



On Asymptotic Behaviour of a Binary Genetic Algorithm

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Abstract. The simple genetic algorithm (SGA) and its convergence analysis are main subjects of the article. A particular SGA is defined on a finite multi-set of individuals (chromosomes) together with mutation and proportional selection operators, each of which with some prescribed probability. The selection operation acts on the basis of the fitness function defined on individuals. Generation of a new population from given one is realized by iterative actions of those operators. Each iteration is written in the form of a transition operator acting on probability vectors which describe probability distributions of all populations. The transition operator is a power of a Markovian matrix. Thanks to the theory of Markov operators [6,9,10] new conditions for asymptotic stability of the transition operator are formulated.

Keywords: simple genetic algorithms, proportional selection, mutation, population, Markovian matrix, asymptotic stability

1 Introduction

In the last two decades there has been growing interest in universal optimization methods realized by genetic and evolutionary algorithms. That algorithms use only limited knowledge about problems to be solved and are constructed on the basis of some similarity to processes realized in nature. Wide applications of those methods in practical solutions of complex optimal problems cause a need to develop theoretical foundations for them. The question of their convergence properties is one of most important issues [2,3,4,5,7,8].

2 Preliminaries

Genetic (GA) as well evolutionary algorithms (EG) perform multi-directional search by maintaining a population of potential solutions, called individuals, and encourage information formation and exchange between these directions. A population, i.e. a set of individuals, undergoes a simulated evolution with a number of steps. In most general case the evolution is due to an iterative action—with some probability distributions—of a composition of three operators: mutation, crossover and selection ones. If a population is regarded as a point in the space Z of (encoded) potential solutions then the effect of one iteration of this composition is to move that population to another point. In this way the action of GA as well as EA is a discrete (stochastic) dynamical system. In the paper we use the term *population* in two meanings; in the first it is a finite multi-set (a set with elements that can repeat) of individuals, in the second it is a frequency vector components of which are composed of fractions, i.e. the ratio of the number of copies of each element $z_k \in Z$ to the total population size. The action of that composition is a random operation on populations.

In the paper we are concerned with a particular case of the simple genetic algorithm (SGA) in which the mutation follows the fitness proportional selection and the crossover is not present. In the case of a binary genetic algorithm (BGA) the mutation can be characterized by the bitwise mutation rate μ —the probability of the mutation of one bit of a chromosome. In SGA with known fitness function the fitness proportional selection can be treated as a multiplication of each component of the frequency vector by

the quotient of the fitness of the corresponding element to the average fitness of the population. This allows to write the probability distribution for the next population in the form of the product of the diagonal matrix with the population (frequency) vector. Moreover, results of the mutation can also be written as a product of another matrix with the population (probability) vector. Finally the composition of both operations is a matrix (cf. (10)), which leads to the general form of the transition operator (cf. (12)) acting on a new probability vector representing a probability distribution of appearance of all populations of the same size equal to the population size *PopSize*. The matrix appearing there turns to be Markovian and each subsequent application of SGA is the same as the subsequent composition of that matrix with itself (cf. (13)). In the paper thanks to the well-developed theory of Markov operator [1,6,9,10] new conditions for the asymptotic stability of the transition operator are formulated and some conclusions are derived.

3 Frequency and Population Vector

In the case of BGA the set of individuals

$$Z = \{z_0, \dots, z_{s-1}\},$$

are *chromosomes* and they form all binary l -element sequences. For a better description one orders them and the set Z with $s = 2^l$, becomes a list, in which its typical element (chromosome) is of the form $z_j = \{0, 0, 1, 0, \dots, 1, 0, 0\}$.

At first by a *population* we understand any multi-set of r chromosomes from Z , then r is the population size: *PopSize*.

Definition 1. *By a frequency vector of population we understand the vector*

$$p = (p_0, \dots, p_{s-1}), \text{ where } p_k = \frac{a_k}{r}, \quad (1)$$

where a_k is a number of copies of the element z_k .

The set of all possible populations now understood in the second meaning as frequency vectors is

$$A = \{p \in \mathbb{R}^s : p_k \geq 0, p_k = \frac{d}{r}, d \in \mathbb{N}, \sum_{k=0}^{s-1} p_k = 1\}. \quad (2)$$

When GA is realized by an action of the so-called transition operator on given population, new population is generated. Since the transition between two subsequent populations is random and is realized by a probabilistic operator, then if one starts with a frequency vector, a probabilistic vector can be obtained, in which p_i may not be rational any more. Hence for our analysis the closure of the set A , namely

$$\bar{A} = \{x \in \mathbb{R}^s : \bigwedge k, x_k \geq 0, \text{ and } \sum_{k=0}^{s-1} x_k = 1\}, \quad (3)$$

is more suitable.

