Theory of the Simple Genetic Algorithm with α -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 heuristic search algorithms can be theoretically described by an infinite population model 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) with fitness-proportional selection, crossover and bitwise mutation. The recently introduced simple genetic algorithm with α -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 α -selection and its intrinsic system model is given. The unique fixed point of the intrinsic system model is derived and its compatibility with the equivalence relation imposed by schemata is shown. In addition to the theoretical analysis experimental results for the simple genetic algorithm with α -selection, uniform crossover and bitwise mutation are presented showing a close agreement to the theoretical predictions.

Key–Words: Simple genetic algorithm, α -selection, random heuristic search, dynamical system model, infinite population model, intrinsic system model, schemata

1 Introduction

As specific instances of random heuristic search (RHS), genetic algorithms mimic biological evolution and molecular genetics in simplified form [1, 9]. These evolutionary algorithms have been successfully applied in a large variety of applications [2, 7, 8, 10]. 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. [9, 12, 13]. According to this infinite population model 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 even for the simple genetic algorithm with fitness-proportional selection, crossover and bitwise mutation.

The simple genetic algorithm (SGA) with α selection recently introduced in [3, 4, 5, 6] 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. In addition to the theoretical analysis experimental results are presented. The paper is organized as follows. The simple genetic algorithm with α -selection, uniform crossover and bitwise mutation 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. Its unique fixed point is derived analytically and its compatibility to the equivalence relation imposed by schemata is shown in Sect. 5. Simulation results for the simple genetic algorithm with α selection, uniform crossover and bitwise mutation are presented in Sect. 6 showing a close agreement between theory and experiment. A brief conclusion is given in Sect. 7.

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 [12]. It is assumed that the genetic algorithm is used for the maximization of a fitness function $f : \Omega \to \mathbb{R}$ which is defined over the search space $\Omega = \mathbb{Z}_2^{\ell} = \{0, 1\}^{\ell}$ consisting of binary ℓ -tuples $(a_0, a_1, \ldots, a_{\ell-1})$.

Each binary ℓ -tuple $(a_0, a_1, \ldots, a_{\ell-1}) = a_0 a_1 \ldots a_{\ell-1}$ 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 $(a_0, a_1, \ldots, a_{\ell-1})^{\mathrm{T}}$. The all-one ℓ -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 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

$$b(t) = \operatorname{argmax} \left\{ f_i : i \in P(t) \right\}$$
(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} .
$$\begin{split} t &:= 0;\\ \text{initialize population } P(0);\\ \text{while end of adaptation } \neq \text{true do}\\ \text{select } \alpha\text{-individual } b(t) \text{ as first parent;}\\ \text{for the creation of } r \text{ offspring do}\\ \text{select second parent } c(t) \text{ randomly;}\\ \text{apply crossover } \chi_{\Omega} \text{ and mutation } \mu_{\Omega}\\ a(t+1) &:= \mu_{\Omega} \left(\chi_{\Omega} \left(b(t), c(t) \right) \right);\\ \text{end}\\ \text{increment } t &:= t+1;\\ \text{end} \end{split}$$

Figure 1: Simple genetic algorithm with α -selection [3, 4, 5, 6].

2.3 Mixing

The *crossover* operator $\chi_{\Omega} : \Omega \times \Omega \to \Omega$ randomly generates an offspring ℓ -tuple $a = (a_0, a_1, \dots, a_{\ell-1})$ according to

$$a = \chi_{\Omega}(b, c) \tag{2}$$

with crossover probability χ from two ℓ -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 ℓ -tuples

$$a = b \otimes m \oplus \overline{m} \otimes c \tag{3}$$

or

$$a = b \otimes \overline{m} \oplus m \otimes c \tag{4}$$

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 $\boldsymbol{\chi} = (\chi_0, \chi_1, \dots, \chi_{n-1})^{\mathrm{T}}$ with [12]

$$\chi_m = \begin{cases} 1 - \chi + \chi \cdot 2^{-\ell} , & m = 0 \\ \chi \cdot 2^{-\ell} , & m > 0 \end{cases} .$$
(5)

