

SIMPLE GENETIC ALGORITHM WITH α -SELECTION

Intrinsic System Model, Fixed Points and the Fixed Point Graph

André Neubauer

*Information Processing Systems Lab, Münster University of Applied Sciences
Stegerwaldstraße 39, D-48565 Steinfurt, Germany*

Keywords: Simple genetic algorithm, α -selection, Random heuristic search, Dynamical system model, Infinite population model, Fixed point graph.

Abstract: Genetic algorithms (GA) are instances of random heuristic search (RHS) which mimic biological evolution and molecular genetics in simplified form. These random search algorithms can be theoretically described with the help of a deterministic dynamical system model by which the stochastic trajectory of a population can be characterized using a deterministic heuristic function and its fixed points. For practical problem sizes the determination of the fixed points is unfeasible even for the simple genetic algorithm (SGA). The recently introduced simple genetic algorithm with α -selection allows the analytical calculation of the unique fixed points of the dynamical system model. In this paper, an overview of the theoretical results for the simple genetic algorithm with α -selection and its corresponding intrinsic system model is given. Further, the connection to the fixed point graph is illustrated which describes the asymptotic behavior of the simple genetic algorithm. In addition to the theoretical analysis experimental results for the simple genetic algorithm with α -selection, uniform crossover and bitwise mutation are presented.

1 INTRODUCTION

As specific instances of random heuristic search (RHS), genetic algorithms mimic biological evolution and molecular genetics in simplified form (Vose, 1999b). Genetic algorithms (GA) process populations of individuals which evolve according to selection and genetic operators like crossover and mutation (Holland, 1992). The algorithm's stochastic dynamics can be described with the help of a dynamical system model introduced by VOSE et al. (Reeves and Rowe, 2003; Vose, 1999b; Vose, 1999a). The population trajectory is attracted by the fixed points of an underlying deterministic heuristic function which also yields the expected next population. However, even for moderate problem sizes the calculation of the fixed points is difficult.

The simple genetic algorithm (SGA) with α -selection recently introduced in (Neubauer, 2009; Neubauer, 2008a; Neubauer, 2008c; Neubauer, 2008b) allows to explicitly derive the fixed points of the heuristic function. In this selection scheme, the best or α -individual is mated with individuals randomly chosen from the current population with uniform probability. For the simple genetic algorithm

with α -selection it is further possible to formulate an intrinsic system model which is compatible with the equivalence relation imposed by schemata. The intrinsic system model provides a means to analyze the genetic algorithm's exploitation and exploration of the search space due to the mixing operation caused by crossover and mutation irrespective of the fitness function.

This paper gives an overview of the theoretical results for the simple genetic algorithm with α -selection and its intrinsic system model. It further outlines the connection to the fixed point graph which describes the asymptotic behavior of the simple genetic algorithm. In addition to the theoretical analysis experimental results are presented. The paper is organized as follows. The simple genetic algorithm with α -selection is described as a specific instance of random heuristic search in Sect. 2 based on the notion of the best individual randomly mating with other individuals in the current population. In Sect. 3 the corresponding dynamical system model is derived based on which the intrinsic system model of the simple genetic algorithm with α -selection is formulated in Sect. 4. Simulation results for the simple genetic algorithm with α -selection, uniform crossover and bitwise mu-

tation are presented showing a close agreement between theory and experiment. The fixed point graph of the simple genetic algorithm with α -selection is illustrated in Sect. 5. A brief conclusion and an outline of future research is given in Sect. 6.

2 SIMPLE GENETIC ALGORITHM WITH α -SELECTION

In this section, the simple genetic algorithm with α -selection, uniform crossover and bitwise mutation is described following the notation and definition of the simple genetic algorithm (SGA) in (Vose, 1999b). It is assumed that the genetic algorithm is used for the maximization of a fitness function $f : \Omega \rightarrow \mathbb{R}$ which is defined over the search space $\Omega = \mathbb{Z}_2^\ell = \{0, 1\}^\ell$ consisting of binary ℓ -tuples $(a_0, a_1, \dots, a_{\ell-1})$.

Each binary ℓ -tuple $(a_0, a_1, \dots, a_{\ell-1}) = a_0 a_1 \dots a_{\ell-1}$ will be identified with the integer $a = a_0 \cdot 2^{\ell-1} + a_1 \cdot 2^{\ell-2} + \dots + a_{\ell-1} \cdot 2^0$ leading to the search space $\Omega = \{0, 1, \dots, n-1\}$ with cardinality $|\Omega| = n = 2^\ell$. The fitness values are given by $f(a) = f_a$. Based on the binary number representation the bitwise modulo-2 addition $a \oplus b$, bitwise modulo-2 multiplication $a \otimes b$ and bitwise binary complement \bar{a} are defined. Vice versa, the integer $a \in \Omega$ is viewed as a column vector $(a_0, a_1, \dots, a_{\ell-1})^T$. The all-one ℓ -tuple $\mathbf{1}$ corresponds to the integer $n-1 = 2^\ell - 1$. The indicator function is defined by $[i = j] = 1$ if $i = j$ and 0 if $i \neq j$.

2.1 Algorithm

The *simple genetic algorithm with α -selection* works over populations $P(t)$ defined as multisets of r individual binary ℓ -tuples $a(t) \in \Omega$. For the creation of offspring individuals in each generation t genetic operators like crossover χ_Ω and mutation μ_Ω are applied to parental individuals (see Fig. 1).

2.2 α -Selection

For the α -selection scheme let

$$b(t) = \operatorname{argmax} \{f_i : i \in P(t)\} \quad (1)$$

be the best individual or α -individual in the current population $P(t)$. In the simple genetic algorithm with α -selection the α -individual $b(t)$ is mated with individuals randomly chosen from the current population $P(t)$ with uniform probability r^{-1} .

```

t := 0;
initialize population P(0);
while end of adaptation ≠ true do
    select  $\alpha$ -individual  $b(t)$  as first parent;
    for the creation of  $r$  offspring do
        select second parent  $c(t)$  randomly;
        apply crossover  $\chi_\Omega$  and mutation  $\mu_\Omega$ 
         $a(t+1) := \mu_\Omega(\chi_\Omega(b(t), c(t)))$ ;
    end
    increment  $t := t + 1$ ;
end
    
```

Figure 1: Simple genetic algorithm with α -selection (Neubauer, 2009; Neubauer, 2008a; Neubauer, 2008c; Neubauer, 2008b).

2.3 Mixing

The *crossover* operator $\chi_\Omega : \Omega \times \Omega \rightarrow \Omega$ randomly generates an offspring ℓ -tuple $a = (a_0, a_1, \dots, a_{\ell-1})$ according to $a = \chi_\Omega(b, c)$ with crossover probability χ from two ℓ -tuples $b = (b_0, b_1, \dots, b_{\ell-1})$ and $c = (c_0, c_1, \dots, c_{\ell-1})$. With the crossover mask $m \in \Omega$ the ℓ -tuples

$$a = b \otimes m \oplus \bar{m} \otimes c \quad (2)$$

or

$$a = b \otimes \bar{m} \oplus m \otimes c \quad (3)$$

are generated one of which is chosen as offspring a with equal probability 2^{-1} . For uniform crossover the crossover mask m is randomly chosen from Ω according to the probability distribution vector $\chi = (\chi_0, \chi_1, \dots, \chi_{n-1})^T$ with (Vose, 1999b)

$$\chi_m = \begin{cases} 1 - \chi + \chi \cdot 2^{-\ell}, & m = 0 \\ \chi \cdot 2^{-\ell}, & m > 0 \end{cases} \quad (4)$$

The bitwise *mutation* operator $\mu_\Omega : \Omega \rightarrow \Omega$, which randomly flips each bit of the ℓ -tuple $a = (a_0, a_1, \dots, a_{\ell-1})$ with mutation probability μ , is defined with the help of the mutation mask $m \in \Omega$ according to $\mu_\Omega(a) = a \oplus m$. The mutation mask m is randomly chosen from Ω according to the probability distribution vector $\mu = (\mu_0, \mu_1, \dots, \mu_{n-1})^T$ with (Vose, 1999b)

$$\mu_m = \mu \mathbf{1}^{Tm} \cdot (1 - \mu)^{\ell - \mathbf{1}^{Tm}} \quad (5)$$

A typical value of the mutation probability is $\mu \sim \frac{1}{\ell}$.

3 DYNAMICAL SYSTEM MODEL

In the *dynamical system model* (Vose, 1999b) the dynamics of the simple genetic algorithm is compactly formulated by defining the population vector

$\mathbf{p} = (p_0, p_1, \dots, p_{n-1})^T$. Each component

$$p_i = \frac{1}{r} \sum_{j \in P} [j = i] \quad (6)$$

gives the proportion of the element $i \in \Omega$ in the current population P . The population vector \mathbf{p} is an element of the simplex

$$\Lambda = \left\{ \mathbf{p} \in \mathbb{R}^n : p_i \geq 0 \wedge \sum_{i \in \Omega} p_i = 1 \right\}. \quad (7)$$

For a population of size r the number of possible population vectors is given by $\binom{n+r-1}{r}$. In the limit of infinite populations with $r \rightarrow \infty$ the population vectors are dense in the simplex Λ . For simplicity we will take the simplex Λ as the defining region of the population vector \mathbf{p} which is strictly valid only for large populations with $r \gg 1$ in the sense of an *infinite population model*.

The simple genetic algorithm is now described as an instance of RHS $\tau : \Lambda \rightarrow \Lambda$ according to $\mathbf{p}(t+1) = \tau(\mathbf{p}(t))$ with τ depending on the random selection and genetic operators. As outlined in (Vose, 1999b) τ can be equivalently represented by a suitable heuristic function $\mathcal{G} : \Lambda \rightarrow \Lambda$ which for a given population vector \mathbf{p} yields the probability distribution $\mathcal{G}(\mathbf{p})$. This probability distribution

$$\mathcal{G}(\mathbf{p})_i = \Pr\{\text{individual } i \text{ is sampled from } \Omega\} \quad (8)$$

is used to generate the next population $\mathbf{p}(t+1)$ in generation $t+1$ from the population $\mathbf{p}(t)$ in generation t as illustrated in Fig. 2. The transition probabilities of the RHS τ are given by the formula (Vose, 1999b)

$$\Pr\{\tau(\mathbf{p}) = \mathbf{q}\} = r! \prod_{i \in \Omega} \frac{\mathcal{G}(\mathbf{p})_i^{rq_i}}{(rq_i)!}. \quad (9)$$

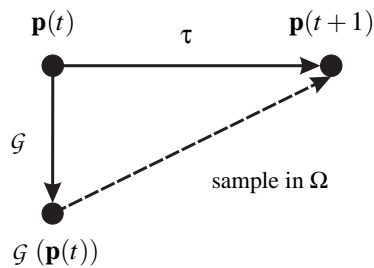


Figure 2: Simple genetic algorithm as RHS τ with heuristic function \mathcal{G} .

The trajectory $\mathbf{p}, \tau(\mathbf{p}), \tau^2(\mathbf{p}), \dots$ approximately follows the trajectory $\mathbf{p}, \mathcal{G}(\mathbf{p}), \mathcal{G}^2(\mathbf{p}), \dots$ of the deterministic dynamical system defined by the heuristic function \mathcal{G} with

$$E\{\tau(\mathbf{p})\} = \mathcal{G}(\mathbf{p}). \quad (10)$$

Because of the corresponding mean quadratic deviation

$$E\{\|\tau(\mathbf{p}) - \mathcal{G}(\mathbf{p})\|^2\} = \frac{1}{r} \cdot (1 - \|\mathcal{G}(\mathbf{p})\|^2) \quad (11)$$

the RHS τ behaves like the deterministic dynamical system model in the limit of infinite populations with $r \rightarrow \infty$. As illustrated by experimental evidence the RHS τ shows punctuated equilibria, i.e. phases of relative stability nearby a fixed point $\omega = \mathcal{G}(\omega)$ of the heuristic function \mathcal{G} disrupted by sudden transitions to another dynamical equilibrium near another fixed point. We call this the *fixed point hypothesis* of genetic algorithms.

3.1 Heuristic

In the simple genetic algorithm with α -selection the α -individual

$$b = \operatorname{argmax}\{f_i : i \in \Omega \wedge p_i > 0\} \quad (12)$$

is selected as the first parent for creation of a new offspring, whereas the second parent is chosen uniformly at random from the current population according to the probability distribution p_j over Ω with $j \in \Omega$. The heuristic function $\mathcal{G}(\mathbf{p})$ follows to

$$\mathcal{G}(\mathbf{p})_i = \sum_{j \in \Omega} p_j \cdot \Pr\{\mu_\Omega(\chi_\Omega(b, j)) = i\}. \quad (13)$$

The probability distributions for crossover χ_Ω and mutation μ_Ω lead to

$$\Pr\{\mu_\Omega(\chi_\Omega(b, j)) = i\} = \sum_{u, v \in \Omega} \mu_v \cdot \frac{\chi_u + \chi_{\bar{u}}}{2} \cdot [b \otimes u \oplus \bar{u} \otimes j = i \oplus v]. \quad (14)$$

By defining the $n \times n$ mixing matrix (Vose, 1999b)

$$M_{i,j} = \sum_{u, v \in \Omega} \mu_v \cdot \frac{\chi_u + \chi_{\bar{u}}}{2} \cdot [i \otimes u \oplus \bar{u} \otimes j = v] \quad (15)$$

this yields $\Pr\{\mu_\Omega(\chi_\Omega(b, j)) = i\} = M_{i \oplus b, i \oplus j}$ and finally

$$\mathcal{G}(\mathbf{p})_i = \sum_{j \in \Omega} p_j \cdot M_{i \oplus b, i \oplus j}. \quad (16)$$

With the permutation matrix $(\sigma_b)_{i,j} = [i \oplus j = b]$ and the twist $(M^*)_{i,j} = M_{i \oplus j, i}$ of the symmetric mixing matrix $M = M^T$ the new population vector is given by

$$\mathbf{q} = \mathcal{G}(\mathbf{p}) = \sigma_b \cdot M^* \cdot \sigma_b \cdot \mathbf{p}. \quad (17)$$

This dynamical system model is illustrated in Fig. 3.

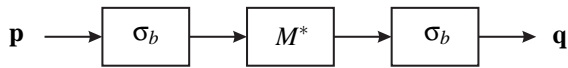


Figure 3: Dynamical system model of the simple genetic algorithm with α -selection (Neubauer, 2008a).

3.2 Mixing Matrix

The calculation of the mixing matrix M can be carried out efficiently with the help of the WALSH transform (Vose and Wright, 1998). For a matrix M the WALSH transform is $\widehat{M} = W \cdot M \cdot W$ with the $n \times n$ WALSH matrix $W_{i,j} = n^{-1/2} \cdot (-1)^{i^T j}$. The WALSH matrix W is symmetric and orthogonal, i.e. $W^{-1} = W^T = W$. The WALSH transform of a vector \mathbf{v} yields $\widehat{\mathbf{v}} = W \cdot \mathbf{v}$. In Fig. 4 the WALSH matrix W is illustrated for $n = 2^6 = 64$.

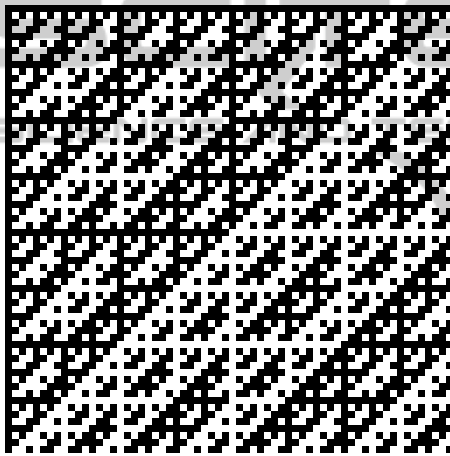


Figure 4: Illustration of the WALSH matrix W for $n = 2^6 = 64$.

For crossover and bitwise mutation the WALSH transform of the mixing matrix M is given by (Vose, 1999b)

$$\widehat{M}_{i,j} = [i \otimes j = 0] \cdot \frac{(1 - 2\mu)^{\mathbf{1}^T(i \oplus j)}}{2} \sum_{k \in \Omega_{\bar{i} \otimes \bar{j}}} (\chi_{k \oplus i} + \chi_{k \oplus j}) \quad (18)$$

with

$$\Omega_k = \{i \in \Omega : i \otimes \bar{k} = 0\} \quad (19)$$

Due to the factor $[i \otimes j = 0]$ the components $\widehat{M}_{i,j}$ are nonzero only if $i \otimes j = 0$ or $j \in \Omega_{\bar{i}}$, respectively. The WALSH transform of the twist of the mixing matrix can be calculated from

$$(M^{*\wedge})_{i,j} = \widehat{M}_{i \oplus j, j} \quad (20)$$

4 INTRINSIC SYSTEM MODEL

The matrix $\sigma_b \cdot M^* \cdot \sigma_b$ of the dynamical system model of the simple genetic algorithm with α -selection in Eq. (17) depends on the mixing matrix M and the α -individual b . Because of $\sigma_b^{-1} = \sigma_b$ this yields the equivalent formulation

$$\sigma_b \mathbf{q} = M^* \cdot \sigma_b \mathbf{p} \quad (21)$$

The permuted population vector $\sigma_b \mathbf{p}$ develops according to the matrix M^* which is independent of the α -individual b . The matrix M^* defines the *intrinsic system model* of the genetic algorithm with α -selection (Neubauer, 2008a).

4.1 Fixed Point

The fixed points of the intrinsic system model are obtained from the eigenvectors of M^* to eigenvalue $\lambda = 1$, i.e.

$$\omega = M^* \cdot \omega \quad (22)$$

The fixed points of the heuristic function \mathcal{G} of the dynamical system model follow from the permutation $\sigma_b \omega$ for a given α -individual b . For the fixed point analysis of the dynamical system model it therefore suffices to analyze the intrinsic system model shown in Fig. 5.

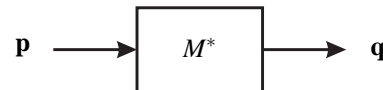


Figure 5: Intrinsic system model of the genetic algorithm with α -selection (Neubauer, 2008a).

To this end, the WALSH transform of both sides of the equation $\mathbf{q} = M^* \cdot \mathbf{p}$ is taken yielding

$$\widehat{\mathbf{q}} = W \cdot \mathbf{q} = W \cdot M^* \cdot W \cdot W \cdot \mathbf{p} = M^{*\wedge} \cdot \widehat{\mathbf{p}} \quad (23)$$

For an eigenvector \mathbf{v} with eigenvalue λ it follows $M^* \cdot \mathbf{v} = \lambda \cdot \mathbf{v}$ and equivalently $M^{*\wedge} \cdot \widehat{\mathbf{v}} = \lambda \cdot \widehat{\mathbf{v}}$, i.e. the matrix M^* and its WALSH transform $M^{*\wedge}$ have the same eigenvalues with eigenvectors which are also related by the WALSH transform.

For crossover and mutation the WALSH transform of the mixing matrix fulfills $\widehat{M}_{i,j} \propto [i \otimes j = 0]$, i.e. \widehat{M} is separative. $M^{*\wedge} = M^{\wedge**}$ is a lower triangular matrix the spectrum of which is given by the first column of \widehat{M} (Vose, 1999b). Since the spectrum of M^* and its WALSH transform $M^{*\wedge}$ are the same this yields the eigenvalues

$$\lambda_i = (M^{*\wedge})_{i,i} = \widehat{M}_{0,i} \quad (24)$$

For crossover and bitwise mutation the eigenvalues are given by

$$\lambda_i = \frac{(1-2\mu)^{1^T i}}{2} \cdot \sum_{k \in \Omega_\tau^T} (\chi_k + \chi_{k \oplus i}) \quad (25)$$

Because of $\lambda_0 = 1$ and

$$0 \leq \lambda_i \leq \frac{1}{2} - \mu < \frac{1}{2} \quad (26)$$

for $1 \leq i \leq n-1$ there exists a single eigenvector ω which is a unique fixed point of the intrinsic system model. For uniform crossover the eigenvalues are obtained from

$$\lambda_i = (1-2\mu)^{1^T i} \cdot \left(\chi \cdot 2^{-1^T i} + \frac{1-\chi}{2} \right) \quad (27)$$

for $1 \leq i \leq n-1$. The fixed points of the heuristic function \mathcal{G} of the simple genetic algorithm with α -selection are obtained from the permutation $\sigma_b \omega$ for a given α -individual b . According to the *fixed point hypothesis* the population will stay near this fixed point $\sigma_b \omega$ and converge to a new fixed point if a better α -individual is found.

The unique fixed point ω of the intrinsic system model can be determined explicitly with the help of the WALSH transform. Due to the relation $\hat{\omega} = M^* \hat{\omega}$ and the lower triangular matrix M^* the WALSH transform of the fixed point can be recursively calculated according to

$$\hat{\omega}_i = \frac{1}{1 - \hat{M}_{0,i}} \cdot \sum_{j=0}^{i-1} \hat{M}_{i \oplus j, j} \cdot \hat{\omega}_j \quad (28)$$

for $1 \leq i \leq n-1$ starting with

$$\hat{\omega}_0 = n^{-1/2} \quad (29)$$

which ensures $\sum_{i \in \Omega} \omega_i = 1$. The unique fixed point ω is then obtained via the inverse WALSH transform $\omega = W \cdot \hat{\omega}$.

The transition in one generation t from population vector $\mathbf{p}(t)$ to population vector $\mathbf{p}(t+1)$ of the random heuristic search τ in Fig. 2 can be detailed for the simple genetic algorithm with α -selection as shown in Fig. 6. Under the assumption of the *fixed point hypothesis* for the intrinsic system model the permuted population vector $\sigma_{b(t)} \mathbf{p}(t)$ will stay near the unique fixed point ω . The population in generation $t+1$ is therefore approximately sampled from the search space Ω according to the probability distribution $\sigma_{b(t)} \omega$ with time-independent fixed point ω and α -individual $b(t)$ as illustrated in Fig. 7.

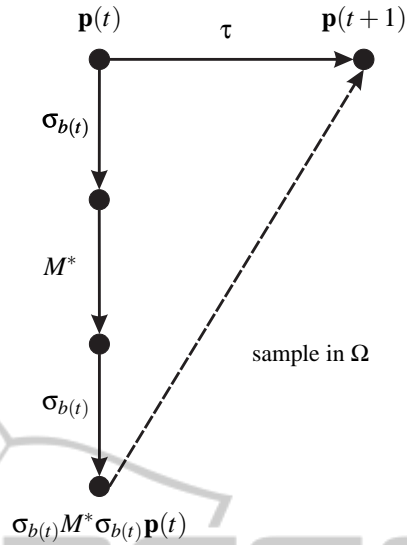


Figure 6: Simple genetic algorithm with α -selection as RHS τ with intrinsic system model M^* .

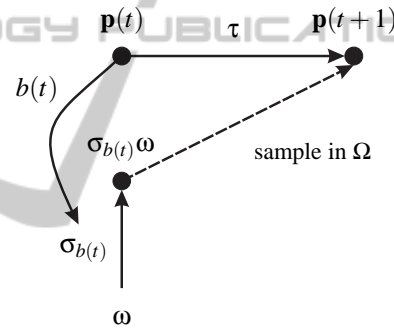


Figure 7: Simple genetic algorithm with α -selection as RHS τ with unique fixed point ω .

4.2 Convergence

The matrix M^* defining the intrinsic system model of the simple genetic algorithm with α -selection has the real eigenvalues $\lambda_0 = 1$ and $0 \leq \lambda_i \leq \frac{1}{2} - \mu < \frac{1}{2}$ for $1 \leq i \leq n-1$. The corresponding JORDAN canonical form of M^* is given by

$$J = S^{-1} M^* S \quad (30)$$

This matrix J consists of simple JORDAN submatrices $J_{v_i}(\lambda_i)$ along the main diagonal and zeros elsewhere, i.e.

$$J = \text{diag}(J_{v_0}(\lambda_0), J_{v_1}(\lambda_1), \dots, J_{v_{\kappa-1}}(\lambda_{\kappa-1})) \quad (31)$$

with the κ distinct eigenvalues λ_i each of algebraic multiplicity v_i . The n columns \mathbf{s}_j of the JORDAN canonical form J form a basis, i.e. the permuted population vector can be formulated as follows

$$\sigma_{b(t)} \mathbf{p}(t) = \sum_{j=0}^{n-1} c_j(t) \cdot \mathbf{s}_j \quad (32)$$

The trajectory of the permuted population vector $\sigma_{b(t)} \mathbf{p}(t)$ can be obtained from the intrinsic system model of the genetic algorithm with α -selection according to

$$\sigma_{b(t)} \mathbf{p}(t) = (M^*)^t \cdot \sigma_{b(0)} \mathbf{p}(0) . \quad (33)$$

Using the expansion of this vector in the basis formed by the columns of the JORDAN canonical form J this leads to (Vose, 1999b)

$$\sigma_{b(t)} \mathbf{p}(t) = \sum_{i=0}^{\kappa-1} \sum_{j=v_i}^{v_{i+1}-1} \mathbf{s}_j \cdot \sum_{k=0}^{\min\{t, j-v_i\}} \binom{t}{k} \cdot \lambda_i^{t-k} \cdot c_{j-k}(0) \quad (34)$$

with

$$v_i = \sum_{j=0}^{i-1} v_j . \quad (35)$$

The convergence of the permuted population vector $\sigma_{b(t)} \mathbf{p}(t)$ to the unique stable fixed point ω of the intrinsic system model of the simple genetic algorithm with α -selection is determined by the eigenvalues λ_i . Because of the single eigenvalue $\lambda_0 = 1$ with algebraic multiplicity $v_0 = 1$ and therefore $v_0 = 0$, $v_1 = 1$ it follows

$$\sigma_{b(t)} \mathbf{p}(t) = \mathbf{s}_0 \cdot c_0(0) + \sum_{i=1}^{\kappa-1} \sum_{j=v_i}^{v_{i+1}-1} \mathbf{s}_j \cdot \sum_{k=0}^{\min\{t, j-v_i\}} \binom{t}{k} \cdot \lambda_i^{t-k} \cdot c_{j-k}(0) \quad (36)$$

for $t \geq 1$. With the remaining eigenvalues λ_i for $1 \leq i \leq n-1$ the convergence properties of the simple genetic algorithm with α -selection can be characterized by introducing the *time constants* τ_i according to

$$\lambda_i^t = e^{-t/\tau_i} \quad (37)$$

leading to

$$\tau_i = -\frac{1}{\ln(\lambda_i)} \leq \frac{2}{1+2\mu} < 2 \quad (38)$$

by taking into account $0 \leq \lambda_i \leq \frac{1}{2} - \mu < \frac{1}{2}$. Due to this upper bound on the time constants τ_i for $1 \leq i \leq n-1$ the permuted population vector $\sigma_{b(t)} \mathbf{p}(t)$ rapidly converges to the unique stable fixed point ω of the intrinsic system model of the simple genetic algorithm with α -selection.

4.3 Experimental Results

In this section, the ONEMAX problem with fitness function

$$f_i = \mathbf{1}^T i \quad (39)$$

is considered, i.e. f_i denotes the number of 1's in the binary representation of $i \in \Omega$. A simple genetic algorithm with α -selection using uniform crossover, bitwise mutation and random initial population is used with the strategy parameters $\ell = 10$, $n = 2^\ell = 1024$, $\chi = 0.75$, $\mu = \ell^{-1}$ and $r = 100$. The unique fixed point ω of the intrinsic system model is shown in Fig. 8.

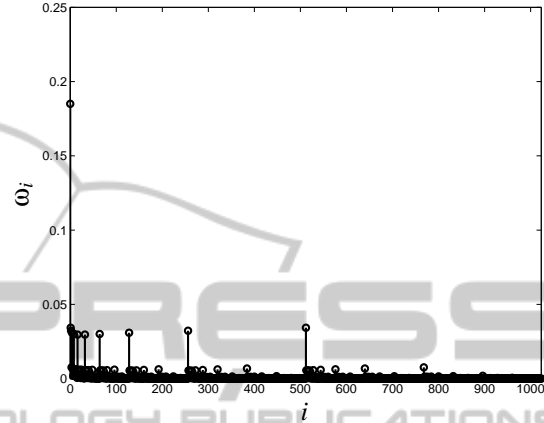


Figure 8: Fixed point of the intrinsic system model of the simple genetic algorithm with α -selection.

The EUCLIDEAN distance of the simulated and permuted population vector $\sigma_{b(t)} \mathbf{p}(t)$ in generation t to the fixed point ω is given by

$$\|\sigma_{b(t)} \mathbf{p}(t) - \omega\| = \sqrt{\sum_{i \in \Omega} \left((\sigma_{b(t)} \mathbf{p}(t))_i - \omega_i \right)^2} . \quad (40)$$

In Fig. 9 this EUCLIDEAN distance is shown for one simulation run. The permuted population vector $\sigma_{b(t)} \mathbf{p}(t)$ rapidly converges to the unique fixed point ω of the intrinsic system model of the simple genetic algorithm with α -selection and stays close to this fixed point.

5 FIXED POINT GRAPH

The stable fixed points of the simple genetic algorithm with α -selection are given by

$$\omega_b = \sigma_b \omega \quad (41)$$

with the unique fixed point ω of the intrinsic system model and $b \in \Omega$. As shown in Sect. 4.3 the trajectory of the simple genetic algorithm with α -selection stays near the fixed points $\sigma_b \omega$ according to the *fixed point hypothesis*.

We will now formulate the connection of the dynamical system model and its fixed points to the fixed

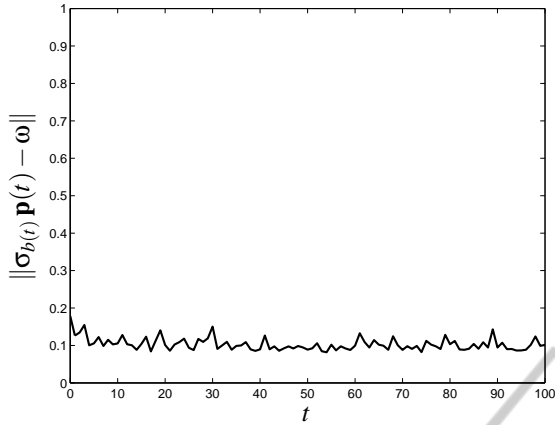


Figure 9: EUCLIDEAN distance $\|\sigma_{b(t)} \mathbf{p}(t) - \omega\|$ over generation t for the simple genetic algorithm with α -selection.

point graph which describes the asymptotic behavior of the simple genetic algorithm (Vose, 1999b). Due to the nature of this paper as a position paper, the following is more speculative than the preceding results. To this end, let \mathcal{F} be the set of fixed points $\omega_b = \sigma_b \omega$ with $b \in \Omega$, i.e.

$$\begin{aligned} \mathcal{F} &= \{\omega_0, \omega_1, \dots, \omega_{n-1}\} \\ &= \{\sigma_0 \omega, \sigma_1 \omega, \dots, \sigma_{n-1} \omega\} . \end{aligned} \quad (42)$$

According to (Vose, 1996; Vose, 1999b) the RHS τ can be modeled by a meta level MARKOV chain \mathcal{C} over the fixed points $\omega_b = \sigma_b \omega$. Let $\rho = \mathbf{p}_0, \mathbf{p}_1, \dots, \mathbf{p}_l$ be a path of length l of population vectors in the simplex Λ . The corresponding *cost* of this path is defined as

$$|\rho| = \sum_{k=1}^l \alpha_{\mathbf{p}_{k-1}, \mathbf{p}_k} \quad (43)$$

with

$$\alpha_{\mathbf{p}, \mathbf{q}} = \sum_{k \in \Omega} q_k \cdot \ln \left(\frac{q_k}{(\mathcal{G}(\mathbf{p}))_k} \right) . \quad (44)$$

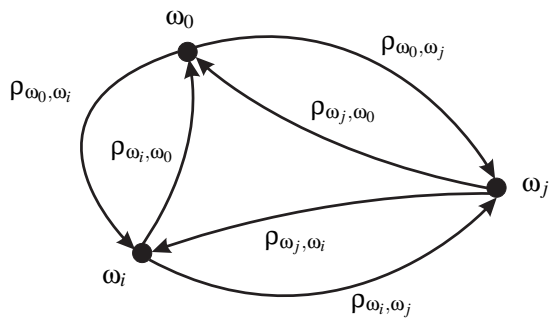


Figure 10: Fixed point graph of the simple genetic algorithm with α -selection as RHS τ .

The *fixed point graph* shown in Fig. 10 is defined as the complete directed graph on the set of stable

fixed points \mathcal{F} with weights

$$\rho_{\omega_i, \omega_j} = \inf \{ |\rho| : \rho \text{ is a path from } \omega_i \text{ to } \omega_j \} . \quad (45)$$

For infinite population size $r \rightarrow \infty$ the steady state distribution of the simple genetic algorithm as RHS τ converges to the steady state distribution of the Markov chain \mathcal{C} over \mathcal{F} . For the determination of this steady state distribution we consider the so-called tributary. The *tributary* T_k is defined as the tree containing every vertex of \mathcal{F} with all its edges pointing towards the root ω_k . The cost of the tributary T_k is given by the sum of its edge weights $\rho_{\omega_i, \omega_j}$. As shown by VOSE in (Vose, 1996; Vose, 1999b) for an infinite population size $r \rightarrow \infty$ the steady state distribution of the simple genetic algorithm is given by the root ω_i of the *minimum cost tributary* T_i (provided it exists).

Due to the simple structure of the dynamical system model of the simple genetic algorithm with α -selection and its stable fixed points $\omega_b = \sigma_b \omega$ future research will focus on the derivation of this steady state distribution for the simple genetic algorithm with α -selection. In view of the rapid convergence of the simple genetic algorithm with α -selection, paths $\rho = \omega_i, \mathbf{p}, \omega_j$ of length $l = 2$ from fixed point $\omega_i = \sigma_i \omega$ to fixed point $\omega_j = \sigma_j \omega$ with interior point $\mathbf{p} \in \Lambda$ are considered. The corresponding cost of this path is given by

$$|\rho| = \alpha_{\omega_i, \mathbf{p}} + \alpha_{\mathbf{p}, \omega_j}$$

or equivalently

$$\begin{aligned} |\rho| &= \sum_{k \in \Omega} p_k \cdot \ln \left(\frac{p_k}{(\mathcal{G}(\omega_i))_k} \right) \\ &+ \sum_{k \in \Omega} (\omega_j)_k \cdot \ln \left(\frac{(\omega_j)_k}{(\mathcal{G}(\mathbf{p}))_k} \right) . \end{aligned} \quad (46)$$

By taking into account

$$\mathcal{G}(\omega_i)_k = (\omega_i)_k = \omega_{i \oplus k} \quad (47)$$

and

$$(\omega_j)_k = \omega_{j \oplus k} \quad (48)$$

if follows

$$|\rho| = \sum_{k \in \Omega} p_k \cdot \ln \left(\frac{p_k}{\omega_{i \oplus k}} \right) + \sum_{k \in \Omega} \omega_{j \oplus k} \cdot \ln \left(\frac{\omega_{j \oplus k}}{(\mathcal{G}(\mathbf{p}))_k} \right) . \quad (49)$$

Under the simplifying assumption of paths $\rho = \omega_i, \mathbf{p}, \omega_j$ of length 2 the weights of the fixed point graph are then approximately given by

$$\begin{aligned} \rho_{\omega_i, \omega_j} &= \inf \left\{ \sum_{k \in \Omega} p_k \cdot \ln \left(\frac{p_k}{\omega_{i \oplus k}} \right) + \right. \\ &\left. \sum_{k \in \Omega} \omega_{j \oplus k} \cdot \ln \left(\frac{\omega_{j \oplus k}}{(\mathcal{G}(\mathbf{p}))_k} \right) : \mathbf{p} \in \Lambda \right\} \end{aligned} \quad (50)$$

with

$$\mathcal{G}(\mathbf{p})_k = \sum_{j \in \Omega} p_j \cdot M_{b \oplus k, j \oplus k} \quad (51)$$

and

$$b = \operatorname{argmax} \{f_i : i \in \Omega \wedge p_i > 0\} . \quad (52)$$

Future research will focus on the analytical derivation of these weights $\rho_{\omega_i, \omega_j}$ and the determination of the minimum cost tributary T_1 leading to the steady state distribution ω_i of the simple genetic algorithm with α -selection.

6 CONCLUSIONS

The intrinsic system model for the simple genetic algorithm with α -selection simplifies the analysis of the dynamical system model of genetic algorithms. It is defined by the mixing matrix M and enables the derivation of the unique fixed point ω . The simplifications are gained because the fitness function f is hidden from the mathematical formulation by making use of the α -individual b . Since b enters the dynamical system model via a permutation σ_b according to $\sigma_b \cdot M^* \cdot \sigma_b$ the intrinsic system model can be formulated with the help of the matrix M^* .

The intrinsic system model provides a means to analyze the genetic algorithm's exploitation and exploration of the search space Ω irrespective of the fitness function f . This model is compatible with the equivalence relation imposed by schemata as shown in (Neubauer, 2008a) by explicitly deriving the coarse-grained system model for a given schemata family. Experimental results for the simple genetic algorithm with α -selection, uniform crossover and bitwise mutation presented in this paper show close agreement to the theoretical predictions with respect to the rapid convergence of the permuted population vector $\sigma_b \mathbf{p}$ to the unique fixed point ω obtained from the intrinsic system model.

It is further conjectured that the structure of the dynamical system model of the simple genetic algorithm with α -selection and its intrinsic system model simplify the determination of the steady state distribution ω_i based on the fixed point graph and the minimum cost tributary T_1 . The analysis of the fixed point graph and the analytical derivation of its weights $\rho_{\omega_i, \omega_j}$ will be the focus of future research.

REFERENCES

Holland, J. H. (1992). *Adaptation in Natural and Artificial Systems – An Introductory Analysis with Applications*

to Biology, Control, and Artificial Intelligence. First MIT Press Edition, Cambridge.

Neubauer, A. (2008a). Intrinsic system model of the genetic algorithm with α -selection. In *Parallel Problem Solving from Nature PPSN X*, Lecture Notes in Computer Science, pages 940–949. Springer.

Neubauer, A. (2008b). Theory of genetic algorithms with α -selection. In *Proceedings of the 1st IAPR Workshop on Cognitive Information Processing – CIP 2008*, pages 137–141.

Neubauer, A. (2008c). Theory of the simple genetic algorithm with α -selection. In *Proceedings of the 10th Annual Genetic and Evolutionary Computation Conference – GECCO 2008*, pages 1009–1016.

Neubauer, A. (2009). Simple genetic algorithm with generalised α^* -selection. In *Proceedings of the International Joint Conference on Computational Intelligence – IJCCI I2009*, pages 204–209.

Reeves, C. R. and Rowe, J. E. (2003). *Genetic Algorithms – Principles and Perspectives, A Guide to GA Theory*. Kluwer Academic Publishers, Boston.

Vose, M. D. (1996). Modeling simple genetic algorithms. *Evolutionary Computation*, 3(4):453–472.

Vose, M. D. (1999a). Random heuristic search. *Theoretical Computer Science*, 229(1-2):103–142.

Vose, M. D. (1999b). *The Simple Genetic Algorithm – Foundations and Theory*. MIT Press, Cambridge.

Vose, M. D. and Wright, A. H. (1998). The simple genetic algorithm and the walsh transform – part i, theory – part ii, the inverse. *Evolutionary Computation*, 6(3):253–273, 275–289.