The Intrinsic System Model of the Simple Genetic Algorithm with \( \alpha \)-Selection, Uniform Crossover and Bitwise Mutation

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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 \( \alpha \)-selection allows the analytical calculation of the unique fixed point of the corresponding intrinsic system model. In this paper, an overview of the theoretical results for the simple genetic algorithm with \( \alpha \)-selection and its intrinsic system model is given. In addition to the theoretical analysis experimental results for the simple genetic algorithm with \( \alpha \)-selection, uniform crossover and bitwise mutation are presented.

Key-Words: Simple genetic algorithm, \( \alpha \)-selection, random heuristic search, dynamical system model, infinite population model, intrinsic system model

1 Introduction

As specific instances of random heuristic search (RHS), genetic algorithms mimic biological evolution and molecular genetics in simplified form. Genetic algorithms (GA) process populations of individuals which evolve according to selection and genetic operators like crossover and mutation. The algorithm’s stochastic dynamics can be described with the help of a dynamical system model introduced by Vose et al. [5, 7, 8]. 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 \( \alpha \)-selection recently introduced in [1, 2, 3, 4] allows to explicitly derive the fixed points of the heuristic function. In this selection scheme, the best or \( \alpha \)-individual is mated with individuals randomly chosen from the current population with uniform probability. For the simple genetic algorithm with \( \alpha \)-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 \( \alpha \)-selection and its intrinsic system model. In addition to the theoretical analysis experimental results are presented. The paper is organized as follows. The simple genetic algorithm with \( \alpha \)-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 \( \alpha \)-selection is formulated in Sect. 4. Simulation results for the simple genetic algorithm with \( \alpha \)-selection, uniform crossover and bitwise mutation are presented in Sect. 5 showing a close agreement between theory and experiment. A brief conclusion is given in Sect. 6.

2 Simple Genetic Algorithm with \( \alpha \)-Selection

In this section the simple genetic algorithm with \( \alpha \)-selection, uniform crossover and bitwise mutation is described following the notation and definition of the
simple genetic algorithm (SGA) in [7]. 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 \( \ell \)-tuples \((a_0, a_1, \ldots, a_{\ell-1})\).

Each binary \( \ell \)-tuple \((a_0, a_1, \ldots, a_{\ell-1})\) will be identified with the integer \( a = a_0 \cdot 2^{\ell-1} + a_1 \cdot 2^{\ell-2} + \ldots + a_{\ell-1} \cdot 2^0 \) leading to the search space \( \Omega = \{0, 1, \ldots, n-1\} \) 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 \( \overline{a} \) are defined. Vice versa, the integer \( a \in \Omega \) is viewed as a column vector \((a_0, a_1, \ldots, a_{\ell-1})^T\). The all-one \( \ell \)-tuple \( 1 \) 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 \( \alpha \)-selection** works over populations \( P(t) \) defined as multisets of \( r \) individual binary \( \ell \)-tuples \( a(t) \in \Omega \). For the creation of offspring individuals in each generation \( t \) genetic operators like crossover \( \chi_\Omega \) and mutation \( \mu_\Omega \) are applied to parental individuals (see Fig. 1).

\[
t := 0; \\
while \ end \ of \ adaptation \neq true \ do \\
\quad select \ \alpha \text{-individual } b(t) \ as \ first \ parent; \\
\quad for \ the \ creation \ of \ r \ offspring \ do \\
\quad \quad select \ second \ parent \ c(t) \ randomly; \\
\quad \quad apply \ crossover \ \chi_\Omega \ and \ mutation \ \mu_\Omega \\
\quad \quad a(t+1) := \mu_\Omega (\chi_\Omega (b(t), c(t))); \\
\quad end \\
increment \ t := t + 1; \\
end
\]

**Figure 1:** Simple genetic algorithm with \( \alpha \)-selection [1, 2, 3, 4].

### 2.2 \( \alpha \)-Selection

For the \( \alpha \)-selection scheme let

\[
b(t) = \arg\max \{ f(i) : i \in P(t) \} \tag{1}
\]

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

### 2.3 Mixing

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

\[
a = b \oplus m \oplus \overline{m} \oplus c \tag{2}
\]

or

\[
a = b \oplus \overline{m} \oplus m \oplus c \tag{3}
\]

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 \( \Omega \) according to the probability distribution vector \( \chi = (\chi_0, \chi_1, \ldots, \chi_n)^T \) with [7]

\[
\chi_m = \begin{cases} 
1 - \chi + \chi \cdot 2^{-\ell}, & m = 0 \\
\chi \cdot 2^{-\ell}, & m > 0
\end{cases} . \tag{4}
\]

The bitwise mutation operator \( \mu_\Omega : \Omega \rightarrow \Omega \), which randomly flips each bit of the \( \ell \)-tuple \( a = (a_0, a_1, \ldots, a_{\ell-1}) \) with mutation probability \( \mu \), 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 \( \Omega \) according to the probability distribution vector \( \mu = (\mu_0, \mu_1, \ldots, \mu_{n-1})^T \) with [7]

\[
\mu_m = \mu_1^T m \cdot (1 - \mu)^{\ell-1} \mu_1^T m . \tag{5}
\]

A typical value of the mutation probability is \( \mu \sim \frac{1}{7} \).