The bitwise *mutation* operator $\mu_{\Omega} : \Omega \to \Omega$, which randomly flips each bit of the ℓ -tuple $a = (a_0, a_1, \ldots, a_{\ell-1})$ with mutation probability μ , is defined with the help of the mutation mask $m \in \Omega$ according to

$$\mu_{\Omega}(a) = a \oplus m \quad . \tag{6}$$

The mutation mask m is randomly chosen from Ω according to the probability distribution vector $\boldsymbol{\mu} = (\mu_0, \mu_1, \dots, \mu_{n-1})^{\mathrm{T}}$ with [12]

$$\mu_m = \mu^{\mathbf{1}^{\mathrm{T}}m} \cdot (1-\mu)^{\ell - \mathbf{1}^{\mathrm{T}}m} .$$
 (7)

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

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3 Dynamical System Model

In the dynamical system model [12] the dynamics of the simple genetic algorithm is compactly formulated by defining the population vector $\boldsymbol{p} = (p_0, p_1, \dots, p_{n-1})^{\mathrm{T}}$. Each component

$$p_i = \frac{1}{r} \sum_{j \in P} [j=i] \tag{8}$$

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

$$\Lambda = \left\{ \boldsymbol{p} \in \mathbb{R}^n : p_i \ge 0 \land \sum_{i \in \Omega} p_i = 1 \right\} \quad . \tag{9}$$

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 $r \to \infty$ 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 p which is strictly valid only for large populations with $r \gg 1$ in the sense of an *infinite population model*.

3.1 Random Heuristic Search

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 τ depending on the random selection and genetic operators. As outlined in [12] τ 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

$$\mathcal{G}(\boldsymbol{p})_i = \Pr\{\text{individual } i \text{ is sampled from } \Omega\}$$
 (10)

is used to generate the next population as illustrated in Fig. 2. The transition probabilities of the RHS τ are given by the formula [12]

$$\Pr\{\tau\left(\boldsymbol{p}\right) = \boldsymbol{q}\} = r! \prod_{i \in \Omega} \frac{\mathcal{G}\left(\boldsymbol{p}\right)_{i}^{rq_{i}}}{(rq_{i})!} \quad . \tag{11}$$

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

$$\mathrm{E}\{\tau\left(\boldsymbol{p}\right)\} = \mathcal{G}\left(\boldsymbol{p}\right) \quad . \tag{12}$$

Because of the corresponding mean quadratic deviation

$$\mathrm{E}\{\left\|\tau\left(\boldsymbol{p}\right) - \mathcal{G}\left(\boldsymbol{p}\right)\right\|^{2}\} = \frac{1}{r} \cdot \left(1 - \left\|\mathcal{G}\left(\boldsymbol{p}\right)\right\|^{2}\right) \quad (13)$$



Figure 2: Simple genetic algorithm as RHS τ with heuristic function \mathcal{G} [12].

the RHS τ behaves like the deterministic dynamical system model in the limit of infinite populations with $r \to \infty$. As illustrated by experimental evidence the RHS τ shows *punctuated equilibria*, i.e. phases of relative stability nearby a fixed point

$$\boldsymbol{\omega} = \mathcal{G}\left(\boldsymbol{\omega}\right) \tag{14}$$

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.

3.2 Heuristic

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

$$b = \operatorname{argmax} \left\{ f_i : i \in \Omega \land p_i > 0 \right\}$$
(15)

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 $\mathcal{G}(p)$ follows to

$$\mathcal{G}(\boldsymbol{p})_{i} = \sum_{j \in \Omega} p_{j} \cdot \Pr\{\mu_{\Omega}\left(\chi_{\Omega}(b, j)\right) = i\} \quad (16)$$

The probability distributions for crossover χ_{Ω} and mutation μ_{Ω} lead to

$$\Pr\{\mu_{\Omega} (\chi_{\Omega}(b, j)) = i\} = \sum_{v \in \Omega} \mu_{v} \cdot \Pr\{\chi_{\Omega}(b, j) = i \oplus v\}$$
$$= \sum_{v \in \Omega} \mu_{v} \sum_{u \in \Omega} \frac{\chi_{u} + \chi_{\overline{u}}}{2} \cdot [b \otimes u \oplus \overline{u} \otimes j = i \oplus v]$$
$$= \sum_{u,v \in \Omega} \mu_{v} \cdot \frac{\chi_{u} + \chi_{\overline{u}}}{2} \cdot [(i \oplus b) \otimes u \oplus \overline{u} \otimes (i \oplus j) = v] .$$
(17)

