# An Analysis of a Simple Genetic Algorithm

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## Abstract

The rate of convergence and the structure of stable populations are studied for a simple, and yet nontrivial, family of genetic algorithms.

## 1 INTRODUCTION

This paper originates in an attempt to use genetic algorithms as an alternative approach to theoretical problems of combinatorial optimization. In Holland's [1] pioneering work it is suggested that genetic algorithms are likely to work well in those cases where some short schemata have fitness exceeding the average and where these schemata combine well by the crossover operator. In this case the crossing-over of two well fitted structures usually results in a well fitted structure. In the context of combinatorial optimization this means that a genetic algorithm (with a genetic operator that is tailor-made for the problem) is likely to be effective when this operator usually merges two given structures of high fitness into a third good structure.

Consider for example the classical problem of finding large matchings in a given graph $G$. Genetic operators with the above-mentioned properties can be described, and it is therefore reasonable to believe that this nontrivial problem of finding a maximum size matching can be effectively solved (or at least approximated) by a genetic algorithm. This line of research quickly runs into serious mathematical difficulties we could not overcome. The present article grew out of our attempts to study similar, simpler systems.

The system under investigation has $n$ independent binary attributes. The fitness of a structure is the number of positive attributes. Evolution in this system is governed by a simple shuffle operator, to be described below. This system stands in sharp contrast with the complicated situations genetic algorithms are usually applied in. Yet its analysis is by no means trivial. Our interest in this system is threefold: First, develop as much rigorous understanding of how it works, in the hope of creating a better basis for the study of similar, but more involved problems. Second, to show that at least the simplest genetic algorithms are amenable to exact mathematical analysis, and develop the suitable techniques. Third, the system turned out to have a measure of beauty.

## 2 THE SYSTEM AND ITS ANALYSIS

### 2.1 DESCRIPTION OF THE SYSTEM

Let $n$ be a natural number. Every structure of our system has exactly $n$ attributes. Each attribute has two possible values (0 and 1) so the set of n attribute may be represented by a binary string of length n. Different structures may have the same set of values for the n attributes.

The *population* will be regarded as a probability distribution over the *kinds* of structures (i.e. over binary strings of length $n$). We shall not estimate in this paper the size needed in order that the population evolved with but a minor deviations from the corresponding distribution.

We define the fitness of a structure to be the number of 1-s it has. Later we shall discuss briefly other fitness functions.

The $\times$ operator (that plays the role of the ordinary crossover operator) acts as follows: given two structures $s_1$ and $s_2$, it produces an offspring structure, whose $i$-th position is determined by the $i$-th position of one of $\{s_1, s_2\}$, each with probability $\frac{1}{2}$.

Note that $\times$ is actually defined for the kinds of populations as well. It will be convenient to extend the domain of $\times$ to pairs of populations. It will be convenient to extend the the domain of $\times$ to the pairs of populations. Denoting symbolically a population $\mathcal{P}$ as $\sum p_i \mathcal{C}_i$, and a population $\mathcal{Q}$ as $\sum q_j \mathcal{C}_j$ where the sum runs over the kinds of structures, the natural definition for $\mathcal{P} \times \mathcal{Q}$ is

$$\mathcal{P} \times \mathcal{Q} = \sum p_i \mathcal{C}_i \times \sum q_j \mathcal{C}_j = \sum \sum p_i q_j (\mathcal{C}_i \times \mathcal{C}_j).$$

Define also $M(\mathcal{P})$ as $\mathcal{P} \times \mathcal{P}$.

Another operator we need is the operator of reevaluation $W$, which is an essential part of Holland's Reproductive Plans. Given a population $\mathcal{P} = \sum p_i \mathcal{C}_i$, $W$ is defined by

$$W\left(\sum p_i \mathcal{C}_i\right) = \sum \left(\frac{f(i) p_i}{\sum f(j) p_j}\right) \mathcal{C}_i.$$

where $f(i)$ stands for fitness of a structure of kind $i$. In other words, each kind in the population increases its part proportionally to its fitness. Note that the sum in the denominator is exactly the average fitness of the population; it will be denoted by $Av(\mathcal{P})$.

In this paper we confine ourselves to symmetrical initial populations (i.e. the populations which remain the same under any permutation of bits). Note that the operators $\times$ and $W$ preserve symmetry. Of special interest to us is the system with the initial population being the uniform distribution over the singletones.