### 3 Dynamical System Model

In the **dynamical system model** [7] the dynamics of the simple genetic algorithm is compactly formulated by defining the population vector \( p = (p_0, p_1, \ldots, p_{n-1})^T \). Each component

\[
p_i = \frac{1}{r} \sum_{j \in P} [j = i] \tag{6}
\]

gives the proportion of the element \( i \in \Omega \) in the current population \( P \). The population vector \( p \) is an element of the simplex

\[
\Lambda = \left\{ p \in \mathbb{R}^n : p_i \geq 0 \land \sum_{i \in \Omega} p_i = 1 \right\} . \tag{7}
\]

For a population of size \( r \) the number of possible population vectors is given by \( \binom{r+n-1}{n} \). In the limit of infinite populations with \( r \rightarrow \infty \) the population vectors are dense in the simplex \( \Lambda \). For simplicity we will
take the simplex $\Lambda$ as the defining region of the population vector $p$ 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 $\tau : \Lambda \to \Lambda$ according to $p(t+1) = \tau (p(t))$ with $\tau$ depending on the random selection and genetic operators. As outlined in [7] $\tau$ can be equivalently represented by a suitable heuristic function $\mathcal{G} : \Lambda \to \Lambda$ which for a given population vector $p$ yields the probability distribution $\mathcal{G} (p)$. This probability distribution

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

is used to generate the next population as illustrated in Fig. 2. The transition probabilities of the RHS $\tau$ are given by the formula [7]

$$\Pr\{\tau (p) = q\} = r! \prod_{i \in \Omega} \frac{\mathcal{G}(p)_{ri}}{(rqi)!}.$$  

![Figure 2: Simple genetic algorithm as RHS $\tau$ with heuristic function $\mathcal{G}$ [7].](image)

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

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

Because of the corresponding mean quadratic deviation

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

the RHS $\tau$ behaves like the deterministic dynamical system model in the limit of infinite populations with $r \to \infty$. As illustrated by experimental evidence the RHS $\tau$ 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 $\alpha$-selection the $\alpha$-individual

$$b = \arg\max \{ f_i : i \in \Omega \wedge p_i > 0 \}$$  

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 $\Omega$ with $j \in \Omega$. The heuristic function $\mathcal{G}(p)$ follows to

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

The probability distributions for crossover $\chi$ and mutation $\mu_\Omega$ lead to

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

By defining the $n \times n$ mixing matrix [7]

$$M_{i,j} = \sum_{u,v \in \Omega} \mu_v \cdot \frac{\chi_u + \chi_v}{2} \cdot [i \otimes u \oplus \overline{u} \otimes j = v]$$

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

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

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

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

This dynamical system model is illustrated in Fig. 3.

![Figure 3: Dynamical system model of the simple genetic algorithm with $\alpha$-selection [2].](image)

### 3.2 Mixing Matrix

The calculation of the mixing matrix $M$ can be carried out efficiently with the help of the WALSH transform [6]. For a matrix $M$ the WALSH transform is $\hat{M} = W \cdot M \cdot W$ with the $n \times n$ WALSH matrix $W_{i,j} = n^{-1/2} \cdot (-1)^{i+j}$. The WALSH matrix $W$ is symmetric and orthogonal, i.e. $W^{-1} = W^T = W$. The WALSH
4 Intrinsic System Model

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

$$\sigma_b \mathbf{q} = M^* \cdot \sigma_b \mathbf{p} .$$

The permuted population vector $\sigma_b \mathbf{p}$ develops according to the matrix $M^*$ which is independent of the $\alpha$-individual $b$. The matrix $M^*$ defines the intrinsic system model of the genetic algorithm with $\alpha$-selection [2]. The fixed points of the intrinsic system model are obtained from the eigenvectors of $M^*$ to eigenvalue $\lambda = 1$, i.e.

$$\omega = M^* \cdot \omega .$$

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

$$\mathbf{p} \rightarrow M^* \rightarrow \mathbf{q}$$

Figure 5: Intrinsic system model of the genetic algorithm with $\alpha$-selection [2].