By defining the $n \times n$ mixing matrix [12]

$$M_{i,j} = \sum_{u,v\in\Omega} \mu_v \cdot \frac{\chi_u + \chi_{\overline{u}}}{2} \cdot [i \otimes u \oplus \overline{u} \otimes j = v]$$
(18)

this yields

$$\Pr\{\mu_{\Omega}\left(\chi_{\Omega}(b,j)\right) = i\} = M_{i \oplus b, i \oplus j} \qquad (19)$$

and finally

$$\mathcal{G}(\boldsymbol{p})_{i} = \sum_{j \in \Omega} p_{j} \cdot M_{i \oplus b, i \oplus j} \quad .$$
 (20)

With the permutation matrix

$$(\sigma_b)_{i,j} = [i \oplus j = b] \tag{21}$$

and the twist

$$(M^*)_{i,j} = M_{i \oplus j,i}$$
 (22)

of the symmetric mixing matrix $M = M^{T}$ the new population vector is given by

$$\boldsymbol{q} = \mathcal{G}\left(\boldsymbol{p}\right) = \sigma_b M^* \sigma_b \cdot \boldsymbol{p} \quad . \tag{23}$$

This dynamical system model is illustrated in Fig. 3.



Figure 3: Dynamical system model of the simple genetic algorithm with α -selection [4].

3.3 Mixing Matrix

The calculation of the mixing matrix M can be carried out efficiently with the help of the WALSH transform [11]. For a matrix M the WALSH transform is $\widehat{M} = W \cdot M \cdot W$ with the $n \times n$ WALSH matrix

$$W_{i,j} = n^{-1/2} \cdot (-1)^{i^T j}$$
 (24)

The WALSH matrix W is symmetric and orthogonal, i.e. $W^{-1} = W^{T} = W$. The WALSH transform of a vector v yields $\hat{v} = W \cdot v$. In Fig. 4 the WALSH matrix W is illustrated for $n = 2^{6} = 64$.

For crossover and bitwise mutation the WALSH transform of the mixing matrix M is given by [12]

$$\widehat{M}_{i,j} = [i \otimes j = 0] \cdot \frac{\sqrt{n}}{2} \cdot \widehat{\mu}_{i \oplus j} \sum_{k \in \Omega_{\overline{i} \otimes \overline{j}}} (\chi_{k \oplus i} + \chi_{k \oplus j}) \quad (25)$$



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

with

$$\Omega_k = \{ i \in \Omega : i \otimes \overline{k} = 0 \} \quad . \tag{26}$$

Due to the factor $[i \otimes j = 0]$ the components $M_{i,j}$ are nonzero only if $i \otimes j = 0$ or $j \in \Omega_{\overline{i}}$, respectively. With the WALSH transform of the mutation mask distribution for bitwise mutation μ_{Ω}

$$\widehat{\mu}_i = n^{-1/2} \cdot (1 - 2\mu)^{\mathbf{1}^{\mathrm{T}}i}$$
 (27)

the WALSH transformed mixing matrix is given by [12]

$$M_{i,j} = [i \otimes j = 0] \cdot \frac{(1 - 2\mu)^{\mathbf{1}^{\mathrm{T}}(i \oplus j)}}{2} \sum_{k \in \Omega_{\overline{i} \otimes \overline{j}}} (\chi_{k \oplus i} + \chi_{k \oplus j}) \quad .$$

$$(28)$$

The WALSH transform of the twist of the mixing matrix can be calculated from

$$\left(M^{*\wedge}\right)_{i,j} = \widehat{M}_{i\oplus j,j} \quad . \tag{29}$$

4 Intrinsic System Model

The matrix $\sigma_b M^* \sigma_b$ of the dynamical system model of the simple genetic algorithm with α -selection in Eq. (23) depends on the mixing matrix M and the α individual b. Because of $\sigma_b^{-1} = \sigma_b$ this yields the equivalent formulation

$$\sigma_b \, \boldsymbol{q} = M^* \cdot \sigma_b \, \boldsymbol{p} \quad . \tag{30}$$

The permuted population vector $\sigma_b p$ develops according to the matrix M^* which is independent of the

 α -individual b, i.e. the diagram in Fig. 5 commutes for a given α -individual b [4]. The matrix M^* defines the *intrinsic system model* of the genetic algorithm with α -selection as shown in Fig. 6 and Fig. 7 [4]. Because of $\sigma_0 = I$ with identity matrix I the intrinsic system model $\boldsymbol{q} = M^* \cdot \boldsymbol{p}$ of the simple genetic algorithm with α -selection corresponds to the underlying dynamical system model $\boldsymbol{q} = \mathcal{G}(\boldsymbol{p}) = \sigma_b M^* \sigma_b \cdot \boldsymbol{p}$ for the best or α -individual b = 0.



Figure 5: Commutativity diagram for the dynamical system model of the simple genetic algorithm with α -selection with heuristic function \mathcal{G} , twist of the mixing matrix M^* and permutation σ_b .



Figure 6: Dynamical system model of the simple genetic algorithm with α -selection and the intrinsic system model.

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

$$\boldsymbol{\omega} = M^* \cdot \boldsymbol{\omega} \quad . \tag{31}$$

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. 7.

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

$$\widehat{\boldsymbol{q}} = W \cdot \boldsymbol{q} = W \cdot M^* \cdot W \cdot W \cdot \boldsymbol{p} = M^{*\wedge} \cdot \widehat{\boldsymbol{p}} \quad . \tag{32}$$

For an eigenvector \boldsymbol{v} with eigenvalue λ it follows $M^* \cdot \boldsymbol{v} = \lambda \cdot \boldsymbol{v}$ and equivalently $M^{*\wedge} \cdot \hat{\boldsymbol{v}} = \lambda \cdot \hat{\boldsymbol{v}}$, i.e.



Figure 7: Intrinsic system model of the genetic algorithm with α -selection [4].

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} [12]. Since the spectrum of M^* and its WALSH transform $M^{*\wedge}$ are the same this yields the eigenvalues

$$\lambda_i = \left(M^{*\wedge}\right)_{i,i} = \widehat{M}_{0,i} \quad . \tag{33}$$

For crossover and bitwise mutation the eigenvalues are given by

$$\lambda_i = \frac{(1-2\mu)^{\mathbf{1}^{\mathrm{T}}i}}{2} \cdot \sum_{k \in \Omega_{\overline{i}}} (\chi_k + \chi_{k \oplus i}) \quad . \tag{34}$$

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

$$\lambda_{i} = (1 - 2\mu)^{\mathbf{1}^{\mathrm{T}}i} \cdot \left(\chi \cdot 2^{-\mathbf{1}^{\mathrm{T}}i} + \frac{1 - \chi}{2}\right) \quad (35)$$

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 *b* 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 $\hat{\omega} = M^{*\wedge} \cdot \hat{\omega}$ and the lower triangular matrix $M^{*\wedge}$ the WALSH transform of the fixed point can be recursively calculated according to

$$\widehat{\omega}_{i} = \frac{1}{1 - \widehat{M}_{0,i}} \cdot \sum_{j=0}^{i-1} \widehat{M}_{i \oplus j,j} \cdot \widehat{\omega}_{j}$$
(36)

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

$$\widehat{\omega}_0 = n^{-1/2} \tag{37}$$

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

$$\boldsymbol{\omega} = \boldsymbol{W} \cdot \widehat{\boldsymbol{\omega}} \quad . \tag{38}$$



Figure 8: Simple genetic algorithm with α -selection as RHS τ with heuristic function \mathcal{G} .



Figure 9: Simple genetic algorithm with α -selection as RHS τ with intrinsic system model M^* .

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. 8 can be detailed for the simple genetic algorithm with α -selection as shown in Fig. 9. 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 $\boldsymbol{\omega}$. The population in generation t + 1 is therefore approximately sampled from the search space Ω according to the probability distribution $\sigma_{b(t)}\boldsymbol{\omega}$ with time-independent fixed point $\boldsymbol{\omega}$ and α -individual b(t) as illustrated in Fig. 10.



Figure 10: Simple genetic algorithm with α -selection as RHS τ with unique fixed point ω .

5 Schemata

In this section coarse-grained system models based on schemata will be explored as equivalence relations [12]. Two equivalent individuals $i \equiv j$ in the search space Ω belong to the same equivalence class $[i] = \{j \in \Omega : j \equiv i\} \in \Omega/\equiv$. This can be expressed with the help of the *quotient map*

$$\Xi_{[i],j} = [i \equiv j] \quad , \tag{39}$$

i.e. $i \equiv j$ if $\Xi_{[i],j} = 1$. Two populations are equivalent if the proportions of individuals in each of the equivalence classes [i] with $i \in \Omega$ are the same in both populations. By using the population vectors p and qin the simplex Λ this corresponds to

$$\boldsymbol{p} \equiv \boldsymbol{q} \quad \Leftrightarrow \\ \forall i \in \Omega : \sum_{j \in \Omega} [i \equiv j] \cdot p_j = \sum_{j \in \Omega} [i \equiv j] \cdot q_j \quad .$$

$$(40)$$

Taking into account $\Xi_{[i],j} = [i \equiv j]$ leads to

$$p \equiv q \quad \Leftrightarrow \quad \Xi p = \Xi q \quad . \tag{41}$$

According to [12] *schemata* can be considered as specific equivalence relations. A *schemata family* is defined with the help of the ℓ -tuple $\xi \in \Omega$ via

$$\Xi_{[i],j} = [j \otimes \xi = i] \tag{42}$$

leading to the $2^{\mathbf{1}^{\mathrm{T}}\xi} \times 2^{\ell}$ matrix Ξ . Here, $i \in \Omega_{\xi} = \{i \in \Omega : i \otimes \overline{\xi} = 0\}$ and $j \in \Omega$. Two individuals $j, k \in \Omega$ are equivalent if they agree on the defining positions according to $j \equiv k \Leftrightarrow j \otimes \xi = k \otimes \xi$. The number of the defining positions is $\mathbf{1}^{\mathrm{T}}\xi$ which yields the cardinality $|\Omega_{\xi}| = 2^{\mathbf{1}^{\mathrm{T}}\xi}$. With $i \in \Omega_{\xi}$ a schema is defined as the equivalence class

$$[i] = i \oplus \Omega_{\overline{\epsilon}} \quad . \tag{43}$$

5.1 Schema Heuristic

Based on the intrinsic system model of the genetic algorithm with α -selection

$$q_i = \sum_{j \in \Omega} p_j \cdot M_{i,i \oplus j} \tag{44}$$

a coarse-grained system model will now be derived. The proportion of the expected next population representing schema $[i] = i \oplus \Omega_{\overline{\xi}}$ with $i \in \Omega_{\xi}$ can be calculated according to

$$\widetilde{q}_{[i]} = (\Xi \boldsymbol{q})_{[i]}$$

$$= \sum_{j \in \Omega} [j \otimes \xi = i] \cdot q_j$$

$$= \sum_{j \in \Omega_{\overline{\xi}}} q_{i \oplus j}$$

$$= \sum_{j \in \Omega_{\overline{\xi}}} \sum_{k \in \Omega} p_k \cdot M_{i \oplus j, i \oplus j \oplus k} \quad .$$
(45)

This yields

$$\widetilde{q}_{[i]} = \sum_{j \in \Omega_{\xi}} \widetilde{p}_{[j]} \cdot (M_{\xi})_{[i], [i \oplus j]}$$
(46)

with $\widetilde{\boldsymbol{p}} = \Xi \boldsymbol{p}$ and the symmetric $2^{\mathbf{1}^{\mathrm{T}}\xi} \times 2^{\mathbf{1}^{\mathrm{T}}\xi}$ schema mixing matrix [12]

$$(M_{\xi})_{[i],[j]} = \sum_{u,v\in\Omega_{\xi}} (\Xi\mu)_{[v]} \cdot \frac{(\Xi\chi)_{[u]} + (\Xi\chi)_{[\overline{u}]}}{2} \cdot [i \otimes u \oplus \overline{u} \otimes j = v]$$
$$= \sum_{u,v\in\Omega_{\xi}} \widetilde{\mu}_{[v]} \cdot \frac{\widetilde{\chi}_{[u]} + \widetilde{\chi}_{[\overline{u}]}}{2} \cdot [i \otimes u \oplus \overline{u} \otimes j = v]$$
(47)

with $\tilde{\chi} = \Xi \chi$ and $\tilde{\mu} = \Xi \mu$. The coarse-grained system model based on schemata for the intrinsic system model of a genetic algorithm with α -selection is therefore given by

$$\widetilde{\boldsymbol{q}} = M_{\boldsymbol{\xi}}^* \cdot \widetilde{\boldsymbol{p}} \quad . \tag{48}$$

The intrinsic system model is compatible with the equivalence relation defined by the schemata family ξ because the diagram in Fig. 11 commutes. This conforms to the observation that the mixing operation of the simple genetic algorithm with crossover and mutation is compatible with this equivalence relation – a property which has been argued as the reason for *implicit parallelism* of genetic algorithms [12, 14].



Figure 11: Commutativity diagram for intrinsic system model M^* with quotient map Ξ .

5.2 Schema Mixing Matrix

The twist of the schema mixing matrix M_{ξ} can be expressed with the help of the twist of the mixing matrix M and the quotient map Ξ according to

$$M_{\xi}^{*} = \frac{2^{\mathbf{1}^{\mathrm{T}}\xi}}{n} \cdot \Xi \cdot M^{*} \cdot \Xi^{\mathrm{T}} \quad . \tag{49}$$

With the $2^{\mathbf{1}^{\mathrm{T}}\xi} \times 2^{\mathbf{1}^{\mathrm{T}}\xi}$ WALSH matrix W_{ξ} over Ω_{ξ} and $i, j \in \Omega_{\xi}$ the WALSH transform $M_{\xi}^{*\wedge} = W_{\xi} \cdot M_{\xi}^* \cdot W_{\xi}$ follows to

$$(M_{\xi}^{*\wedge})_{[i],[j]} = (\widehat{M}_{\xi})_{[i\oplus j],[j]}$$
 (50)

 $M_{\xi}^{*\wedge}$ is obtained from $M^{*\wedge}$ by choosing rows and columns with indices in Ω_{ξ} , i.e.

$$(M_{\xi}^{*\wedge})_{[i],[j]} = (M^{*\wedge})_{i,j} \quad .$$
 (51)

5.3 Schema Fixed Point

The matrix M_{ξ}^* and its WALSH transform $M_{\xi}^{*\wedge}$ have the same eigenvalues. Because of (51) for a lower triangular matrix $M^{*\wedge}$ the matrix $M_{\xi}^{*\wedge}$ is also lower triangular. The corresponding eigenvalues are obtained from

$$\lambda_{[i]} = (M_{\xi}^{*\wedge})_{[i],[i]} = (M^{*\wedge})_{i,i} = \lambda_i$$
 (52)

with $i \in \Omega_{\xi}$, i.e. the eigenvalues $\lambda_{[i]}$ correspond to the eigenvalues λ_i . There exists a single eigenvalue $\lambda_{[0]} = 1$ which leads to the unique *schema fixed point*

$$\widetilde{\boldsymbol{\omega}} = M_{\boldsymbol{\xi}}^* \cdot \widetilde{\boldsymbol{\omega}} \quad . \tag{53}$$

The unique schema fixed point $\tilde{\omega}$ can be determined explicitly with the help of the WALSH transform by taking into account that $M_{\xi}^{*\wedge}$ is a lower triangular matrix. By making use of the relation $\hat{\widetilde{\omega}} = M_{\xi}^{*\wedge} \cdot \hat{\widetilde{\omega}}$ the WALSH transform of the schema fixed point can be recursively calculated according to

$$\boxed{\widehat{\widetilde{\omega}}_{[i]} = \frac{1}{1 - \widehat{M}_{0,i}} \cdot \sum_{j \in \Omega_{\xi} \cap \{0,1,\dots,i-1\}} \widehat{M}_{i \oplus j,j} \cdot \widehat{\widetilde{\omega}}_{[j]}}}$$
(54)

with $i \in \Omega_{\xi}$ starting with

$$\widehat{\widetilde{\omega}}_{[0]} = 2^{-\mathbf{1}^{\mathrm{T}}\xi/2} \tag{55}$$

which ensures $\sum_{i\in\Omega_{\xi}}\widetilde{\omega}_{[i]}=1$. The schema fixed point is then obtained via the inverse WALSH transform

$$\widetilde{\boldsymbol{\omega}} = W_{\boldsymbol{\xi}} \cdot \widetilde{\boldsymbol{\omega}} \quad . \tag{56}$$

6 Experimental Results

In this section the ONEMAX problem with fitness function

$$f_i = \mathbf{1}^{\mathrm{T}} i \tag{57}$$

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 listed in Tab. 1.

Table 1: Strategy parameters for the simple genetic algorithm with α -selection.

ℓ	$n=2^\ell$	χ	μ	r
10	1024	1.0	ℓ^{-1}	100

6.1 Intrinsic System Model

The intrinsic system model of the simple genetic algorithm with α -selection is defined by the twist of the mixing matrix M^* which leads to the unique fixed point ω shown in Fig. 12. The largest fraction of the population according to the largest component ω_i of the fixed point ω occurs at the individual i = 0. This is in line with the observation that the intrinsic system model of the simple genetic algorithm with α -selection corresponds to the underlying dynamical system model for the best or α -individual b = 0.

According to the *fixed point hypothesis* the permuted population vector $\sigma_{b(t)} \mathbf{p}(t)$ will stay near this fixed point $\boldsymbol{\omega}$. The corresponding distance between the permuted population vector $\sigma_{b(t)} \mathbf{p}(t)$ in generation t to the fixed point $\boldsymbol{\omega}$ can be measured by the EUCLIDean distance which is defined by

$$\left\|\sigma_{b(t)} \boldsymbol{p}(t) - \boldsymbol{\omega}\right\| = \sqrt{\sum_{i \in \Omega} \left(\left(\sigma_{b(t)} \boldsymbol{p}(t)\right)_i - \omega_i \right)^2} .$$
(58)

In Fig. 13 the EUCLIDean distance $\|\sigma_{b(t)} \mathbf{p}(t) - \boldsymbol{\omega}\|$ is shown for one simulation run of the simple genetic algorithm with α -selection and strategy parameters as in Tab. 1 for 100 generations. The permuted population



Figure 12: Fixed point ω of the intrinsic system model of the simple genetic algorithm with α -selection.

vector $\sigma_{b(t)} \mathbf{p}(t)$ stays close to the unique fixed point $\boldsymbol{\omega}$ of the intrinsic system model of the simple genetic algorithm with α -selection. There is a close match between the theoretical prediction and the experimental result, thereby confirming the *fixed point hypothesis*.



Figure 13: EUCLIDean distance $\|\sigma_{b(t)} \boldsymbol{p}(t) - \boldsymbol{\omega}\|$ over generation t for the simple genetic algorithm with α -selection.

6.2 Schemata

For numerical calculations the equivalence class or schema $[i] \in \Omega/\equiv$ is identified with $i \in \Omega_{\xi}$. The elements of Ω_{ξ} are numbered in ordinary binary fashion, e.g. for $\ell = 5$ and $\xi = 13$ we identify $\{0\underline{0}000, 0\underline{0}001, 0\underline{0}100, 0\underline{0}101, 0\underline{1}000, 0\underline{1}001, 0\underline{1}100, 0\underline{1}101\}$ with the set $\{000, 001, 010, 011, 100, 101, 110, 111\}$ of binary 3-tuples or index numbers $\{0, 1, 2, 3, 4, 5, 6, 7\}$, respectively.

The schemata family for $\ell = 10$ assumed in the following experiment is defined by the binary ℓ -tuple

 $\xi=0000000\underline{111}$ or $\xi=7,$ respectively. The corresponding $2^3\times 2^3$ schema system matrix M_ξ is given by

the WALSH transform \widehat{M}_{ξ} of which follows to

 $\widehat{M}_{\xi} =$

The WALSH transform of the twist of the schema mixing matrix $M_{\xi}^{*\wedge}$ is a lower triangular matrix

in line with the theoretical predictions.

The unique schema fixed point $\widetilde{\omega}$ of the coarsegrained system model of the simple genetic algorithm with α -selection defined by the ℓ -tuple ξ is shown in Fig. 14. The largest fraction of the population representing schema [i] within the schemata family according to the largest component $\widetilde{\omega}_{[i]}$ of the schema fixed point $\widetilde{\omega}$ occurs at the schema [i] = [0]. This again is in line with the observation that the intrinsic system model of the simple genetic algorithm with α -selection corresponds to the underlying dynamical system model for the best or α -individual b = 0.

The EUCLIDean distance of the simulated and permuted schema population vector $\Xi \sigma_{b(t)} \mathbf{p}(t)$ in generation t to the schema fixed point $\widetilde{\boldsymbol{\omega}}$ is

$$\left\|\Xi \sigma_{b(t)} \boldsymbol{p}(t) - \widetilde{\boldsymbol{\omega}}\right\| = \sqrt{\sum_{i \in \Omega_{\xi}} \left(\left(\Xi \sigma_{b(t)} \boldsymbol{p}(t)\right)_{[i]} - \widetilde{\omega}_{[i]} \right)^2} \quad . \tag{59}$$



Figure 14: Schema fixed point $\tilde{\omega}$ of the intrinsic system model of the simple genetic algorithm with α -selection for schemata family $\xi = 7$.

