag{3}
\end{equation*}
$$

where Walsh function $W_{i j}$ is

$$
\begin{equation*}
W_{i j} \equiv W_{i}(j)=\prod_{k=1}^{\ell}(-1)^{i(k) \cdot j(k)} \tag{4}
\end{equation*}
$$

and we call $\tilde{x}_{i}$ as Walsh coefficient. When it is necessary to show the number of bit ones and their positions in $i$

$$
k=|i|, \quad 1 \leq b_{1}<\ldots<b_{k} \leq \ell
$$

we use the notation

$$
\begin{equation*}
\tilde{x}_{i}(t)=\tilde{x}^{(k)}\left[b_{1}, \ldots, b_{k}\right](t), \tag{5}
\end{equation*}
$$

where $k$ is the degree of Walsh coefficient.
Substituting $W_{0 j}=1$ into equation (3), and using the normalization condition (2), we have the zeroth order Walsh coefficient $\tilde{x}_{0}$

$$
\begin{equation*}
\tilde{x}_{0}(t)=\sum_{j=0}^{n-1} x_{j}(t)=1 \tag{6}
\end{equation*}
$$

The following relation will be used later

$$
\begin{equation*}
\tilde{x}^{(k)}\left[b_{1}, b_{2} \ldots b_{k}\right]=\sum_{j=0}^{n-1} \prod_{m=1}^{k}(-1)^{j\left(b_{m}\right)} x_{j} \tag{7}
\end{equation*}
$$

where $j\left(b_{1}\right), \ldots, j\left(b_{k}\right)$ stand for the bit values of $j$ at the positions of ones in $i$.

### 2.3 Evolution Equation

In proportionate selection, the frequency of genotype $B_{i}$ at generation $t+1$ is given in terms of frequencies at generation $t$

$$
\begin{equation*}
x_{i}(t+1)=\frac{f_{i}}{\bar{f}(t)} x_{i}(t) \quad(i=0, \ldots, n-1), \tag{8}
\end{equation*}
$$

where $f_{i}$ is a fitness of $B_{i}$, and the average fitness of the population $\bar{f}(t)$

$$
\begin{equation*}
\bar{f}(t)=\sum_{i=0}^{n-1} f_{i} x_{i}(t) \tag{9}
\end{equation*}
$$

There is a very important relation for the selection process. The change in average fitness per generation

$$
\Delta \bar{f}(t)=\bar{f}(t+1)-\bar{f}(t)
$$

is given by

$$
\begin{align*}
\Delta \bar{f}(t) & =\frac{1}{\bar{f}(t)} V(f)  \tag{10}\\
V(f) & =\sum_{i} f_{i}^{2} x_{i}(t)-\bar{f}(t)^{2}
\end{align*}
$$

This is a version of Fisher's fundamental theorem of natural selection [13]. Fisher's theorem means that the increase in the average fitness is proportional to the ratio of the variance of fitness $V(f)$ to its average.

The Walsh transform of the evolution equation (8) becomes

$$
\begin{equation*}
\widehat{S} \tilde{x}_{i}(t)=\frac{1}{n \bar{f}(t)} \sum_{j=0}^{n-1} \tilde{f}_{j} \tilde{x}_{i \oplus j}(t) \tag{11}
\end{equation*}
$$

where $\oplus$ is the bitwise exclusive-or operation, and $\widehat{S}$ shows the effect of selection symbolically. The fitness $\tilde{f}_{i}$ is the Walsh transform of $f_{i}$

$$
\begin{equation*}
\tilde{f}_{i}=\sum_{j=0}^{n-1} W_{i j} f_{j} \tag{12}
\end{equation*}
$$

The average fitness is given by

$$
\begin{equation*}
\bar{f}(t)=\frac{1}{n} \sum_{j=0}^{n-1} \tilde{f}_{j} \tilde{x}_{j}(t) \tag{13}
\end{equation*}
$$

The change in the frequency under mutation is

$$
\begin{equation*}
x_{i}(t+1)=\sum_{j=0}^{n-1} M_{i j} x_{j}(t) \tag{14}
\end{equation*}
$$

where the mutation matrix $M_{i j}$ stands for the probability of mutation from $B_{j}$ to $B_{i}$ over one generation. An $(i, j)$ th element of $M$ is a function of the Hamming distance $d(i, j)$ between strings $i$ and $j$.

$$
\begin{equation*}
M_{i j}=(1-p)^{\ell-d(i, j)} p^{d(i, j)}, \tag{15}
\end{equation*}
$$

where $p$ denotes the mutation rate at one bit position over one generation.
The matrix $M_{i j}$ can be diagonalized by Walsh functions

$$
\sum_{i^{\prime}=0}^{n-1} \sum_{j^{\prime}=0}^{n-1} W_{i i^{\prime}} M_{i^{\prime} j^{\prime}} W_{j^{\prime} j}=n(1-2 p)^{|i|} \delta_{i, j}
$$

Thus the Walsh transform of the evolution equation under mutation (14) is

$$
\begin{equation*}
\widehat{M} \tilde{x}_{i}(t)=(1-2 p)^{|i|} \tilde{x}_{i}(t) \tag{16}
\end{equation*}
$$

where $\widehat{M}$ symbolically shows the effect of mutation.
The evolution equation under crossover can be given in terms of crossover tensor $C$

$$
\begin{equation*}
x_{k}(t+1)=\sum_{i=0}^{n-1} \sum_{j=0}^{n-1} C(k \mid i, j) x_{i}(t) x_{j}(t) \tag{17}
\end{equation*}
$$

Using the Walsh transformation, we can express the effect of crossover in a very simple form 58

$$
\begin{equation*}
\widehat{C} \tilde{x}_{k}(t)=\sum_{i=0}^{n-1} c_{i, i \oplus k} \tilde{x}_{i}(t) \tilde{x}_{i \oplus k}(t), \tag{18}
\end{equation*}
$$

where $\widehat{C}$ denotes the effect of crossover. The factor $c_{i j}$ is given by

$$
\begin{equation*}
c_{i j}=(1-\chi) \frac{\delta(i)+\delta(j)}{2}+\chi c_{i j}(\chi=1) \tag{19}
\end{equation*}
$$

where $\chi$ is a crossover rate, and $c_{i j}(\chi=1)$ is the value of $c_{i j}$ with $\chi=1$. The discrete $\delta$ function is defined for integer $m$

$$
\delta(m)= \begin{cases}1 & (m=0) \\ 0 & (m \neq 0)\end{cases}
$$

For one-point crossover, we obtain [5]
$-i=0$ or $j=0$

$$
\begin{equation*}
c_{i j}(\chi=1)=\frac{1}{2(\ell-1)}\{\operatorname{lo}(i)-\operatorname{hi}(i)+\operatorname{lo}(j)-\operatorname{hi}(j)\} \tag{20}
\end{equation*}
$$

The functions hi $(i)$ and $\operatorname{lo}(i)$ are defined as

$$
\begin{aligned}
\mathrm{hi}(i) & = \begin{cases}1 & (i=0) \\
i_{\max } & (\text { otherwise }),\end{cases} \\
\mathrm{lo}(i) & = \begin{cases}\ell & (i=0) \\
i_{\min } & (\text { otherwise })\end{cases}
\end{aligned}
$$

where $i_{\max }$ and $i_{\min }$ stand for the leftmost and rightmost ones in $i$, respectively.
$-i \neq 0$ and $j \neq 0$

$$
c_{i j}(\chi=1)= \begin{cases}\left(i_{\min }-j_{\max }\right) / 2(\ell-1) & \left(i_{\min }>j_{\max }\right)  \tag{21}\\ \left(j_{\min }-i_{\max }\right) / 2(\ell-1) & \left(j_{\min }>i_{\max }\right) \\ 0 & \text { (otherwise) }\end{cases}
$$

For uniform crossover, we have a very simple expression

$$
\begin{equation*}
c_{i j}=(1-\chi) \frac{\delta(i)+\delta(j)}{2}+\chi \prod_{m=1}^{\ell} \frac{\delta\{i(m)\}+\delta\{j(m)\}}{2} . \tag{22}
\end{equation*}
$$

## 3 Schema Theorem

After introducing schemata and Holland's schema theorem [2], we describe the new schema theorem obtained by Walsh transformation [7].

A schema $\mathcal{H}$ represents a set of genotypes. It is given by three types of symbols, 0,1 and $*$. The bits 0 and 1 are defining bits, and $*$ is a wild card that allows both 0 and 1 . The order of schema $\mathcal{O}(\mathcal{H})$ is the number of defining bits, and the defining length $\mathcal{L}(\mathcal{H})$ is the distance between the rightmost and leftmost defining bits.

The most famous example of the schema theorem is Holland's one with onepoint crossover [2].

$$
\begin{equation*}
h(\mathcal{H}, t+1) \geq h(\mathcal{H}, t) \frac{f(\mathcal{H})}{\bar{f}(t)}\left\{1-\chi \frac{\mathcal{L}(\mathcal{H})}{\ell-1}-p \mathcal{O}(\mathcal{H})\right\} \tag{23}
\end{equation*}
$$

where $h(\mathcal{H}, t)$ is the relative frequency of the schema $\mathcal{H}$ at generation $t$, and $f(\mathcal{H})$ is the average fitness of genotypes included in $\mathcal{H}$.

We also use the notation showing explicitly the order of schema, the positions of defining bits, and their bit values,

$$
\mathcal{H}=\mathcal{H}^{(k)}\left[i\left(b_{1}\right), i\left(b_{2}\right), \ldots, i\left(b_{k}\right)\right]
$$

Here, $k=\mathcal{O}(\mathcal{H})$, and $1 \leq b_{1}<b_{2}<\ldots<b_{k} \leq \ell$ are positions of defining bits. In a similar manner, we use the notation for the relative frequency $h(\mathcal{H})$,

$$
h(\mathcal{H})=h^{(k)}\left[i\left(b_{1}\right), i\left(b_{2}\right), \ldots, i\left(b_{k}\right)\right] .
$$

Then we derive the new schema theorem by using the Walsh transformation. When $i$ and $j$ take binary values, 0 and 1 , the condition of $i=j$ is given by

$$
\delta(i-j)=\frac{1}{2}\left\{1+(-1)^{i}(-1)^{j}\right\} .
$$

From this, we can obtain an expression for the frequency $h(\mathcal{H})$ of the first order schema $\mathcal{H}^{(1)}\left[i\left(b_{1}\right)\right]$. Using the normalization condition (2) and definition (7), we have

$$
\begin{aligned}
h^{(1)}\left[i\left(b_{1}\right)\right] & =\sum_{j=0}^{n-1} \delta\left(i\left(b_{1}\right)-j\left(b_{1}\right)\right) x_{j} \\
& =\sum_{j=0}^{n-1} \frac{1}{2}\left\{x_{j}+(-1)^{i\left(b_{1}\right)}(-1)^{j\left(b_{1}\right)} x_{j}\right\} \\
& =\frac{1}{2}\left\{1+(-1)^{i\left(b_{1}\right)} \tilde{x}^{(1)}\left[b_{1}\right]\right\} .
\end{aligned}
$$

For the $L$ th order schema, noting

$$
h^{(L)}\left[i\left(b_{1}\right), i\left(b_{2}\right), \ldots, i\left(b_{L}\right)\right]=\sum_{j=0}^{n-1} \prod_{m=1}^{L} \delta\left(i\left(b_{m}\right)-j\left(b_{m}\right)\right) x_{j},
$$

and expanding the products of the delta functions, we have a new expression for the schema frequency in terms of the Walsh coefficients. Giving the positions of all defining bits $S=\left\{b_{1}, \ldots, b_{L}\right\}$, and its subset $S^{\prime}=\left\{b_{1}^{\prime}, \ldots, b_{k}^{\prime}\right\}$, we have

$$
\begin{align*}
& h^{(L)}\left[i\left(b_{1}\right), \ldots, i\left(b_{L}\right)\right] \\
& =\frac{1}{2^{L}} \sum_{S^{\prime} \in \mathcal{P}(S)}(-1)^{i\left(b_{1}^{\prime}\right)+\cdots+i\left(b_{k}^{\prime}\right)} \tilde{x}^{(k)}\left[b_{1}^{\prime}, \ldots, b_{k}^{\prime}\right], \tag{24}
\end{align*}
$$

where $\mathcal{P}(S)$ is the power set of the set $S$. The power set is a set of all subsets of a given set. Thus the summation is taken over all subsets $S^{\prime}$ of $S$.

For example, the second order term is

$$
\begin{aligned}
& h^{(L)}\left[i\left(b_{1}\right), i\left(b_{2}\right)\right] \\
= & \frac{1}{4}\left\{1+(-1)^{i\left(b_{1}\right)} \tilde{x}^{(1)}\left[b_{1}\right]+(-1)^{i\left(b_{2}\right)} \tilde{x}^{(1)}\left[b_{2}\right]\right. \\
+ & \left.(-1)^{i\left(b_{1}\right)+i\left(b_{2}\right)} \tilde{x}^{(2)}\left[b_{1}, b_{2}\right]\right\}
\end{aligned}
$$

The inverse transformation is given by

$$
\begin{align*}
& (-1)^{i\left(b_{1}\right)+\cdots+i\left(b_{L}\right)} \tilde{x}^{(L)}\left[b_{1}, \ldots, b_{L}\right] \\
& =\sum_{S^{\prime} \in \mathcal{P}(S)}(-1)^{L-k} 2^{k} h^{(k)}\left[i\left(b_{1}^{\prime}\right), \ldots, i\left(b_{k}^{\prime}\right)\right] . \tag{25}
\end{align*}
$$

It becomes possible to derive the schema evolution equation for genetic operators. From the evolution equation of the Walsh coefficient under mutation (16), we obtain

$$
\begin{align*}
& \widehat{M} h^{(L)}\left[i\left(b_{1}\right), \ldots, i\left(b_{L}\right)\right] \\
& =\sum_{S^{\prime} \in \mathcal{P}(S)}(1-2 p)^{k} p^{L-k} h^{(k)}\left[i\left(b_{1}^{\prime}\right), \ldots, i\left(b_{k}^{\prime}\right)\right] . \tag{26}
\end{align*}
$$

For the first order Walsh coefficients, we have

$$
\begin{equation*}
\widehat{M} h^{(1)}\left[i\left(b_{1}\right)\right]=(1-2 p) h^{(1)}\left[i\left(b_{1}\right)\right]+p \tag{27}
\end{equation*}
$$

For crossover, we give here the final results of the schema theorem under uniform crossover. The process of derivation is described in [7. We use an integer $i(\mathcal{H})$ as another representation of the schema $\mathcal{H}$

$$
\begin{equation*}
\{0,1\} \rightarrow 1, \quad\{*\} \rightarrow 0 \tag{28}
\end{equation*}
$$

For example, the new representation of $\mathcal{H}=* 10 *$ is $i(\mathcal{H})=<0,1,1,0\rangle$. Though this representation does not distinguish between 0 and 1 , it may not bring any confusion in the case of crossover process.

The schema theorem for crossover can be given by

$$
\begin{equation*}
\widehat{C} h(k)=\sum_{i=0}^{n-1} c_{i, i \oplus k} h(i) h(i \oplus k), \tag{29}
\end{equation*}
$$

The integers $i$ and $k$ in $h(k)$ and $h(i)$ are the binary expression of schema (28), and please consider that

$$
i=i(\mathcal{H}), \quad k=k(\mathcal{H})
$$

The coefficient $c_{i, i \oplus k}$ is zero when $i$ and $i \oplus k$ both take the value of one at the same bit position.

We will use a shorthand notation

$$
h^{(1)}\left[i_{k}=1\right] \rightarrow \mathrm{h}\left(1_{k}\right), \quad h^{(1)}\left[i_{k}=0\right] \rightarrow \mathrm{h}\left(0_{k}\right)
$$

In this analysis, the notion of linkage [14] is very important, and the linkage disequilibrium coefficient $D$ is defined as

$$
\begin{equation*}
D[k, m]=h^{(2)}\left[1_{k}, 1_{m}\right]-\mathrm{h}\left[1_{k}\right] \mathrm{h}\left[1_{m}\right] . \tag{30}
\end{equation*}
$$

This quantity shows the correlation between alleles at different loci. When each gene evolves independently, a population is in linkage equilibrium, while if there are any correlations among genes at different loci, it is in linkage disequilibrium. When the population is in linkage equilibrium, all $D$ coefficients are zero, $D[k, m]=0$.

If we set the crossover rate $\chi=1$, the effect of crossover is given by [8]. For uniform crossover,

$$
\begin{equation*}
\widehat{C} D[k, m]=\frac{1}{2} D[k, m] . \tag{31}
\end{equation*}
$$

We note that crossover has an effect of reducing the magnitude of $D$. The action of mutation on $D$ is given by

$$
\begin{equation*}
\widehat{M} D[k, m]=(1-2 p)^{2} D[k, m] \tag{32}
\end{equation*}
$$

and we see that mutation also reduces the magnitude of $D$.

## 4 Multiplicative Landscape

This section gives some mathematical results for GAs on the multiplicative landscape obtained by the schema theorem. The fitness function of multiplicative form is defined as

$$
\begin{equation*}
f_{i}=(1-s)^{|i|}=\prod_{k=1}^{\ell}(1-s)^{i(k)}, \quad(0<s<1) \tag{33}
\end{equation*}
$$

where $s$ is a parameter of the strength of selection. We consider a maximization problem on this landscape. In [12], we have shown that the evolution equation of genotypes can be solved exactly for GAs under the action of selection with the multiplicative fitness and mutation. We will obtain here an exact schema evolution.

### 4.1 Schema Analysis

We assume that the population is in linkage equilibrium state at generation $t$, and it will later become clear that this is an essential assumption in the following analysis. Thus we have

$$
\begin{equation*}
x_{i}=\prod_{m=1}^{\ell} \mathrm{h}\{i(m)\} \tag{34}
\end{equation*}
$$

and the average fitness is

$$
\bar{f}(t)=\bar{f}^{(e q)}
$$

where the average fitness in equilibrium is also given in the product form

$$
\begin{equation*}
\bar{f}^{(e q)}=\prod_{m=1}^{\ell}\left\{\mathrm{h}\left(0_{m}\right)+(1-s) \mathrm{h}\left(1_{m}\right)\right\}=\prod_{m=1}^{\ell}\left\{1-s \mathrm{~h}\left(1_{m}\right)\right\} \tag{35}
\end{equation*}
$$

Then we may define the fitness function at each bit as

$$
g_{k}=1-s \mathrm{~h}\left(1_{k}\right) .
$$

The Walsh transform of the fitness function is obtained as

$$
\begin{equation*}
\tilde{f}_{i}=\prod_{m=1}^{\ell}\left\{1+(-1)^{i(m)}(1-s)\right\} \tag{36}
\end{equation*}
$$

In the next subsection, without assuming linkage equilibrium, we will obtain the exact expression for the average fitness using this equation.

Under this assumption, we can obtain the schema equation of the first order schemata for selection. Substituting equation (36) into evolution equation for selection (11), we have

$$
\begin{equation*}
\widehat{S} \tilde{x}_{i}(t)=\prod_{m=1}^{\ell} \frac{\beta\{i(m)\}}{\beta\left(0_{m}\right)} \tag{37}
\end{equation*}
$$

Here, the function $\beta\{i(m)\}$ is defined as

$$
\beta\{i(m)\}=\mathrm{h}\left(0_{m}\right)+(-1)^{i(m)}(1-s) \mathrm{h}\left(1_{m}\right) .
$$

Then we can derive the schema equation of the $L$ th order schemata. With the set of defining bits $S=\left\{b_{1}, \ldots, b_{L}\right\}$, we have

$$
\begin{equation*}
\widehat{S} h^{(L)}\left[i\left(b_{1}\right), \ldots, i\left(b_{L}\right)\right]=\prod_{m \in S} \frac{a\{i(m)\} \mathrm{h}\{i(m)\}}{\mathrm{h}\left(0_{m}\right)+(1-s) \mathrm{h}\left(1_{m}\right)}, \tag{38}
\end{equation*}
$$

where $a(0)=1$ and $a(1)=1-s$. For $\mathrm{h}\left(1_{k}\right)$, the effect of selection is

$$
\widehat{S} \mathrm{~h}\left(1_{k}\right)=\frac{(1-s) \mathrm{h}\left(1_{k}\right)}{1-s \mathrm{~h}\left(1_{k}\right)} .
$$

It is important to note that the schemata after selection also satisfy the condition of linkage equilibrium. From equations (26) and (29), we can also verify that the schemata after mutation and crossover satisfy the condition of equilibrium. Thus, if the population is in linkage equilibrium at $t=0$, then it always satisfies the condition of equilibrium.

The change in the fitness function $g_{k}$ under the action of selection is

$$
\Delta g_{k}(t) \equiv \widehat{S} g_{k}(t)-g_{k}(t)
$$

and we have

$$
\begin{equation*}
\Delta g_{k}(t)=\frac{v_{k}(t)}{g_{k}(t)} \tag{39}
\end{equation*}
$$

where the variance $v_{k}$ is

$$
v_{k}=s^{2} \mathrm{~h}\left(1_{k}\right)\left\{1-\mathrm{h}\left(1_{k}\right)\right\} .
$$

### 4.2 Schema Representation of Average Fitness

We will discuss here the direct effects of crossover and mutation on the average fitness. By using equations (13) and (25), the average fitness $\bar{f}(t)$ can be given in terms of schema frequencies. After some calculations, we have

$$
\begin{equation*}
\bar{f}(t)=\bar{f}^{(e q)}+s^{2} \Delta^{(2)}-s^{3} \Delta^{(3)}+\ldots+(-s)^{\ell} \Delta^{(\ell)} \tag{40}
\end{equation*}
$$

The contribution of the $m$ th order term is given by

$$
\Delta^{(m)}=\sum_{k_{1}} \sum_{<k_{2}} \ldots \sum_{<k_{m}} D\left[k_{1}, k_{2}, \ldots, k_{m}\right]
$$

where the linkage equilibrium coefficient of the order $m$ is given by the schema frequencies

$$
\begin{equation*}
D\left[k_{1}, k_{2}, \ldots, k_{m}\right]=h^{(m)}\left(1_{k_{1}}, 1_{k_{2}}, \ldots, 1_{k_{m}}\right)-\mathrm{h}\left(1_{k_{1}}\right) \mathrm{h}\left(1_{k_{2}}\right) \cdots \mathrm{h}\left(1_{k_{m}}\right) \tag{41}
\end{equation*}
$$

When we use a small value of $s$, the equation is approximately given by

$$
\begin{equation*}
\bar{f}(t) \approx \bar{f}^{(e q)}+s^{2} \sum_{k_{1}} \sum_{<k_{2}} D\left[k_{1}, k_{2}\right] . \tag{42}
\end{equation*}
$$

We have shown in the paper [15] that the variance $V$ of Hamming distance from the optimum solution can be given by the sum of additive variance $V_{a}$ and epistatic variance $V_{e}$

$$
\begin{equation*}
V=V_{a}+V_{e} \tag{43}
\end{equation*}
$$

where

$$
V_{a}=\sum_{k=1}^{\ell} \mathrm{h}\left(1_{k}\right)\left\{1-\mathrm{h}\left(1_{k}\right)\right\}
$$

and

$$
V_{e}=2 \sum_{k_{1}} \sum_{<k_{2}} D\left[k_{1}, k_{2}\right] .
$$

Though we use the term "variance", the epistatic variance $V_{e}$ can take negative values.

If we use a small value of $s$, we obtain the variance of the fitness $V(f)$

$$
\begin{equation*}
V(f)=s^{2}\left(V_{a}+V_{e}\right)+s^{3}(\cdots)+\ldots \approx s^{2}\left(V_{a}+V_{e}\right) \tag{44}
\end{equation*}
$$

The variance $V(f)$ in the linkage equilibrium is given by

$$
\begin{equation*}
V^{(e q)}=\left.\bar{f}^{(e q)}\right|_{s \rightarrow 2 s-s^{2}}-\bar{f}^{(e q)} \cdot \bar{f}^{(e q)} \tag{45}
\end{equation*}
$$



Fig. 1. Numerical experiments for $\bar{f}(t)$. Thick lines for the experiments with crossover, and thin lines without crossover. Solid lines for $\bar{f}(t)$, and dotted lines for $\bar{f}{ }^{(e q)}$. The mutation rate $p=0.001$, selection parameter $s=0.2$, and $N=200$.


Fig. 2. The sum of the second order linkage disequilibrium coefficients, $s^{2} V_{e}$, with ( $\chi=1$ ) and without ( $\chi=0$ ) crossover.


Fig. 3. Variance of fitness. $V(f)$ and $V^{(e q)}$ with $(\chi=1)$ and without $(\chi=0)$ crossover. Solid lines and dotted lines show $V(f)$ and $V^{(e q)}$, respectively.

## 5 Experiments

We carried out numerical experiments of GA on the multiplicative landscape, and their results were compared with the theory in the previous section. The population size $N$ was 200 , and bit length was $\ell=8$. The selection parameter was $s=0.2$. We used the mutation rates $p$ of 0.001 , and uniform crossover. The effect of crossover was studied by comparing the experiments with the crossover rates $\chi=0$ and 1 . At $t=0$, we used the initial value of $\mathrm{h}\left(1_{k}\right)=1 / 8$. The calculations were performed repeatedly with the same parameters, and their results were averaged over 100 runs.

Figure 1 demonstrates the average fitness obtained in four types of calculations. Thick solid line shows $\bar{f}(t)$ with crossover $\chi=1$, and thin solid line without crossover $\chi=0$. Thick dotted line is for $\bar{f}^{(e q)}$ with crossover, and thin dotted line without crossover. We cannot observe the thick dotted line because it is masked by the thick solid line. The effect of crossover is very significant in these experiments. We see that crossover works as a beneficial operator. The effect of linkage disequilibrium is very small, and $\bar{f}(t) \approx \bar{f}^{(e q)}$ in experiments with and without crossover. This result seems to suggest that the effect of linkage disequilibrium is negligibly small. However, this is not the case.

Figure 2 gives $s^{2} V_{e}$ with and without crossover. $V_{e}$ shows the degree of linkage disequilibrium of the second order. When crossover is active, $V_{e}$ is almost 0 . On the other hand, if $\chi=0, V_{e}$ takes negative values of large magnitude.

In Fig. 3, the variance of fitness $V(f)$ is shown. The variances in linkage equilibrium $V^{(e q)}$ calculated by equation (45) are given in dotted lines. There is
large difference in the results with (thick lines) and without (thin lines) crossover. The GA with crossover demonstrates the large value of $V(f)$, and the dotted line for $V^{(e q)}$ is masked by the solid line for $V(f)$. When crossover is absent, the effect of linkage disequilibrium becomes large, and as a result $V(f)$ is small. The contribution of linkage is negative, and we observe large difference between $V(f)$ and $V^{(e q)}$. Fisher's theorem states that the large variance of fitness can give good performance [15], and this explains the fast increase of $\bar{f}(t)$ in GA with crossover in Fig.1.

## 6 Conclusion

In this paper, we have shown that the exact schema theorem can be obtained for the GA on the multiplicative landscape. In this problem, if we ignore the effect of random sampling, the assumption of linkage equilibrium holds at all generations when the initial state is in linkage equilibrium. Therefore, the system is completely determined by the first order schemata $\mathrm{h}\left(1_{k}\right)$. However, in the practical calculations, there appears the stochastic effect, and we have to take into account the effect of linkage disequilibrium.

Crossover works as a beneficial operator in this problem. It reduces the magnitude of $D$ coefficients, and as a result accelerates the speed of evolution by increasing the total variance $V(f)$. This is an indirect effect of crossover.

On the other hand, there is a direct effect of linkage given by equation (40). However, this effect is very small as shown in Fig. 1 in our experiments.

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