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

$$\hat{\mathbf{q}} = W \cdot \mathbf{q} = W \cdot M^* \cdot W \cdot \mathbf{p} = M^{*\hat{\chi}} \cdot \hat{\mathbf{p}} .$$

For an eigenvector $\mathbf{v}$ with eigenvalue $\lambda$ it follows $M^* \cdot \mathbf{v} = \lambda \cdot \mathbf{v}$ and equivalently $M^{*\hat{\chi}} \cdot \hat{\mathbf{v}} = \lambda \cdot \hat{\mathbf{v}}$, i.e. the matrix $M^*$ and its WALSH transform $M^{*\hat{\chi}}$ 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 $\hat{M}_{i,j} \propto [i \otimes j = 0]$, i.e. $\hat{M}$ is separative. $M^{*\hat{\chi}} = M^{\hat{\chi}**}$ is a lower triangular matrix the spectrum of which is given by the first column of $\hat{M}$ [7]. Since the spectrum of $M^*$ and its WALSH transform $M^{*\hat{\chi}}$ are the same this yields the eigenvalues

$$\lambda_i = (M^{*\hat{\chi}})_{i,i} = \hat{M}_{0,i} .$$

For crossover and bitwise mutation the eigenvalues are given by

$$\lambda_i = (1 - 2\mu)^{1^{T_i}} \cdot \sum_{k \in \Omega_b} (\chi_k + \chi_{k\oplus i}) .$$

Because of $\lambda_0 = 1$ and $0 \leq \lambda_i \leq \frac{1}{2} - \mu < \frac{1}{2}$ for $1 \leq i \leq n - 1$ there exists a single eigenvector $\omega$ which is a unique fixed point of the intrinsic system model. For uniform crossover the eigenvalues are obtained from

$$\lambda_i = (1 - 2\mu)^{1^{T_i}} \left( \chi \cdot 2^{-1^{T_i}} + \frac{1 - \chi}{2} \right)$$

for $1 \leq i \leq n - 1$. The fixed points of the heuristic function $G$ of the simple genetic algorithm with $\alpha$-selection are obtained from the permutation $\sigma_b \omega$ for a
given $\alpha$-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 $\alpha$-individual is found.

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

$$\widehat{\omega}_i = \frac{1}{1 - M_{0,i}} \cdot \sum_{j=0}^{i-1} M_{i,j} \cdot \widehat{\omega}_j$$

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

$$\widehat{\omega}_0 = n^{-1/2}$$

which ensures $\sum_{i=0}^{n} \omega_i = 1$. The unique fixed point $\omega$ is then obtained via the inverse WALSH transform $\omega = W \cdot \widehat{\omega}$.

The transition in one generation $t$ from population vector $p(t)$ to population vector $p(t+1)$ of the random heuristic search $\tau$ in Fig. 6 can be detailed for the simple genetic algorithm with $\alpha$-selection as shown in Fig. 7. Under the assumption of the fixed point hypothesis for the intrinsic system model the permuted population vector $\sigma_{b(t)}p(t)$ will stay near the unique fixed point $\omega$. The population in generation $t+1$ is therefore approximately sampled from the search space $\Omega$ according to the probability distribution $\sigma_{b(t)}\omega$ with time-independent fixed point $\omega$ and $\alpha$-individual $b(t)$ as illustrated in Fig. 8.

### 5 Experimental Results

In this section the ONEMAX problem with fitness function $f_i = 1^T i$ 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 $\alpha$-selection using uniform crossover, bitwise mutation and random initial population is used with the strategy parameters $\ell = 10$, $n = 2^\ell = 1024$, $\chi = 1.0$, $\mu = \ell^{-1}$ and $r = 100$. The unique fixed point $\omega$ of the intrinsic system model is shown in Fig. 9.

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

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

In Fig. 10 this EUCLIDEAN distance is shown for one simulation run. The permuted population vector $\sigma_{b(t)}p(t)$ stays close to the unique fixed point $\omega$ of the intrinsic system model of the simple genetic algorithm with $\alpha$-selection.

![Figure 6: Simple genetic algorithm with $\alpha$-selection as RHS $\tau$ with heuristic function $\mathcal{G}$](image)

![Figure 7: Simple genetic algorithm with $\alpha$-selection as RHS $\tau$ with intrinsic system model $M^\ast$.](image)

![Figure 8: Simple genetic algorithm with $\alpha$-selection as RHS $\tau$ with unique fixed point $\omega$.](image)
6 Conclusion

The intrinsic system model for the simple genetic algorithm with $\alpha$-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 $\omega$. The simplifications are gained because the fitness function $f$ is hidden from the mathematical formulation by making use of the $\alpha$-individual $b$. Since $b$ enters the dynamical system model via a permutation $\sigma_b$ 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 $\Omega$ irrespective of the fitness function $f$. This model is compatible with the equivalence relation imposed by schemata as shown in [2] by explicitly deriving the coarse-grained system model for a given schemata family. Experimental results for the simple genetic algorithm with $\alpha$-selection, uniform crossover and bitwise mutation presented in this paper show close agreement to the theoretical predictions obtained from the intrinsic system model.

References:


