

A Fixed Point Analysis of a Gene Pool GA with Mutation

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1 Introduction

A major goal of genetic algorithm theory is a tractable model of a GA that gives quantitative predictions over multiple generations. The Vose dynamical system model is exact in the infinite-population limit, but it is intractable for quantitative results due to the fact that the number of variables in the model is exponential in the string length. What is needed is a “coarse-grained” model that reduces the number of variables in the model. One natural way to attempt to coarse-grain a GA model is to look at the representations of schemata, especially low-order schemata. The sum of the frequencies of the individuals in a schemata is commonly referred to as the “schema sum” of the schema. One would like to track schema sums over multiple generations.

There are now “exact schema theorems” that can give the exact expected schema sum in the next generation of a genetic algorithm after starting with a finite population. However, these schema theorems still cannot be applied to give exact results for realistic string lengths for more than one generation. The problem is that after one generation an “infinite population” results, and the cardinality of a schema is exponential in the number of variable positions in the schema. The infinite population will generally have a positive probability for all of these points of the schema, and the next generation schema sum depends both on the probabilities and the fitnesses of these points.

Crossover does not change the schema sums of order 1 schemata. Stated another way, it preserves the frequencies of each allele. The effect of crossover on a population is to move the population closer to

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linkage equilibrium. In a linkage equilibrium population, the representation of any string is determined by the allele frequencies. Geiringer's theorem shows that the limit of repeated applications of crossover is a population in linkage equilibrium (also known as Robbins' proportions).

When gene pool recombination is applied to a population, the population goes to linkage equilibrium in one step. This can be achieved by choosing genes from the population rather than from two specific parents. After a gene pool recombination step, the complete state of the population is determined by the allele frequencies, and the number of these variables is linear rather than exponential in the string length. Thus, the gene pool GA can be much more tractable for analysis than the two-parent recombination GA.

For the ones-counting (ONEMAX) and the needle-in-the-haystack (NEEDLE) fitness functions, explicit formulas are given for all fixed points. To our knowledge, this is the first time that formulas for fixed points have been given for a GA that involves selection, recombination, and mutation and for arbitrary string length. We show that the unique fixed point for any linear fitness function is asymptotically stable. For the NEEDLE fitness function, we show that there can be either one or three fixed points (after a possible small perturbation of the needle height). If there is one fixed point, it is stable. If there are three fixed points, then two are asymptotically stable and one is unstable. When the model goes from three fixed points to one by a parameter change (mutation rate or needle height), "phase transition" behavior can happen where the model jumps to single remaining stable fixed point. This could correspond the "punctuated equilibrium" behavior of a finite population GA.

When the fitness function has a sufficiently compact representation in the Walsh basis, we show that the gene pool GA infinite population model reduces to ℓ variables where ℓ is the string length. This class of fitness functions includes linear functions and functions of unitation.

A gene pool recombination GA can either be used as an approximation to a two-parent recombination GA or as an alternative GA. We show empirically that the gene pool GA is a good approximation to a two-parent recombination GA for some fitness functions. (What "some" means is yet to be determined.) In addition, the gene pool GA can suggest general properties of recombination that can then be tested for the two-parent GA.

(Comment: this paragraph is redundant with the previous paragraph.) A gene pool GA can either be used as a practical GA for solving problems, or the model of the GA can be used as an approximation to the model for a GA with two parent recombination. We show empirically that the gene pool model closely approximates the full infinite population model for linear fitness (and maybe for the needle-in-the-haystack fitness??). Mühlenbein and Mahnig [Mühlenbein and Mahnig, 1999] suggest that a GA based on gene pool recombination can handle a wider range of practical problems by combining epistatically linked variables in the fitness function into metavariables, thereby reducing epistasis and making the fitness function closer to linear.

Our analysis is all in terms of the Walsh basis. The Walsh basis allows us to incorporate mutation into the model. The previous work on the gene pool GA has been for a recombination-selection GA with no mutation.

2 Notation

Square brackets $[\cdot \cdot \cdot]$ are used to denote an indicator function: if $expr$ is an expression which may be true or false, then

$$[expr] = \begin{cases} 1 & \text{if } expr \text{ is true} \\ 0 & \text{otherwise} \end{cases}$$

The search space Ω consists of all binary strings of length ℓ . The binary representation of a string induces a correspondence from the elements of Ω to the set of integers from 0 to $2^\ell - 1$. Let $N = 2^\ell$. The bitwise mod 2 sum of two strings j and k is denoted by $j \oplus k$; Ω is a group under this operation. The identity element is the string of zeros, which will be denoted by 0 . The string of all ones will be denoted by $\mathbf{1}$. The bitwise product of strings j and k is denoted by $j \otimes k$. The ones-complement of k is denoted by \bar{k} .

The number of ones in a binary string k is denoted by $\#k$.

For each $u \in \Omega$, $\Omega_u = \{i \in \Omega : i \otimes u = 0\}$; Ω_u is the set of binary strings which have a 1 only in positions where u has a 1. Note that Ω_u is a subgroup of Ω .

Let $\mathcal{L} = \{j \in \Omega : \#j = 1\}$ and let $\mathcal{L}_k = \{j \in \mathcal{L} : j \otimes k = i\}$.

A population (a multiset of Ω) is represented as a population vector x indexed by Ω ; x_j is the fraction of the population which is string j . Thus, if $\ell = 2$ and the population as a multiset is $\{00, 01, 01, 11\}$, then the corresponding population vector is $\langle 1/4, 1/2, 0, 1/4 \rangle$.

All population vectors are contained in the simplex $\Lambda = \{x : \sum_{j \in \Omega} x_j = 1 \text{ and } x_j \geq 0 \text{ for all } j\}$.

A schema is a coset of Ω_k for some $k \in \Omega$. In other words, $\Omega_k \oplus v = \{i \oplus v : i \in \Omega_k\}$ is the schema determined by k and v , where k is a mask for the variable positions and v specifies the fixed positions. Without loss of generality, we can assume that $k \otimes v = 0$. In traditional notation, a schema is denoted by a string from the alphabet $\{0, 1, *\}$, where $*$ is a ‘‘don’t care’’ symbol. The traditional notation schema $1*0**1$ is $\Omega_{010110} \oplus 100001$.

Let $S(x, u)_v$ denote the schema sum of the schema $\Omega_{\bar{u}} \oplus v$ relative to the population x . In other words,

$$S(x, u)_v = \sum_{i \in \Omega_{\bar{u}} \oplus v} x_i = \sum_{i \in \Omega_{\bar{u}}} x_{i \oplus v}$$

Thus, u is a mask for the fixed positions of the schema, and we assume that $v \otimes \bar{u} = 0$. Since $v \in \Omega_u$, $S(x, u)$ can be regarded as a vector indexed over Ω_u . $S(x, u)$ is the vector of schema sums of the family of competing schemata whose variable positions are determined by \bar{u} .

The k th Walsh matrix W_k is an 2^k by 2^k matrix defined by $(W_k)_{i,j} = 2^{-k/2} (-1)^{\#(i \otimes j)}$. The Walsh matrix is symmetric and $W_k = (W_k)^{-1}$. When W is used without a subscript, it will denote W_ℓ .

If x is a population vector, then the Walsh transform of x is Wx and is denoted by \hat{x} . Let e_0, e_1, \dots, e_{N-1} be the standard basis vectors for \mathbb{R}^N . Then the vectors $\hat{e}_0, \hat{e}_1, \dots, \hat{e}_{N-1}$ form the Walsh basis for \mathbb{R}^N . If x is a vector then $\hat{x} = Wx$ is expressed in the Walsh basis. In other words, x_j is the j th coordinate of x in the standard basis and \hat{x}_j is the j th coordinate of x in the Walsh basis. If A is a 2^ℓ by 2^ℓ matrix, then WAW is the Walsh transform of A and is denoted by \hat{A} .

Let Ξ_u denote the projection from vectors indexed over Ω to vectors indexed over Ω_u . Thus, if $k \in \Omega_u \subseteq \Omega$, then $\Xi_u(x)_k = x_k$. It may be convenient for the reader to think of Ω_u as corresponding to the integers in the range from 0 to $2^{\#u} - 1$, and in this case Ξ_u can be thought of as doing the appropriate reindexing.

3 Basic Results

This section gives some basic results relating schema averages, the Walsh representation of a population, and properties of a population that is at linkage equilibrium.

Lemma 1 *If $x \in \Lambda$, then $|\hat{x}_k| \leq 2^{-\ell/2}$ for all $k \in \Omega$.*

Proof: The simplex Λ is the convex hull of the basis vectors e_0, e_1, \dots, e_{N-1} of the standard basis. The vectors $\hat{e}_0, \hat{e}_1, \dots, \hat{e}_{N-1}$ are the same geometric points expressed in the Walsh basis, so the simplex is still the convex hull of these points. But these correspond to the columns of the Walsh matrix, and every entry of the Walsh matrix is $\pm 2^{-\ell/2}$. Thus \hat{x}_k is a convex combination of $2^{-\ell/2}$ and $-2^{-\ell/2}$. \square

This lemma is a technical lemma that is useful in proofs about the Walsh transform.

Lemma 2

$$\sum_{j \in \Omega_u} (-1)^{\#(j \otimes w)} = \begin{cases} 2^{\#u} & \text{if } w \in \Omega_{\bar{u}} \\ 0 & \text{otherwise} \end{cases}$$

Proof: Suppose that $w \in \Omega_{\bar{u}}$. This implies that $j \otimes w = 0$ for all $j \in \Omega_u$. Thus, the summation is equal to the number of elements in Ω_u , which is $2^{\#u}$.

Now suppose $w \notin \Omega_{\bar{u}}$. Then we can write $w = q \oplus v$ where $\#q = 1$, $q \in \Omega_u$, and $q \otimes v = 0$. Note that $\Omega_q = \Omega_{u \otimes q} = \{0, q\}$. Then

$$\sum_{j \in \Omega_u} (-1)^{\#(j \otimes w)} = \sum_{i \in \Omega_{u \otimes q}} \sum_{k \in \Omega_{u \otimes \bar{q}}} (-1)^{\#((i \oplus k) \otimes (q \oplus v))} \quad (1)$$

$$= \sum_{i \in \Omega_{u \otimes q}} (-1)^{\#(i \otimes q)} \sum_{k \in \Omega_{u \otimes \bar{q}}} (-1)^{\#(k \otimes v)} \quad (2)$$

$$= \sum_{k \in \Omega_{u \otimes \bar{q}}} (-1)^{\#(k \otimes v)} - \sum_{k \in \Omega_{u \otimes \bar{q}}} (-1)^{\#(k \otimes v)} = 0 \quad (3)$$

Equation (2) follows from (1) since $(i \oplus k) \otimes (q \oplus v) = (i \otimes q) \oplus (k \otimes v)$, and since $\#((i \otimes q) \oplus (k \otimes v)) \pmod{2} = \#(i \otimes q) + \#(k \otimes v) \pmod{2}$. Equation (3) follows from (2) since $\Omega_q = \Omega_{u \otimes q} = \{0, q\}$. \square

The next theorem shows the close relationship between the schema sums of a population and Walsh coefficients of the population. Since the Walsh transform is invertible, it can also be used to compute the Walsh coefficients \hat{x}_i for $i \in \Omega_u$ from the schema sum vector $S(x, u)$.

Theorem 3 *If x is a population and $u \in \Omega$,*

$$S(x, u) = 2^{\#\bar{u}/2} W_{\#u} \Xi_u(\hat{x})$$

Proof:

$$\begin{aligned}
W_{\#u} \Xi_u(\hat{x})_k &= 2^{-\#u/2} \sum_{j \in \Omega_u} (-1)^{\#(k \otimes j)} \Xi_u(\hat{x})_j \\
&= 2^{-\#u/2} \sum_{j \in \Omega_u} (-1)^{\#(k \otimes j)} 2^{-\ell/2} \sum_{v \in \Omega} (-1)^{\#(j \otimes v)} x_v \\
&= 2^{-\ell/2 - \#u/2} \sum_{v \in \Omega} x_v \sum_{j \in \Omega_u} (-1)^{\#(j \otimes v) + \#(j \otimes k)} \tag{4} \\
&= 2^{-\ell/2 - \#u/2} \sum_{v \in \Omega} x_v \sum_{j \in \Omega_u} (-1)^{\#(j \otimes (v \oplus k))} \tag{5} \\
&= 2^{-\ell/2 - \#u/2} \sum_{w \in \Omega} x_{w \oplus k} \sum_{j \in \Omega_u} (-1)^{\#(j \otimes w)} \\
&= 2^{-\ell/2 - \#u/2} \sum_{w \in \Omega_{\bar{u}}} x_{w \oplus k} \sum_{j \in \Omega_u} (-1)^{\#(j \otimes w)} \quad \text{by lemma 2} \\
&= 2^{-\ell/2 - \#u/2} \sum_{w \in \Omega_{\bar{u}}} x_{w \oplus k} 2^{\#u} \quad \text{by lemma 2} \\
&= 2^{-\ell/2 + \#u/2} \sum_{w \in \Omega_{\bar{u}}} x_{w \oplus k} \\
&= 2^{-\#\bar{u}/2} \sum_{w \in \Omega_{\bar{u}}} x_{w \oplus k} \\
&= 2^{-\#\bar{u}/2} S(x, u)_k
\end{aligned}$$

Equation 5 follows from 4 since $\#(j \otimes v) + \#(j \otimes k) \pmod{2} = \#(j \otimes (v \oplus k)) \pmod{2}$. \square

The following corollary relates the schema sums of the order 1 schemata and the order 1 Walsh coefficients. It follows easily from theorem 3.

Corollary 4 *If $u \in \mathcal{L}$,*

$$S(x, u) = \left\langle \frac{1}{2}(1 + 2^{\ell/2} \hat{x}_u), \frac{1}{2}(1 - 2^{\ell/2} \hat{x}_u) \right\rangle$$

Another way of stating this corollary is:

$$S(x, u)_v = \frac{1}{2} \left(1 + (-1)^{\#v} 2^{\ell/2} \hat{x}_u \right)$$

Definition 5 *A population x is in linkage equilibrium if*

$$x_k = \prod_{u \in \mathcal{L}} S(x, u)_{k \otimes u}$$

Thus, a population is in linkage equilibrium if the frequency of each string is the product of the corresponding 1 schema averages. For example, the population $\frac{1}{64} \langle 19, 5, 29, 11 \rangle$ (with Walsh basis representation $\frac{1}{32} \langle 16, 8, -4, -1 \rangle$) is in linkage equilibrium.

Lemma 6 Let u be an element of Ω , let b be a vector indexed over \mathcal{L}_u , and let a be any real number. Then

$$\sum_{k \in \Omega_u} \prod_{i \in \mathcal{L}_u} (a + (-1)^{\#(i \otimes k)} b_i) = (2a)^{\#u}$$

Proof: The proof is by induction on $\#u$. First assume that $\#u = 1$. Then $\Omega_u = \{0, u\}$ and $\mathcal{L}_u = \{u\}$. So the summation is

$$(a + (-1)^{\#(u \otimes 0)} b_u) + (a + (-1)^{\#(u \otimes u)} b_u) = (a + b_u) + (a - b_u) = 2a$$

If $\#u > 1$, we can write $u = j \oplus v$ where $\#j = 1$ and $\#v = \#u - 1$. Then

$$\begin{aligned} \sum_{k \in \Omega_u} \prod_{i \in \mathcal{L}_u} (a + (-1)^{\#(i \otimes k)} b_i) &= \sum_{k \in \Omega_v} \prod_{i \in \mathcal{L}_u} (a + (-1)^{\#(i \otimes (k \oplus 0))} b_i) + \sum_{k \in \Omega_v} \prod_{i \in \mathcal{L}_u} (a + (-1)^{\#(i \otimes (k \oplus j))} b_i) \\ &= (a + b_j) \sum_{k \in \Omega_v} \prod_{i \in \mathcal{L}_v} (a + (-1)^{\#(i \otimes k)} b_i) + (a - b_j) \sum_{k \in \Omega_v} \prod_{i \in \mathcal{L}_v} (a + (-1)^{\#(i \otimes k)} b_i) \\ &= 2a \sum_{k \in \Omega_v} \prod_{i \in \mathcal{L}_v} (a + (-1)^{\#(i \otimes k)} b_i) = (2a)(2a)^{\#v} = (2a)^{\#u} \end{aligned}$$

□

Lemma 7 Let u be an element of Ω , let b be a vector indexed over \mathcal{L}_u , and let a be any real number. Then

$$\sum_{k \in \Omega_u} (-1)^{\#k} \prod_{i \in \mathcal{L}_u} (a + (-1)^{\#(i \otimes k)} b_i) = 2^{\#u} \prod_{i \in \mathcal{L}_u} b_i$$

Proof: The proof is by induction on $\#u$. First assume that $\#u = 1$. Then $\Omega_u = \{0, u\}$ and $\mathcal{L}_u = \{u\}$. So the summation is

$$(a + (-1)^{\#(u \otimes 0)} b_u) + (-1)^{\#u} (a + (-1)^{\#(u \otimes u)} b_u) = (a + b_u) - (a - b_u) = 2b_u$$

If $\#u > 1$, we can write $u = j \oplus v$ where $\#j = 1$ and $\#v = \#u - 1$. Then

$$\begin{aligned} \sum_{k \in \Omega_u} (-1)^{\#k} \prod_{i \in \mathcal{L}_u} (a + (-1)^{\#(i \otimes k)} b_i) &= \sum_{k \in \Omega_v} (-1)^{\#k} \prod_{i \in \mathcal{L}_u} (a + (-1)^{\#(i \otimes (k \oplus 0))} b_i) - \sum_{k \in \Omega_v} (-1)^{\#k} \prod_{i \in \mathcal{L}_u} (a + (-1)^{\#(i \otimes (k \oplus j))} b_i) \\ &= (a + b_j) \sum_{k \in \Omega_v} (-1)^{\#k} \prod_{i \in \mathcal{L}_v} (a + (-1)^{\#(i \otimes k)} b_i) - (a - b_j) \sum_{k \in \Omega_v} (-1)^{\#k} \prod_{i \in \mathcal{L}_v} (a + (-1)^{\#(i \otimes k)} b_i) \\ &= 2b_j \sum_{k \in \Omega_v} (-1)^{\#k} \prod_{i \in \mathcal{L}_v} (a + (-1)^{\#(i \otimes k)} b_i) = (2b_j)2^{\#v} \prod_{i \in \mathcal{L}_v} b_i = 2^{\#u} \prod_{i \in \mathcal{L}_u} b_i \end{aligned}$$

□

The next theorem gives the sum of the frequencies over any schema.

Theorem 8 *If population x is in linkage equilibrium, and if $u, v \in \Omega$ with $v \otimes \bar{u} = 0$, then*

$$S(x, u)_v = 2^{-\#u} \prod_{i \in \mathcal{L}_u} \left(1 + (-1)^{\#(i \otimes v)} 2^{\ell/2} \hat{x}_i \right)$$

Proof:

$$\begin{aligned} S(x, u)_v &= \sum_{k \in \Omega_{\bar{u}}} x_{k \oplus v} \\ &= \sum_{k \in \Omega_{\bar{u}}} \prod_{i \in \mathcal{L}} S(x, i)_{(k \oplus v) \otimes i} \\ &= \left(\prod_{i \in \mathcal{L}_u} S(x, i)_{v \otimes i} \right) \left(\sum_{k \in \Omega_{\bar{u}}} \prod_{j \in \mathcal{L}_{\bar{u}}} S(x, j)_{k \otimes j} \right) \end{aligned} \quad (6)$$

$$= \left(\prod_{i \in \mathcal{L}_u} \frac{1}{2} \left(1 + (-1)^{\#(v \otimes i)} 2^{\ell/2} \hat{x}_i \right) \right) \left(\sum_{k \in \Omega_{\bar{u}}} \prod_{j \in \mathcal{L}_{\bar{u}}} \frac{1}{2} \left(1 + (-1)^{\#(k \otimes j)} \hat{x}_j \right) \right) \quad (7)$$

$$= \left(2^{-\#u} \prod_{i \in \mathcal{L}_u} \left(1 + (-1)^{\#(v \otimes i)} 2^{\ell/2} \hat{x}_i \right) \right) \left(2^{-\#\bar{u}} \sum_{k \in \Omega_{\bar{u}}} \prod_{j \in \mathcal{L}_{\bar{u}}} \left(1 + (-1)^{\#(k \otimes j)} \hat{x}_j \right) \right)$$

Equation (7) follows from (6) by Corollary 4.

The summation in the last equation is equal to $2^{\#\bar{u}}$ by lemma 6, so the theorem follows. \square

Corollary 9 *Let x be in linkage equilibrium. For any $v \in \Omega$,*

$$x_v = 2^{-\ell} \prod_{i \in \mathcal{L}} \left(1 + (-1)^{\#(i \otimes v)} 2^{\ell/2} \hat{x}_i \right)$$

Proof: Any point is a schema with all positions fixed. Thus, we can apply theorem 8 with u as the string of all ones, and in this case $x_v = S(x, u)_v$. \square

Theorem 10 *If population x is in linkage equilibrium, then*

$$\hat{x}_k = 2^{(\#k-1)\ell/2} \prod_{i \in \mathcal{L}_k} \hat{x}_i$$

Proof: When $\#k = 0$, $\prod_{i \in \mathcal{L}_0} = 1$ so the theorem says that $\hat{x}_0 = 2^{-\ell/2}$. This is true by the Walsh transform formula and since $\sum_i x_i = 1$.

For $\#k > 0$,

$$\begin{aligned}
\widehat{x}_k &= 2^{-\ell/2} \sum_{v \in \Omega} (-1)^{\#(k \otimes v)} x_v \\
&= 2^{-\ell/2} \sum_{v \in \Omega} (-1)^{\#(k \otimes v)} \prod_{u \in \mathcal{L}} S(x, u)_{u \otimes v} \\
&= 2^{-\ell/2} \sum_{i \in \Omega_k} \sum_{j \in \Omega_{\bar{k}}} (-1)^{\#(k \otimes (i \oplus j))} \prod_{u \in \mathcal{L}} S(x, u)_{u \otimes (i \oplus j)} \\
&= 2^{-\ell/2} \left(\sum_{i \in \Omega_k} (-1)^{\#(k \otimes i)} \prod_{u \in \mathcal{L}_k} S(x, u)_{u \otimes i} \right) \left(\sum_{j \in \Omega_{\bar{k}}} (-1)^{\#(k \otimes j)} \prod_{u \in \mathcal{L}_{\bar{k}}} S(x, u)_{u \otimes j} \right) \\
&= 2^{-\ell/2} \left(\sum_{i \in \Omega_k} (-1)^{\#i} \prod_{u \in \mathcal{L}_k} \frac{1}{2} (1 + (-1)^{\#(u \otimes i)} 2^{\ell/2} \widehat{x}_u) \right) \left(\sum_{j \in \Omega_{\bar{k}}} \prod_{u \in \mathcal{L}_{\bar{k}}} \frac{1}{2} (1 + (-1)^{\#(u \otimes j)} 2^{\ell/2} \widehat{x}_u) \right)
\end{aligned}$$

For the first summation, $k \otimes i = i$ since $i \in \Omega_k$. Thus, lemma 7 applies and shows that the summation is $2^{\#k\ell/2} \prod_{u \in \mathcal{L}_k} \widehat{x}_u$.

For the second summation, $\#(k \otimes j)$ is always zero since $j \in \Omega_{\bar{k}}$. Thus, lemma 6 applies and shows that the summation is 1.

□

4 The Gene Pool Model in the Walsh Basis

In this paper, one generation of the gene pool GA will consist of the following three steps:

1. Gene pool recombination.
2. Proportional selection.
3. Mutation.

The dynamical system model will be described by a function $\mathcal{G} : \Lambda \rightarrow \Lambda$. \mathcal{G} is a composition of \mathcal{M} , \mathcal{F} , and \mathcal{U} (i. e., $\mathcal{G} = \mathcal{U} \circ \mathcal{F} \circ \mathcal{M}$). The \mathcal{M} , \mathcal{F} , and \mathcal{U} functions are described below.

4.1 Proportional selection

Following [Vose, 1999], the effect of proportional selection can be described by a function $\mathcal{F} : \Lambda \rightarrow \Lambda$. The probability that an individual $k \in \Omega$ is chosen to be in the new population is $\mathcal{F}(x)_k$. Or stated another way, if proportional selection is applied to a population x , then the expected frequency vector for the resulting population is $\mathcal{F}(x)$.

If $f \in \mathbb{R}^n$ is the fitness function (i. e., f_k is the fitness of k) then

$$\mathcal{F}(x) = \frac{F x}{f^T x}$$

where F is the diagonal matrix such that $F_{k,k} = f_k$.

The average fitness $f^T x$ when computed in the Walsh basis is the same: $\widehat{f^T x} = (f^T W)(Wx) = f^T x$. Thus,

$$\widehat{\mathcal{F}(x)} = \frac{WFx}{\widehat{f^T x}} = \frac{WFWWx}{\widehat{f^T x}} = \frac{\widehat{F}\widehat{x}}{\widehat{f^T x}}$$

Lemma 11 For any $i, j \in \Omega$,

$$\widehat{F}_{i,j} = 2^{-\ell/2} \widehat{f}_{i \oplus j}$$

Proof:

$$\begin{aligned} \widehat{F}_{i,j} &= 2^{-\ell} \sum_{u \in \Omega} (-1)^{\#(u \otimes i)} \sum_{v \in \Omega} (-1)^{\#(v \otimes j)} F_{u,v} \\ &= 2^{-\ell} \sum_{u \in \Omega} (-1)^{\#(u \otimes i)} \sum_{v \in \Omega} (-1)^{\#(v \otimes j)} [u = v] F_{u,u} \\ &= 2^{-\ell} \sum_{u \in \Omega} (-1)^{\#(u \otimes i)} (-1)^{\#(u \otimes j)} f_u \\ &= 2^{-\ell} \sum_{u \in \Omega} (-1)^{\#(u \otimes (i \oplus j))} f_u \\ &= 2^{-\ell/2} \widehat{f}_{i \oplus j} \end{aligned}$$

□

Let σ_k denote the $2^\ell \times 2^\ell$ matrix defined by $(\sigma_k)_{i,j} = [i \oplus k = j]$. Then it is easy to show that $(\sigma_k x)_i = x_{i \oplus k}$.

Corollary 12

$$\widehat{F}(x)_k = \frac{\sum_{i \in \Omega} \widehat{f}_{i \oplus k} \widehat{x}_i}{2^{\ell/2} \widehat{f^T x}} = \frac{\sum_{i \in \Omega} \widehat{f}_i \widehat{x}_{i \oplus k}}{2^{\ell/2} \widehat{f^T x}} = \frac{\widehat{f^T \sigma_k x}}{2^{\ell/2} \widehat{f^T x}}$$

4.2 Mutation

Following [Wright, 1999], the effect of mutation can be described by a function $\mathcal{U} : \Lambda \rightarrow \Lambda$. the probability that an individual $k \in \Omega$ is chosen to be in the new population is $\mathcal{U}(x)_k$.

If the probability that a bit is mutated (flipped) is μ , then the probability that an individual $i \in \Omega$ is mutated to an individual j is $\mu^{\#(i \oplus j)} (1 - \mu)^{\ell - \#(i \oplus j)}$. Thus, we can define a $2^\ell \times 2^\ell$ mutation matrix U with $U_{i,j} = \mu^{\#(i \oplus j)} (1 - \mu)^{\ell - \#(i \oplus j)}$, and $\mathcal{U}(x) = Ux$.

Following Vose (section 4.3 of [Vose, 1999]), we define a vector μ indexed over Ω by

$$\mu_i = (\mu)^{\#i} (1 - \mu)^{\ell - \#i}$$

(Whether μ denotes the scalar mutation rate or the mutation vector should be clear from the context.)

The following lemma is Theorem 6.9 of [Vose, 1999].

Lemma 13

$$\widehat{\mu}_k = 2^{-\ell/2}(1 - 2\mu)^{\#k}$$

The Walsh transform of U is easily shown to be diagonal.

Lemma 14

$$\widehat{U}_{i,j} = [i = j](1 - 2\mu)^{\#i}$$

Proof: Let V be the matrix defined by $V_{i,j} = [i = j](1 - 2\mu)^{\#i}$. Note that $V_{i,i} = 2^{\ell/2}\widehat{\mu}_i$. It is sufficient to show that $\widehat{V} = U$.

Since F in lemma 11 is an arbitrary diagonal matrix, we can apply lemma 11 to V . Thus,

$$\widehat{V}_{i,j} = 2^{-\ell/2} \left(2^{-\ell/2} \widehat{\mu}_{i \oplus j} \right) = \mu_{i \oplus j} = (\mu)^{\#(i \oplus j)} (1 - \mu)^{\ell - \#(i \oplus j)} = U_{i,j}$$

□

Theorem 15

$$\widehat{\mathcal{U}(x)}_k = (1 - 2\mu)^{\#k} \widehat{x}_k$$

4.3 Gene pool recombination

To implement gene pool recombination in a finite population GA, the order 1 schema sums $S(x, u)$ for $\#u = 1$ are computed from the current population x . Then each individual of the new population is constructed by choosing each bit according to the probabilities determined by these schema sums. Thus, the probability that the bit at position i is 0 is $S(x, 2^i)_0$ and the probability that the bit at position i is 1 is $S(x, 2^i)_{2^i}$.

In the infinite population model, the population y resulting from applying gene pool recombination to population x has the properties that $S(y, u) = S(x, u)$ and $\widehat{y}_u = \widehat{x}_u$ for $\#u = 1$. In addition, y is at linkage equilibrium. Thus, the higher order schema sums and Walsh coefficients of the population after gene pool recombination can be computed from theorems 8 and 10.

As with proportional selection and mutation, we can describe gene pool recombination through a function $\mathcal{M} : \Lambda \rightarrow \Lambda$. By theorem 10, we have:

$$\widehat{\mathcal{M}(x)}_k = 2^{(\#k-1)\ell/2} \prod_{i \in \mathcal{L}_k} \widehat{x}_i = 2^{-\ell/2} \prod_{i \in \mathcal{L}_k} 2^{\ell/2} \widehat{x}_i$$

4.4 The gene pool GA for a general fitness vector

We make the assumption that the fitness of every individual is positive. Since proportional selection is invariant under multiplication of the fitness by a positive constant, we can assume that the minimum fitness is 1. Thus, the fitness vector f can be written in the form

$$f = \mathbf{1} + \sum_{k \in \Omega} (f_k - 1) e_k$$

The Walsh transform of $\mathbf{1}$ is $2^{\ell/2}e_0$, where e_0 represents the vector with a 1 in the first position and zeros in all other positions. Thus,

$$\widehat{f}_i = \begin{cases} 2^{\ell/2} + 2^{-\ell/2} \sum_{j \in \Omega} (f_j - 1) & \text{if } i = 0 \\ 2^{-\ell/2} \sum_{j \in \Omega} (-1)^{\#(j \otimes i)} (f_j - 1) & \text{if } i \neq 0 \end{cases}$$

Let $y = \mathcal{M}(x)$. First we will calculate $\widehat{\mathcal{F}(y)}$ using Corollary 12.

$$\begin{aligned} \widehat{\mathcal{F}(y)}_k &= \frac{\widehat{f}^T \sigma_k \widehat{y}}{2^{\ell/2} \widehat{f}^T \widehat{y}} \\ &= \frac{\sum_{i \in \Omega} \widehat{y}_i \widehat{f}_{i \oplus k}}{\sum_{i \in \Omega} \widehat{y}_i \widehat{f}_i} \\ &= \frac{2^{\ell/2} \widehat{y}_k + 2^{-\ell/2} \sum_{i \in \Omega} \widehat{y}_i \sum_{j \in \Omega} (-1)^{\#(j \otimes (i \oplus k))} (f_j - 1)}{2^{\ell/2} + \sum_{i \in \Omega} \widehat{y}_i \sum_{j \in \Omega} (-1)^{\#(j \otimes i)} (f_j - 1)} \\ &= \frac{2^{\ell/2} \widehat{y}_k + \sum_{j \in \Omega} (-1)^{\#(j \otimes k)} (f_j - 1) 2^{-\ell/2} \sum_{i \in \Omega} (-1)^{\#(i \otimes j)} \widehat{y}_i}{2^{\ell/2} + \sum_{j \in \Omega} (f_j - 1) \sum_{i \in \Omega} (-1)^{\#(j \otimes i)} \widehat{y}_i} \\ &= \frac{2^{\ell/2} \widehat{y}_k + \sum_{j \in \Omega} (-1)^{\#(j \otimes k)} (f_j - 1) y_j}{2^{\ell/2} + \sum_{j \in \Omega} (f_j - 1) 2^{\ell/2} y_j} && \text{by the Walsh transform formula} \\ &= \frac{2^{\ell/2} \widehat{y}_k + \sum_{i \in \Omega} (-1)^{\#(i \otimes k)} (f_i - 1) \prod_{j \in \mathcal{L}} (1 + (-1)^{\#(i \otimes j)} 2^{-\ell/2} \widehat{y}_j)}{2^\ell + \sum_{i \in \Omega} (f_i - 1) \prod_{j \in \mathcal{L}} (1 + (-1)^{\#(i \otimes j)} 2^{-\ell/2} \widehat{y}_j)} && \text{by Corollary 9} \end{aligned}$$

Since $\widehat{y}_j = \widehat{x}_j$ for $j \in \mathcal{L}$, and since $\mathcal{G}(x) = \mathcal{U}(\mathcal{F}(\mathcal{M}(x))) = \mathcal{U}(\mathcal{F}(y))$, for $k \in \mathcal{L}$,

$$\widehat{\mathcal{G}(x)}_k = (1 - 2\mu) \frac{2^{\ell/2} \widehat{x}_k + \sum_{i \in \Omega} (-1)^{\#(i \otimes k)} (f_i - 1) \prod_{j \in \mathcal{L}} (1 + (-1)^{\#(i \otimes j)} 2^{-\ell/2} \widehat{x}_j)}{2^\ell + \sum_{i \in \Omega} (f_i - 1) \prod_{j \in \mathcal{L}} (1 + (-1)^{\#(i \otimes j)} 2^{-\ell/2} \widehat{x}_j)} \quad (8)$$

This formula is a recurrence that defines the infinite population gene pool GA model in terms of the variables \widehat{x}_k for $k \in \mathcal{L}$. It allows us to compute $\mathcal{G}(x)$ efficiently when most of the fitnesses of individuals are the same.

The notation can be simplified by doing a change of variables. Let $\widehat{z}_k = 2^{\ell/2} \widehat{x}_k$ for $k \in \mathcal{L}$. Note that while \widehat{x}_k ranges from $-2^{-\ell/2}$ to $2^{-\ell/2}$ for x in the simplex, \widehat{z}_k ranges from -1 to 1 . Then the recurrence in terms of these variables is

$$\widehat{\mathcal{G}(z)}_k = (1 - 2\mu) \frac{2^\ell \widehat{z}_k + \sum_{i \in \Omega} (-1)^{\#(i \otimes k)} (f_i - 1) \prod_{j \in \mathcal{L}} (1 + (-1)^{\#(i \otimes j)} \widehat{z}_j)}{2^\ell + \sum_{i \in \Omega} (f_i - 1) \prod_{j \in \mathcal{L}} (1 + (-1)^{\#(i \otimes j)} \widehat{z}_j)} \quad (9)$$

5 The NEEDLE and BINEEDLE fitness functions

The NEEDLE (needle-in-the-haystack) fitness function assigns a fitness of $1 + a$ (where $a > 0$) to the string of all zeros, and assigns a fitness of 1 to all other strings. The BINEEDLE fitness function assigns fitness $1 + a$ to the string of all zeros, $1 + b$ to the string of all ones, and 1 to all other strings.

Comment: A summary of previous work on the NEEDLE fitness function, the Eigen model, and on quasispecies should go here.

Equation (9) can be specialized to the case of the bineedle fitness function:

$$\widehat{\mathcal{G}}(z) = (1 - 2\mu) \frac{2^\ell \widehat{z}_k + a \prod_{i \in \mathcal{L}} (1 + \widehat{z}_i) - b \prod_{i \in \mathcal{L}} (1 - \widehat{z}_i)}{2^\ell + a \prod_{i \in \mathcal{L}} (1 + \widehat{z}_i) + b \prod_{i \in \mathcal{L}} (1 - \widehat{z}_i)} \quad (10)$$

The recurrence leads immediately to the fixed point equations:

$$\widehat{z}_k \left(2^{\ell+1} \mu + a \prod_{i \in \mathcal{L}} (1 + \widehat{z}_i) + b \prod_{i \in \mathcal{L}} (1 - \widehat{z}_i) \right) = (1 - 2\mu) \left(a \prod_{i \in \mathcal{L}} (1 + \widehat{z}_i) - b \prod_{i \in \mathcal{L}} (1 - \widehat{z}_i) \right) \quad (11)$$

Lemma 16 *If $\mu > 0$ and if z is a fixed point of \mathcal{G} which is in the interior of the simplex, then \widehat{z} is symmetric in the sense that all components of \widehat{z} are equal.*

Proof: Since z is in the interior of the simplex, $|\widehat{z}_k| < 1$ for all $k \in \mathcal{L}$. Thus, $\prod_{i \in \mathcal{L}} (1 + \widehat{z}_i) > 0$ and $\prod_{i \in \mathcal{L}} (1 - \widehat{z}_i) > 0$ for all $k \in \mathcal{L}$.

All components \widehat{z}_k of \widehat{z} satisfy:

$$\widehat{z}_k = \frac{(1 - 2\mu) (a \prod_{i \in \mathcal{L}} (1 + \widehat{z}_i) - b \prod_{i \in \mathcal{L}} (1 - \widehat{z}_i))}{2^{\ell+1} \mu + a \prod_{i \in \mathcal{L}} (1 + \widehat{z}_i) + b \prod_{i \in \mathcal{L}} (1 - \widehat{z}_i)} \quad (12)$$

The right side of this equation is the same for all k . □

Thus, equation (12) can be simplified by replacing all components of \widehat{z} with a scalar variable w . The resulting equation is:

$$2^{\ell+1} \mu w + a(w - 1 + 2\mu)(1 + w)^\ell + b(w + 1 - 2\mu)(1 - w)^\ell = 0 \quad (13)$$

If the GA model is started with a symmetric population, symmetry will be maintained. In this case, the recurrence equations can also be written in terms of the symmetric variable w .

$$\mathcal{G}(w) = (1 - 2\mu) \frac{2^\ell w + a(1 + w)^\ell - b(1 - w)^\ell}{2^\ell + a(1 + w)^\ell + b(1 - w)^\ell} \quad (14)$$

Next we investigate the stability of the fixed points.

Definition 17 *Suppose that $g : \mathbb{R}^N \rightarrow \mathbb{R}^N$ defines a discrete-time dynamical system. A fixed point x of g is **asymptotically stable** if there is a neighborhood of x so that for any y in this neighborhood, $\lim_{t \rightarrow \infty} g^t(y) = x$.*

In other words, if the dynamical system is started sufficiently close to x , it converges to x .

If g is differentiable, the differential of g is the $N \times N$ matrix defined by

$$(dg)_{i,j} = \frac{\partial g_i}{\partial x_j}$$

The differential dg_x at x is obtained by evaluating the partial derivatives at x .

A fixed point x will be called **hyperbolic** if dg_x exists and the maximum modulus of the eigenvalues of dg_x is not 1. It is well known that if all of the eigenvalues of dg_x have modulus less than 1, then x is an asymptotically stable fixed point of g .

Thus, we are interested in computing $d\mathcal{G}_{\hat{z}}$ for the fixed points \hat{z} of \mathcal{G} . (Since we are interested in stability in the simplex, we cannot just compute the 1-dimensional derivative of the symmetric version of \mathcal{G} .) The differential will be computed by differentiating formula (10).

Lemma 18 *Let $P = \prod_{i \in \mathcal{L}}(1 + z_i)$, $Q = \prod_{i \in \mathcal{L}}(1 - z_i)$, $P_j = \prod_{i \in \mathcal{L} \setminus \{j\}}(1 + z_i)$ and $Q_j = -\prod_{i \in \mathcal{L} \setminus \{j\}}(1 - z_i)$. Then for $j \neq k$,*

$$\frac{\partial \widehat{\mathcal{G}}(z)_k}{\partial \hat{z}_j} = (1 - 2\mu) \frac{2^\ell a(1 - \hat{z}_k)P_j - 2^\ell b(1 + \hat{z}_k)Q_j - 2abPQ_j + 2abQP_j}{(2^\ell + aP + bQ)^2}$$

$$\frac{\partial \widehat{\mathcal{G}}(z)_k}{\partial \hat{z}_k} = (1 - 2\mu) \frac{2^{2\ell} + 2^\ell aP + 2^\ell bQ + 2^\ell a(1 - \hat{z}_k)P_k - 2^\ell b(1 + \hat{z}_k)Q_k - 2abPQ_k + 2abQP_k}{(2^\ell + aP + bQ)^2}$$

Furthermore, both of these partial derivatives are nonnegative for $0 \leq \mu \leq 1/2$ and \hat{z} representing a point in the simplex.

Proof: Note that $\frac{\partial P}{\partial \hat{z}_j} = P_j$ and $\frac{\partial Q}{\partial \hat{z}_j} = Q_j$. Then the computation of the partials is straightforward but tedious. For \hat{z} in the simplex, $-1 \leq \hat{z}_i \leq 1$ by lemma 1 and by the definition of \hat{z}_i in terms of \hat{x}_i , and this implies that P , Q , P_j and $-Q_j$ are all nonnegative. \square

Lemma 19 *Let $P = (1+w)^\ell$, $Q = (1-w)^\ell$, $P' = \ell(1+w)^{\ell-1}$, $Q' = -\ell(1-w)^{\ell-1}$. Then the derivative of the symmetric \mathcal{G} defined in equation (14) is given by:*

$$\frac{d\mathcal{G}}{dw} = (1 - 2\mu) \frac{2^{2\ell} + 2^\ell aP + 2^\ell bQ + 2^\ell a(1-w)P' - 2^\ell b(1+w)Q' - 2abPQ' + 2abQP'}{(2^\ell + aP + bQ)^2}$$

Lemma 20 *Let A be an $n \times n$ matrix where all of the diagonal entries are equal to a and all of the off-diagonal entries are equal to b . Then the eigenvalues of A are $a + (n-1)b$ with multiplicity 1 and $a - b$ with multiplicity $n-1$.*

Proof: The eigenvalues of a matrix are unchanged if a multiple of one column is added to another column. We will apply these operations to transform A into an upper triangular matrix.

First, add the sum of columns 2 to n to column 1. now every entry of column 1 is $a + (n-1)b$. Then add column n to each of columns 2 to $n-1$. This makes the matrix upper triangular except for the last column, and the diagonal entries in columns 2 to $n-1$ are $a - b$. Add $-b/(a + (n-1)b)$ times column 1 to column n . This makes all off-diagonal entries of column n equal to zero and makes the diagonal entry equal to $a - b$. So the matrix is now upper triangular, the first diagonal entry is $a + (n-1)b$, and the remaining diagonal entries are $a - b$.

The eigenvalues of a triangular matrix are the diagonal entries. \square

Lemma 21 *At a symmetric point \widehat{z} where $\widehat{z}_k = w$ for all $k \in \mathcal{L}$,*

$$\frac{d\mathcal{G}}{dw} = \frac{\partial \widehat{\mathcal{G}}(z)_k}{\partial \widehat{z}_k} + (\ell - 1) \frac{\partial \widehat{\mathcal{G}}(z)_k}{\partial \widehat{z}_j}$$

Thus, the largest modulus eigenvalue of $d\mathcal{G}_{\widehat{z}}$ is equal to $\frac{d\mathcal{G}}{dw}$.

Proof: The formula follows by comparing the formulas from lemmas 18 and 19. Lemma 20 shows that the largest modulus eigenvalue of $d\mathcal{G}_{\widehat{z}}$ is the right side of the formula. \square

The next theorem says that the fixed points of the dynamical system are determined by solving a single-variable degree $\ell + 1$ polynomial, and the stability of hyperbolic fixed points can be determined by evaluating the derivative of a single-variable degree $\ell + 1$ polynomial.

Theorem 22 *The fixed points of the dynamical system determined by equation (10) are symmetric and are determined by solving equation (13). If a fixed point is hyperbolic, then it is stable if and only if the derivative of the symmetric \mathcal{G} evaluated at the fixed point is less than 1.*

Proof: The symmetry follows from lemma 16. The stability statement follows from lemma 21. \square

6 The fixed points for the NEEDLE fitness

In this section we analyze the fixed points for the NEEDLE fitness. Thus, $b = 0$. One way to understand the fixed points is to plot the symmetric fixed point equation (13) as a function of a . Thus, we rewrite equation (13) by solving for a .

$$a = \frac{2^{\ell+1} \mu w}{(1 - w - 2\mu)(1 + w)^\ell} \quad (15)$$

Figure 1 shows a plotted as a function of w for $\ell = 9$, $\mu = 0.03$. For a fixed value of a_f , the w values for the fixed points can be found by intersecting the horizontal line $a = a_f$ with the graph (or by solving substituting a_f for a in equation (13) and solving for w). For example, for $a = 1$, there are fixed points at 0.0425, 0.4478, and 0.8287.

The (w, a) points where the curve has a zero slope can be critical values. As a increases through such a value, pair of fixed points can appear or disappear. The points (w_0, a_0) and (w_1, a_1) in figure 1 are such points. For $a < a_1$, there is one fixed point in the interval $[0, 1]$; for $a_1 < a < a_0$ there are three fixed points; and for $a_0 < a$ there is one fixed point.

Thus, it is useful to find those points where this curve has slope 0. First, we solve equation (13) for a . Then we differentiate with respect to w and set the derivative to 0, and solve for w .

$$\frac{da}{dw} = \frac{2^{\ell+1} \mu (1 - w - 2\mu)(1 + w)^\ell + 2^{\ell+1} \mu w (1 + w)^\ell - 2^{\ell+1} \ell w (1 - w - 2\mu)(1 + w)^{\ell-1}}{((1 - w - 2\mu)(1 + w)^\ell)^2} = 0 \quad (16)$$

The equation simplifies to:

$$\ell w_c^2 + (2\ell\mu - 2\mu - \ell + 1)w_c + (1 - 2\mu) = 0$$

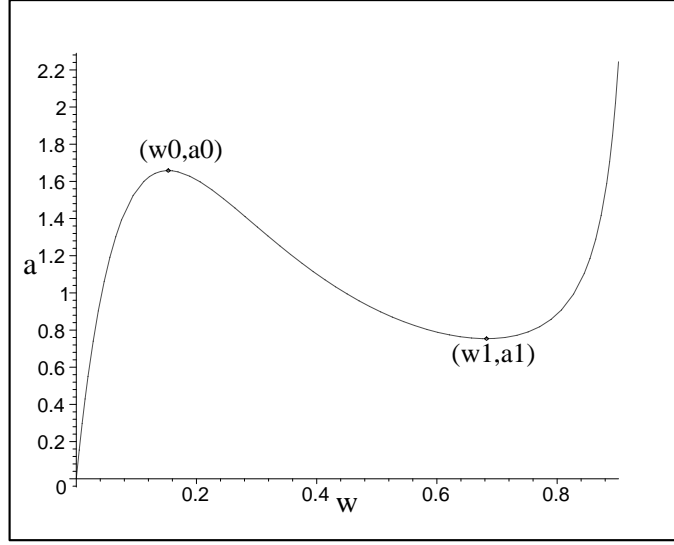


Figure 1: Values of parameter a that will give a fixed point as a function of w . $\ell = 9, \mu = 0.03$.

The solutions are given by

$$w_c = \frac{-2\ell\mu + 2\mu + \ell - 1 \pm \sqrt{4\mu^2 - 4\mu + 16\ell\mu - 8\ell\mu^2 + 1 - 6\ell + \ell^2 - 4\ell^2\mu + 4\ell^2\mu^2}}{2\ell}$$

The critical values for a can be found by substituting these critical values for w into (15). For example, for $\ell = 9, \mu = 0.03$, the critical points shown in figure 1 are $(w_0, a_0) = (0.1530, 1.658)$, $(w_1, a_1) = (0.6825, 0.7536)$.

For a fixed value of a_{fixed} , the critical values for the mutation rate μ can be found by substituting the formula for w_c written as a function of μ into (13), and also substituting a_{fixed} for a , and solving for μ . For example, for $\ell = 9$ and $a = 1$, the critical mutation values are $\mu_c = 0.01861$ and $\mu_c = 0.037540$. Below the lower critical mutation rate, there is one fixed point population near the needle (which is stable). Between the two critical mutation rates, there are three fixed point populations, one stable near the needle, one unstable, and one stable which is near a random population.

By analyzing equation (15), we can give a definitive characterization of the fixed points.

Theorem 23 *If $0 < \mu < 1/2$, then there can be at most 3 fixed points. For a and μ where there is one fixed point, it is stable. Where there are three fixed points, they are stable, unstable, and stable when ordered by w values. If there are 2 fixed points, then a small perturbation of either a or μ can give one fixed point.*

Proof: For $w < 0$, the graph of (15) is below the $a = 0$ axis, so there are no fixed points under our assumption that $a > 0$.

The graph of (15) crosses the $a = 0$ axis only at $w = 0$. Thus, for fixed μ and sufficiently small $a > 0$, there must be a single fixed point near $w = 0$ (the center of the simplex). As w approaches $1 - 2\mu$ from

the left, the graph goes to positive infinity. Thus, for fixed μ and sufficiently large a , there must be a single fixed point near $1 - 2\mu$.

We have already seen that there are at most two points where the graph has zero slope. Thus, the graph can have at most one local maximum and one local minimum, and for fixed μ , a horizontal line corresponding to a fixed a value can intersect the curve in at most 3 points.

Theorem 22 shows that the stability of the fixed points in the simplex is the same as the stability of equation (14) with $b = 0$. The graph of (14) starts above the diagonal and ends below the diagonal. Each intersection of the graph with the diagonal gives a fixed point, and if the slope of the graph at the intersection has absolute value less than 1, the fixed point is stable.

Thus, after a small perturbation of a , the graph must either cross the diagonal once from above the diagonal to below, or cross the diagonal three times, once from above to below, once from below to above, and once from above to below. Furthermore, we can assume that the derivative at the crossing point is not equal to 1.

Since $\frac{dG}{dw} > 0$ from equation (14), at a fixed point where the graph crosses the diagonal from above to below must be stable. A fixed point where the graph crosses from below to above must be unstable. \square

Thus, we have exactly characterized the fixed points for the gene pool model on the NEEDLE fitness function. For fixed values of a and μ , the location of the fixed points can be found using equation (6). For a fixed value of μ , the range of values of a which give bistability can be found, and for a fixed value of a the range of values of μ which give bistability can be found.

The population distribution at a fixed point can be found using Corollary 9. *Comment: I can derive the exact distribution under mutation/selection, only I have to numerically solve a system of equations to find the distribution. I have been able to do this.*

The whole system exhibits what is known as hysteresis. In a system with varying parameters, the state of the system depends on the history of how that state was reached in parameter space. For example, suppose that the system is started with a random population and a mutation rate between the upper and lower mutation rates. It will then converge to the random fixed point. If the mutation is lowered below the lower critical mutation rate, the system will jump to the needle fixed point, and if the mutation is then raised back to its original value, the system will stay on the needle fixed point.

Figure 2 shows how the critical values change for a fixed string length as the mutation changes. The horizontal axis is w , and the vertical axis is a . The curves correspond to mutation rates of 0.02, 0.03, 0.04, 0.05. For a given a value a_{fixed} , intersecting the horizontal line $a = a_{fixed}$ with the curve gives the fixed points for those a and μ values.

Figure 3 shows the region of bistability in (μ, a) space for $\ell = 9$. The horizontal axis is the mutation rate μ and the vertical axis is the needle height parameter a . Between the two curves, the system is bistable. underneath the lower curve, only the needle fixed point is stable. Above the upper curve, only the random fixed point is stable.

Figure 4 shows how the bistability phenomenon depends on the string length. The upper and lower critical mutation rates for $a = 1$ are plotted as a function of string length for string lengths from 7 to 20. (There is no bistability for $a = 1$ for $\ell < 7$. There is a small bistability region for small a for $\ell = 6$. There does not seem to be any bistability for $\ell < 6$.)

We see that the upper critical mutation rate decreases slowly as a function of string length. The lower

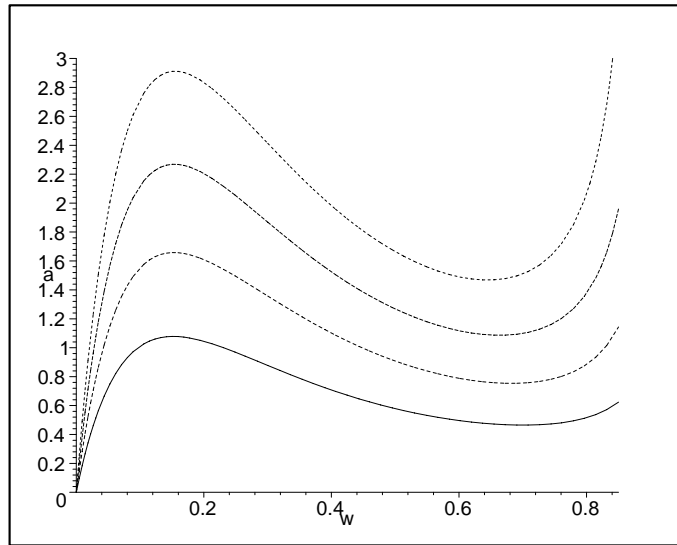


Figure 2: Values of parameter a that will give a fixed point as a function of w for $\mu = 0.02, 0.03, 0.04, 0.05$, $\ell = 9$.

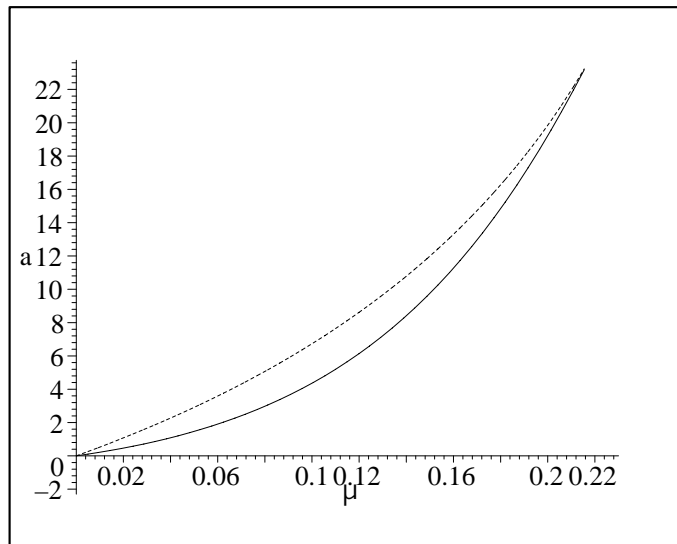


Figure 3: Region of bistability in (μ, a) space for $\ell = 9$.

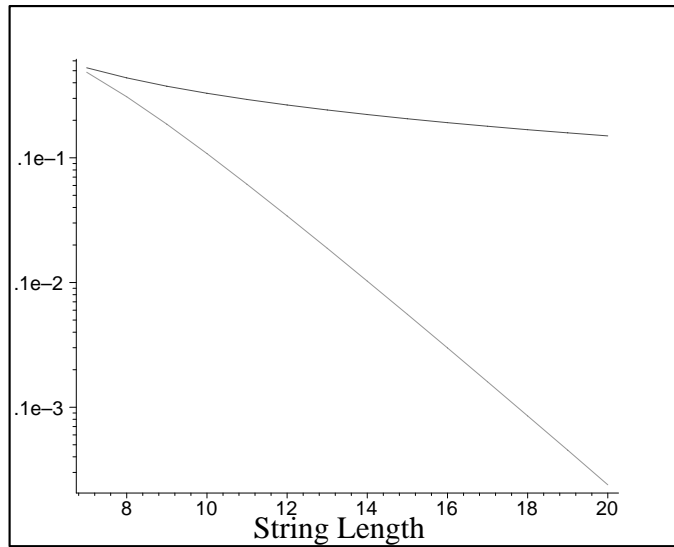


Figure 4: Upper and lower critical mutation rates as a function of string length for $a = 1$

critical mutation rate decreases rapidly. The graph is approximately a straight line on the semilog plot, so this indicates that it is decreasing exponentially.

References

- [Mühlenbein and Mahnig, 1999] Mühlenbein, H. and Mahnig, T. (1999). The factorized distribution algorithm for additively decomposed functions. In Angeline, P. J., Michalewicz, Z., Schoenauer, M., Yao, X., and Zalzal, A., editors, *Proceedings of the Congress of Evolutionary Computation*, volume 1, pages 752–759, Mayflower Hotel, Washington D.C., USA. IEEE Press.
- [Vose, 1999] Vose, M. D. (1999). *The Simple Genetic Algorithm: Foundations and Theory*. MIT Press, Cambridge, MA.
- [Wright, 1999] Wright, A. H. (1999). The exact schema theorem. Technical report, University of Montana, Missoula, MT 59812, USA.