To finish the description of the system, we need to define how it evolves. Given the initial population $\mathcal{P}_0$, $\mathcal{P}_{n+1}$ is

$$\mathcal{P}_{n+1} = W(\mathcal{P}_n) \times W(\mathcal{P}_n) = MW(\mathcal{P}_n).$$

We follow the Reproductive Plan of Holland [1], with a generation replaced in a time-step by the generation of its offsprings. Since the system we have obtained has short above average schemata, there is every reason to believe that the population $\mathcal{P}_n$ converges to distribution having the whole weight on the string '11...111' ($n$ 1-s). The main object of the following sections is to provide a mathematical foundation for this feeling.

Another object of interest are the populations arising from some iterative acting of $M$ on some initial population, and the populations satisfying $\mathcal{P} \times \mathcal{P} = \mathcal{P}$. (Such populations will be called *stable*). Their importance will be revealed later.

## 2.2 HOMOGENEOUS REPRESENTATION

The representation of the the original system as given in section 2.1 is not convenient to work with. Therefore we shall use two other representations. The first is described in this section and the second in the next section. To every symmetric population $\mathcal{P}$ attach a vector $v = (a_0, a_1, ..., a_n)$ where $a_i$ is a total weight of binary strings with exactly $i$ 1-s. The $a_i$-s satisfy two conditions :
$(a)$ $a_i \geq 0$; $(b)$ $\sum_{i=0}^{n} a_i = 1$ .

Call a $(n+1)$-vector *legal* if its entries satisfy the two conditions. There is a one-to-one correspondence between the symmetric populations and the legal $(n+1)$-vectors. Moreover, since the symmetric populations are closed under W and $\times$ , our original system induces a new system over these vectors. The induced system is a genetic algorithm as well. When there is no place for confusion, we use for the induced operators the same symbols as for the original operators.

The original definition of $W(\mathcal{P})$ takes form
$W(v) = W(a_0, a_1, ..., a_n) = (0, \frac{a_1}{Av(v)}, \frac{2a_2}{Av(v)}, ..., \frac{na_n}{Av(v)})$;
$Av(v) = Av(a_0, a_1, ..., a_n) = \sum_{i=0}^{n} i a_i$.

The introduced representation simplifies the investigation of our system, but it has its own drawbacks. The main problem lies in the description of the operator $\times$. Its direct definition would be hard to work with. This problem will be solved in the following section, using a different basis. Meanwhile we note that for two legal vectors $v$ and $u$, $v \times u = (B_0(v,u), B_1(v,u), ..., B_n(v,u))$ where each $B_i(v,u)$ is a symmetric bilinear form with nonnegative coefficients. Their sum is defined by a $(n+1)\times(n+1)$ matrix with all entries equal 1.

### 2.3 CHANGE OF BASIS

The operator $\times$ is inconvenient to work with. In this section we present a basis, more suitable for both $\times$ and $W$.

Let us return to the original system. For a population $\mathcal{P}$ define the random variable $X_i$, $(i = 1, \ldots, n)$ to be the $i$-th coordinate of a random string in $\mathcal{P}$. Define $e_k$, $(k = 0, 1, ..., n)$ to be

$$e_0 = 1; \quad e_k = Pr(\wedge_{i=1}^{k}(X_i = 1)).$$

Note that because of the symmetry of $\mathcal{P}$ we could use in the definition of $e_k$ any $k$-tuple of $X_i$-s with different indices.

We wish to express $e_k$-s in terms of $a_i$-s. Let $A_k$ be a set of all strings in $\mathcal{P}$ having exactly $k$ 1-s, and let $s$ be a random string. For $k > 0$ we have:

$$e_k = Pr(\wedge_{i=1}^{k}(X_i = 1)) =$$

$$\sum_{j=0}^{n} Pr(\wedge_{i=1}^{k}(X_i = 1)|\ s \in A_j)\ Pr(s \in A_j) =$$

$$\sum_{j=k}^{n} \frac{\binom{n-k}{j-k}}{\binom{n}{j}} a_j.$$

Simplifying the above we obtain the equations $(k = 0, 1, ..., n)$

$$e_k = \sum_{i=0}^{n} \frac{i(i-1)...(i-k+1)}{n(n-1)...(n-k+1)} a_i = \frac{1}{\binom{n}{k}} \sum_{i=k}^{n} \binom{i}{k} a_i. \tag{1}$$

Thus the $e_k$-s are obtained from the $a_k$-s by a linear transformation. Since the transformation matrix is lower triangular with nonzero values on the diagonal, it is regular.

In what follows, we call the standard form of a vector the $a\text{-}form$, and its form in the new basis the $e\text{-}form$.

The following class of populations plays a key role in the investigation of our system:

**Definition 2.1** *Let $\mathcal{P}(\alpha)$ be the symmetric population such that*
*(1) $Pr(X_i = 1) = \alpha$ for $i = 1, 2, 3, ...n$.*
*(2) $X_i$ are independent.*

Such populations exist for every $\alpha$ between 0 and 1. They have a simple structure. For example, the probability of a binary string '1101...0' in $\mathcal{P}(\alpha)$ is $\alpha\alpha(1-\alpha)\alpha...(1-\alpha)$. If $v(\alpha)$ is a vector in the $e$-form corresponding to $\mathcal{P}(\alpha)$, then, of course, $v(\alpha) = (1, \alpha, \alpha^2, ..., \alpha^n)$.

**Lemma 2.1** *$\mathcal{P}(\alpha) \times \mathcal{P}(\beta) = \mathcal{P}(\frac{\alpha+\beta}{2})$ where $\alpha, \beta$ are reals in $[0,1]$.*

**Proof:** First, note that since the $\times$ operator acts independently on different coordinates, it preserves their independence. Second, it is evident that $E(X_i)$ in $\mathcal{P} \times \mathcal{Q}$ always equals the average of $E(X_i)$-s in $\mathcal{P}$ and $\mathcal{Q}$. Since $X_i$ is a binary random variable, $Pr(X_i) = E(X_i)$. ∎

**Theorem 2.1** *Let $v = (e_0, e_1, ..., e_n)$, $u = (d_0, d_1, ..., d_n)$ be two vectors in the e-form, and $v \times u = (F_0(v,u), F_1(v,u),$ Then $F_k(v,u)$ is a a bilinear form $\frac{1}{2^k}\sum_{i=0}^{k}\binom{k}{i} e_i d_{k-i}$.*

**Proof:** From the lemma 2.1 we know the statement is true if $v$ and $u$ are of the special form $v = (1, \alpha, \alpha^2, ..., \alpha^n), u = (1, \beta, ..., \beta^n)$ . Indeed, in this case $F_k(v,u) = (\frac{\alpha+\beta}{2})^k = \frac{1}{2^k}\sum_{i=0}^{k}\binom{k}{i}\alpha^i\beta^{k-i}$. To conclude the proof it is sufficient to notice that a basis for $R^{n+1}$ can be constructed of such vectors. Since any basis completely determines the coefficients of a bilinear form, the theorem is established. ∎

It remains to determine the form of the operator $W$ in the new basis.

**Proposition 2.1** *Let $v = (1, e_1, ..., e_n)$ be a vector in e-form. Then the k-th coordinate of $W(v)$ is given by $\left(\frac{n-k}{n}\frac{e_{k+1}}{e_1} + \frac{k}{n}\frac{e_k}{e_1}\right)$ for $k = 0, 1, ..., n$ (regard $e_{n+1}$ as 0).*

**Proof:** The proposition can be verified directly by using the $a$-form of $v$, obtaining the $a$-form of $W(v)$, and going back to the $e$-form. ∎

Before we go on, we establish some additional properties of the $e_k$-s.

From equation 1 we see that $e_1 = \frac{Av(\mathcal{P})}{n}$. Since we are mainly interested in $Av(\mathcal{P})$, the $e_1$ is a very important parameter. Note that $e_1$ is preserved under $M$ ($\times$ preserves average) and is changed to $(\frac{n-1}{n}\frac{e_2}{e_1} + \frac{1}{n})$ under $W$.

As follows from the above paragraph, $e_2$ has a big influence on the next population's average. Note that $M$ changes $e_2$ to $\frac{1}{2}(e_2 + e_1^2)$.

¿From the definition of the $e_k$-s it follow that they constitute a nonnegative nonincreasing sequence. Therefore if $e_k = 0$ in some legal vector in the $e$-form, than $e_{k+1} = ... = e_n = 0$.

**Proposition 2.2** *Let* $v = (e_0, e_1, ..., e_n)$ *be some legal vector in e-form, and denote* $W(v)$ *by* $(e_0^{'}, e_1^{'}, ..., e_n^{'})$ . *Then*

$$\frac{e_k^{'}}{e_{k-1}^{'}} \geq \frac{e_k}{e_{k-1}} \qquad (k = 1, 2, .., n).$$

*(Regard* $\frac{0}{0}$ *as 0).*

**Proof:** We can express (using proposition 2.1) the $e_k^{'}$-s in terms of $e_k$-s. Our statement assumes the form :

$$\frac{(n-k)e_{k+1} + ke_k}{(n-k+1)e_k + (k-1)e_{k-1}} \geq \frac{e_k}{e_{k-1}}.$$

If $e_k = 0$ the inequality holds trivially ; otherwise we obtain an equivalent statement

$$(n-k)\frac{e_{k+1}}{e_k} + 1 \geq (n-k+1)\frac{e_k}{e_{k-1}}.$$

Expressing the $e_k$-s in terms of the $a_i$-s (via equation 1) and taking the common denominator in the left side, the inequality is equivalent to :

$$\frac{\sum_{i=0}^{n} i(i-1)...(i-k+1)(i-k+1)a_i}{\sum_{i=0}^{n} i(i-1)...(i-k+1)a_i} \geq$$

$$\frac{\sum_{i=0}^{n} i(i-1)...(i-k+2)(i-k+1)a_i}{\sum_{i=0}^{n} i(i-1)...(i-k+2)a_i}.$$

The numerator of the left side is the same as denominator of the right side. Observe that the ratio of the $i$-th terms in the left side ($i-k+1$ or 0) is equal to that of the right side. Therefore the last inequality is a direct consequence of the following lemma:

**Lemma 2.2** *Let* $\alpha, a_i, b_i, c_i$ *be nonnegative reals* $(i = 1, ..., n)$ *and suppose that for every* $i$, $\frac{a_i}{b_i} \geq \alpha\frac{b_i}{c_i}$ *(regard* $\frac{0}{0}$ *as* 0*). Then*

$$\frac{\sum_{i=1}^{n} a_i}{\sum_{i=1}^{n} b_i} \geq \alpha \frac{\sum_{i=1}^{n} b_i}{\sum_{i=1}^{n} c_i} .$$

**Proof:** The statement follows from the Cauchy - Shwarz inequality with $x_i = \sqrt{\frac{a_i}{\alpha}}$ , $y_i = \sqrt{\frac{c_i}{\alpha}}$. ∎

**Corollary 2.1** *In the same notation of the proposition we have :* $e'_1 \geq e_1,\ e'_2 \geq e_2, ..., e'_n \geq e_n$.

## 2.4 A LOWER BOUND ON $Av(\mathcal{P}_r)$

The parameter $\frac{e_2}{e_1}$ is very important since the average of the next population depends only on it. The following lemma helps us to estimate its value. In this and the following sections only the $e$-form will be used.

**Lemma 2.3** *Let* $(e_0, e_1, ..., e_n)$ *be the vector representing a nonzero population* $\mathcal{P}$. *Denote by* $(e_0^{'}, e_1^{'}, ...e_n^{'})$ *the representation of* $W(\mathcal{P})$, *and by* $(e_0^*, e_1^*, ...e_n^*)$ *the representation of* $MW(\mathcal{P})$. *Then*

$$\frac{e_2^*}{e_1^*} \geq \left(\frac{2n-1}{2n}\right)\frac{e_2}{e_1} + \frac{1}{2n} .$$

**Proof:**

$$\frac{e_2^*}{e_1^*} \overset{(1)}{=} \frac{e_2^{'} + e_1^{'\,2}}{2e_1^{'}} = \frac{1}{2}e_1^{'} + \frac{1}{2}\frac{e_2^{'}}{e_1^{'}} \overset{(2)}{\geq}$$

$$\frac{1}{2}e_1^{'} + \frac{1}{2}\frac{e_2}{e_1} \overset{(3)}{=} \frac{1}{2}\left(\left(\frac{n-1}{n}\right)\frac{e_2}{e_1} + \frac{1}{n}\right) + \frac{1}{2}\frac{e_2}{e_1} =$$

$$\left(\frac{2n-1}{2n}\right)\frac{e_2}{e_1} + \frac{1}{2n} .$$

(1) is an expression of $e_1$ and $e_2$ in $MW(\mathcal{P})$ in terms of $W(\mathcal{P})$ ;

(2) is an application of the proposition 2.2;
(3) is an expression of $e_1$ in $W(\mathcal{P})$ in terms of $\mathcal{P}$. ∎

We can prove now the main theorem of this section. Call a population *zero free* if the weight of the string '00...000' is zero.

**Theorem 2.2** *Let $\mathcal{Q}$ be some zero-free population and $\mathcal{Q}^+ = WM(\mathcal{Q})$ . Then*

$$n - Av(\mathcal{Q}^+) \quad \leq \quad ( n - Av(\mathcal{Q})) \left(1 - \frac{1}{2n}\right) \quad .$$

**Proof:** Since $n - Av(\mathcal{Q})$ equals $n(1-e_1)$, it is sufficient to prove the corresponding inequality for the $e_1$-s.

For every zero-free population $\mathcal{Q}$ there exists population $\mathcal{Q}^-$ such that $W(\mathcal{Q}^-) = \mathcal{Q}$.

Denote the $e$-form of $\mathcal{Q}^-$ by $(e_0, e_1, ..., e_n)$, the $e$-form of $\mathcal{Q}$ by $(e_0^{'}, e_1^{'}, ..., e_n^{'})$, the $e$-form of $M(\mathcal{Q})$ by $(e_0^*, e_1^*, ..., e_n^*)$ and the $e$-form of $\mathcal{Q}^+$ by $(e_0^+, e_1^+, ..., e_n^+)$.

( $\mathcal{Q}^+ = WM(\mathcal{Q}) = WMW(\mathcal{Q}^-)$ ).

Again we write a sequence of inequalities:

$$1 - e_1^+ \overset{(1)}{=} \left(\frac{n-1}{n}\right)\left(1 - \frac{e_2^*}{e_1^*}\right) \overset{(2)}{\leq}$$

$$\left(\frac{n-1}{n}\right)\left(1 - \frac{e_2}{e_1}\right)\left(1 - \frac{1}{2n}\right) \overset{(3)}{=}$$

$$(1 - e_1^{'}) \left(1 - \frac{1}{2n}\right) \quad .$$

Where
(1) is a representation of $e_1^+$ in $WM(\mathcal{Q})$ in terms of $M(\mathcal{Q})$ ;
(2) is an application of the previous lemma;
(3) is an expression of $e_1$ in $W(\mathcal{Q}^-)$ in terms of $\mathcal{Q}^-$ . ∎

**Corollary 2.2**

$$Av(\mathcal{P}_r) \;\geq\; n-( n-Av(\mathcal{P}_1)) \left(1 - \frac{1}{2n}\right)^{r-1} \;\geq$$

$$n - (n - Av(\mathcal{P}_1)) \exp\left(-\frac{r-1}{2n}\right).$$

**Proof:** The proof follows directly from the theorem above and the observation that $Av(\mathcal{P}_{i+1}) = Av(\mathcal{Q}_i)$ for all natural $i$. (As usual, $\mathcal{Q}_i = W(\mathcal{P}_i), \mathcal{P}_i = M(\mathcal{Q}_{i-1})$.) ∎

The above corollary may be restated in the following form:
For every initial nonzero population $\mathcal{P}_0$, $2n \ln \frac{n}{\epsilon}$ generations shall always sufice to raise the average of the population to $1 - \epsilon$.

## 2.5 AN UPPER BOUND ON $Av(\mathcal{P}_r)$

Our aim now is to prove that there are populations which do not improve too fast. A class of *normal* populations will play a central role.

**Definition 2.2** *A population is called normal if* $e_0 \geq \frac{e_1}{e_0} \geq \frac{e_2}{e_1} \geq ... \geq \frac{e_n}{e_{n-1}}$ .
*($\frac{0}{0}$ is regarded as 0 .)*

Such populations exist. The simplest example is the uniform distribution on singletones, represented (in the $e$-form) by $(\frac{1}{n}, 0, 0, ..., 0)$.

**Theorem 2.3** *The property of normality is preserved under the operators $\times$ and $W$.*

The proof for $W$ is routine; one needs only to express the entries of $W(\mathcal{P})$ in terms of those of $\mathcal{P}$ and use the normality of $\mathcal{P}$.

Much more delicate is the proof that if $\mathcal{P}$ and $\mathcal{Q}$ are both normal, so is $\mathcal{P} \times \mathcal{Q}$. Unexpectedly enough, the result is actually proven by Walkup [2], in the paper on the binomial convolutions of Polya sequences. (The $PF_2$ sequences in this paper correspond to our normal sequences.)

**Lemma 2.4** *Let $(e_0, e_1, ...e_k)$ be nonzero normal population $\mathcal{P}$. Then, in the notions of the lemma 2.3,*

$$\frac{e_2^*}{e_1^*} \;\leq\; \left(\frac{n-1}{n}\right)\frac{e_2}{e_1} + \frac{1}{n} \;.$$

**Proof:**

$$\frac{e_2^*}{e_1^*} \overset{(1)}{=} \frac{e_2' + {e_1'}^2}{2e_1'} = \frac{1}{2}e_1' + \frac{1}{2}\frac{e_2'}{e_1'} \overset{(2)}{\leq}$$
$$\frac{1}{2}e_1' + \frac{1}{2}e_1' = e_1' \overset{(3)}{=} \left(\frac{n-1}{n}\right)\frac{e_2}{e_1} + \frac{1}{n} .$$

(1) is an expression of $e_1$ and $e_2$ in $MW(\mathcal{P})$ in terms of $W(\mathcal{P})$ ;
(2) uses the normality preservation under $W$ (${e_1'}^2 \geq e_2'$);
(3) is an expression of $e_1$ in $W(\mathcal{P})$ in terms of $\mathcal{P}$. ∎

We are now in the position to prove the following theorem :

**Theorem 2.4** *Let $\mathcal{P}_0$ be some nonzero normal population. Then all $\mathcal{P}_i$ and $\mathcal{Q}_i$ are normal, and for all natural $r$*

$$n - Av(\mathcal{Q}_{r+1}) \geq (n - Av(\mathcal{Q}_r))\left(1 - \frac{1}{n}\right) .$$

**Proof:** Using notations analogous to those of the theorem 2.2, ( $e^+$ for $\mathcal{Q}_{r+1}$, $e^*$ for $\mathcal{P}_{r+1}$, $e'$ for $\mathcal{Q}_r$, $e$ for $\mathcal{P}_r$ ), we obtain

$$1 - e_1^+ \overset{(1)}{=} \left(\frac{n-1}{n}\right)\left(1 - \frac{e_2^*}{e_1^*}\right) \overset{(2)}{\geq}$$
$$\left(\frac{n-1}{n}\right)\left(1 - \frac{e_2}{e_1}\right)\left(1 - \frac{1}{n}\right) \overset{(3)}{=}$$
$$(1 - e_1')\left(1 - \frac{1}{n}\right) .$$

Where
(1) is a representation of $e_1^+$ in $\mathcal{Q}_{r+1}$ in terms of $\mathcal{P}$ ;
(2) uses the normality preservation and the previous lemma;
(3) is an expression of $e_1$ in $\mathcal{Q}_r$ in terms of $\mathcal{P}_r$ . ∎

**Corollary 2.3** *Suppose that $\mathcal{P}_0$ is a normal population. Then*

$$Av(\mathcal{P}_r) \leq n - (n - Av(\mathcal{P}_1))\left(1 - \frac{1}{n}\right)^{r-1} \leq$$
$$n - (n - Av(\mathcal{P}_1))\exp\left(-\frac{r-1}{n+1}\right) .$$

**Proof:** The statement follow from the theorem we just have proved, and the fact that $Av(\mathcal{Q}_{i-1}) = Av(\mathcal{P}_i)$ for all natural $i$. ∎

This corollary, together with the corollary 2.2, shows that our bounds are tight for systems with normal $\mathcal{P}_0$.

## 2.6 STABLE POPULATIONS AND ONE GENERAL REMARK ON THE LOWER BOUND

**Theorem 2.5** *For any $\alpha$ in the interval [0,1] $\mathcal{P}(\alpha)$ is only stable population with $e_1 = \alpha$. Moreover, if we start with any $\mathcal{P}$ with $e_1 = \alpha$ and apply $M$ repeatedly, the population converges to $\mathcal{P}(\alpha)$. (Recall that $M$ preserves $e_1$.) In the metrics $d(\mathcal{P}, \mathcal{Q}) = \sum_{k=0}^{n} |e_k - d_k|$ this convergence is exponentially fast.*

**Proof:** We already know from theorem 2.1 that $\mathcal{P}(\alpha)$ is stable. If we prove the second part of the theorem, the uniqueness will be established.

We sketch the proof of the second part. Let $(e_0, e_1, ..., e_n)$ be our initial population. Denote by $e_k^{(r)}$ the $e_k$ after $r$ applications of $M$. Let $\alpha$ be $e_1$. Our goal is to prove that $|e_k^{(r)} - \alpha^k|$ tends to zero exponentially fast.

¿From the theorem 2.1 we know that $e_k^{(1)} = \sum_{i=0}^{k} \frac{\binom{k}{i}}{2^k} e_i e_{k-i}$. Observe that if $e_i = \alpha^i$ for $i = 0, 1, ..., (k-1)$ then $e_k^{(1)} = \frac{2^{k-1}-1}{2^{k-1}}\alpha^k + \frac{1}{2^{k-1}}e_k$.

By above observation, after $t$ applications of $M$, $|e_2 - \alpha^2|$ is $O(2^{-t})$. Since by now $e_2$ does not differ significantly from $\alpha^2$, another $\frac{t}{2}$ applications of $M$ cause $|e_3 - \alpha^3|$ to be $O(2^{-t})$. Meanwhile $|e_2 - \alpha^2|$ is already $O(2^{-1.5t})$. Advancing in the same fashion, after $(t + \frac{t}{2} + ...\frac{t}{2^n}) < 2t$ applications of $M$, for every $k \leq n$ $|e_k - \alpha^k|$ cannot be significantly bigger than $O(2^{-t})$. ∎

After we have found the stable populations and established a fast convergence to the stable population under action of $M$, we wish to outline a direction that might lead to a lower bound on $Av(\mathcal{P}_r)$ for other fitness functions.

We know that the operator $W$ improves the population. It seems that in many cases a more general thing is true :

**Conjecture 2.1** *Let $\mathcal{R}$ be a population, $S$ is an operator obtained by a concatenation of the $W$-s and the $M$-s in a certain order, $S^-$ is obtained exactly in the same way as $S$, with one $W$ left out. Then* $Av(\ S(\mathcal{R}))\ \geq\ Av(\ S^-(\mathcal{R}))$ .

Suppose that our fitness function $f$ is such that the conjecture holds. Suppose, further, that $W$ is not sensitive to small changes. Then we could obtain a lower bound on $Av(\mathcal{P}_r)$ in the following way:

Define a function $F$ as $F(\alpha) = Av(\ W(\mathcal{P}(\alpha)))$.

Define $k$ to be a natural number, such that $k$ consecutive applications of $M$ cause any population $\mathcal{P}$ to approach (in terms of the $W$'s sensitivity) some $\mathcal{P}(\alpha)$. Then $Av(\mathcal{P}_r)\ \geq\ F^{*(\frac{r}{k})}(\beta) - \epsilon$, where $\beta = Av(\mathcal{P}_0)$ and $F^{*m}$ is the $m$-th iteration of $F$.

Indeed, $\mathcal{P}_r = MWMW...MW(\mathcal{P}_0)$. By erasing all the $W$-s standing in the places not divisible by $k$, we cannot (by the conjecture) decrease the average. But now we have $\frac{r}{k}$ blocks of the type $WMMM...M$. The result follows from the definition of $k$.

# 3 CONCLUSION

The main focus of this paper is the applications of genetic algorithms to combinatorial optimization. The concrete system under study is very simple. Yet, investigating it hopefully teaches us something worthwhile about genetic algorithms in general.

A few interesting questions arise from our work. For example, what do stable populations look like? When does iterated applications of $M$ converge ?

It is our hope to be able to investigate in the future some more complex genetic algorithms related to classical combinatorial problems. For example, genetic algorithms systems which produce maximum weight independent set of matroids by synthesizing complex structures from simple ones. We already know of a genetic algorithm that causes maximum size independent set of a matroid to evolve with a high probability in $O(n^2)$ steps.

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