This EUCLIDean distance $\|\Xi \sigma_{b(t)} p(t) - \widetilde{\omega}\|$ is shown in Fig. 15 for one simulation run. The permuted schema population vector $\Xi \sigma_{b(t)} p(t)$ stays close to the unique schema fixed point $\widetilde{\omega}$ of the coarse-grained system model of the simple genetic algorithm with α -selection according to the *fixed point hypothesis*. There is again a close match between the theoretical prediction and the experimental result.



Figure 15: EUCLIDean distance $\|\Xi \sigma_{b(t)} \boldsymbol{p}(t) - \widetilde{\boldsymbol{\omega}}\|$ over generation *t* for the simple genetic algorithm with α -selection and schemata family $\xi = 7$.

7 Conclusion

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 explicit derivation of the unique fixed point ω . The simplifications are gained because the fitness function 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 the system matrix $\sigma_b M^* \sigma_b$ the intrinsic system model can be formulated with the help of the twist of the mixing matrix M^* . It has to be observed, however, that the permutation σ_b depends on the α -individual b and therefore on the population vector p.

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 which was shown by explicitly deriving the coarse-grained system model for a given schemata family ξ . 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 obtained from the intrinsic system model.

References:

- HOLLAND, J.H.: Adaptation in Natural and Artificial Systems – An Introductory Analysis with Applications to Biology, Control, and Artificial Intelligence. Cambridge: First MIT Press Edition, 1992
- [2] KUMSAWAT, P.; ATTAKITMONGCOL, K.; SRIKAEW, A.: An Optimal Robust Digital Image Watermarking Based on Genetic Algorithms in Multiwavelet Domain. In: WSEAS Transactions on Signal Processing. Iss. 1, Vol. 5, pp. 42-51, 2009
- [3] NEUBAUER, A.: Simple Genetic Algorithm with Generalised α^* -Selection. In: Proceedings of the International Joint Conference on Computational Intelligence – IJCCI 2009. Madeira, Portugal: pp. 204-209, 2009
- [4] NEUBAUER, A.: Intrinsic System Model of the Genetic Algorithm with α-Selection. In: RUDOLPH, G.; JANSEN, T.; LUCAS, S.; POLONI, C.; BEUME, N. (Eds.): Parallel Problem Solving from Nature PPSN X. Berlin: Springer-Verlag, pp. 940-949, 2008

- [5] NEUBAUER, A.: Theory of the Simple Genetic Algorithm with α-Selection. In: Proceedings of the 10th Annual Genetic and Evolutionary Computation Conference – GECCO 2008. Atlanta, USA: pp. 1009-1016, 2008
- [6] NEUBAUER, A.: Theory of Genetic Algorithms with α-Selection. In: Proceedings of the 1st IAPR Workshop on Cognitive Information Processing – CIP 2008. Santorini, Greece: pp. 137-141, 2008
- [7] PAN, C.-H.: An Efficient MIMO Detection Algorithm Employed in Imperfect Noise Estimation. In: WSEAS Transactions on Communications. Iss. 8, Vol. 8, pp. 941-958, 2009
- [8] POPESCU, M.-C.; POPESCU, L.; MAS-TORAKIS, N.: Applications of Genetic Algorithms. In: WSEAS Transactions on Information Science and Applications. Iss. 11, Vol. 6, pp. 1782-1791, 2009
- [9] REEVES, C.R.; ROWE, J.E.: Genetic Algorithms – Principles and Perspectives, A Guide to GA Theory. Boston: Kluwer Academic Publishers, 2003
- [10] REIS, C.; TENREIRO MACHADO, K.A.: Crossing Genetic and Swarm Intelligence Algorithms to Generate Logic Circuits. In: WSEAS Transactions on Computers. Iss. 9, Vol. 8, pp. 1419-1428, 2009
- [11] VOSE, M.D.; WRIGHT, A.H.: The Simple Genetic Algorithm and the Walsh Transform Part I Theory, Part II The Inverse. In: Evolutionary Computation. Vol. 6, No. 3, pp. 253-273, 275-289, 1998
- [12] VOSE, M.D.: The Simple Genetic Algorithm

 Foundations and Theory. Cambridge: MIT Press, 1999
- [13] VOSE, M.D.: Random Heuristic Search. In: Theoretical Computer Science. Vol. 229, No. 1-2, pp. 103-142, 1999
- [14] VOSE, M.D.; WRIGHT, A.H.; ROWE, J.E.: *Implicit Parallelism.* In: Genetic and Evolu- tionary Computation Conference GECCO 2003. Springer Lecture Notes in Computer Science, pp. 1003-1014, 2003