4 Selection Operator

Optimization problem at hand is characterized by a goal (or cost) function. If we transform it by a standard operation to a nonnegative function we will get the so-called *fitness function* $f : Z \rightarrow \mathbb{R}^+$. If we assume the first genetic operator is the *fitness proportional selection*, then the probability that the element z_k from a given population p will appear in the next population equals

$$\frac{f(z_k)p_k}{\bar{f}(p)}, \quad (4)$$

where $\bar{f}(p)$ is the *average population fitness* denoted by

$$\bar{f}(p) = \sum_{k=0}^{s-1} f(z_k)p_k. \quad (5)$$

Then the transition from the population p into the new one, say q , can be given by

$$q = \frac{1}{\bar{f}(p)} \mathbf{S}p, \quad (6)$$

where the matrix \mathbf{S} of the size s , has on its main diagonal the entries

$$S_{kk} = f(z_k). \quad (7)$$

Matrix \mathbf{S} describes *selection operator* [5,7,8].

5 Mutation Operator

The second genetic operator we consider the *binary uniform mutation* with a parameter μ as the probability of changing bits 0 into 1 or vice versa. If the chromosome z_i differs from z_j at c positions then the probability of mutation of the element z_j into the element z_i is

$$U_{ij} = \mu^c (1 - \mu)^{l-c}. \quad (8)$$

Then we may define a matrix

$$\mathbf{U} = [U_{ij}],$$

with U_{ij} as in (8) and U_{ii} —the probability of the surviving of the element (individual) z_i . In general one requires

1.

$$U_{ij} \geq 0;$$

2.

$$\sum_{i=0}^{s-1} U_{ij} = 1, \text{ for all } j. \quad (9)$$

6 Transition Operator

When we have the specific population p , then it means p is a frequency vector and $p \in \Lambda$. If the mutation and selection (random) operators are applied to it they could lead p out the set Λ . The action of the genetic algorithm at the first and at all subsequent steps is the following: if we have a given population p then we sample with returning r -elements from the set Z , and the probability of sampling the elements z_0, \dots, z_{s-1} is described by the vector $G(p)$, where

$$G(p) = \frac{1}{\bar{f}(p)} \mathbf{U} \mathbf{S} p. \quad (10)$$

This r -element vector is our new population q .

Let us denote by W the set of all possible r -element populations composed of elements selected from the set Z , where elements in the population could be repeated. This set is finite and let its cardinality be M . It can be shown that the number M is given by some combinatoric formula, cf. [12]. Let us order all populations, then we identify the set W with the list $W = \{w^1, \dots, w^M\}$. Typical $w^k, k = 1, 2, \dots, M$ is some population for which we used the notation p in the previous section. That population will be identified with its frequency vector or probabilistic vector. This means that for given population $p = w^k = (w_0^k, \dots, w_{s-1}^k)$, the number w_i^k , for $i \in \{0, \dots, s-1\}$, denotes the probability of sampling from the population w^k the individual z_i . If p is a frequency vector then the number w_i^k the fraction of the individual z_i in the population w^k .

Beginning our implementation of BGA from an arbitrary population $p = w^k$ in the next stage each population w^1, \dots, w^M can appear with the probability, which can be determined from our analysis. In particular, if in the next stage the population has to be q , with the position l on our list W (it means $q = w^l$), then this probability [7,11,12] is equal

$$r! \prod_{j=0}^{s-1} \frac{(\mathcal{G}(p)_j)^{r q_j}}{(r q_j)!}. \quad (11)$$

After two steps, every population w^1, \dots, w^M will appear with some probability, which is a double composition of this formula. It will be analogously in the third step and so on. This formula gives a possibility of determining all elements of a matrix \mathbf{T} which defines the probability distribution of appearance of populations in the next steps, if we have current probability distribution of the populations. With our choice of denotations for the populations p and q , the element (l, k) of the matrix will give transition probability from the population with the number k into the population with the number l . It is important that elements of the matrix are determined once forever, independently of the number of steps. The transition between elements of different pairs of populations is described by different probabilities (11) represented by different elements of the matrix. We can see that the nonnegative, square matrix \mathbf{T} of dimension M , with elements p_{lk} , $l, k = 1, 2, \dots, M$ has the property: the probability distribution of all M populations in the step t is given by the formula

$$\mathbf{T}^t u \quad t = 0, 1, 2, \dots$$

Let us denote by

$$\Gamma = \{x \in \mathbb{R}^M : \forall k x_k \geq 0 \text{ oraz } \|x\| = 1\},$$

where $\|x\| = x_1 + \dots + x_M$, for $x = (x_1, \dots, x_M)$, the set of new M -dimensional probabilistic vectors. A particular component of the vector x represents the probability of the appearance of this population from the list W of all M populations. The set Γ is composed of the all possible probability distributions for M populations. Then described implementation transforms, at every step, the set Γ into the same.

Notice that if at the beginning we start our SGA at a specific population p , which attains the place j -th on our list W , i.e. $p = w^j$, then the vector u will denote the particular situation of the population distribution in the step zero 0 if

$$u = (0, \dots, 0, 1, 0, \dots, 0) \in \mathbb{R}^m.$$

On the set Γ the basic, fundamental *transition operator*,

$$T(\cdot) : \mathbf{I}N \times \Gamma \rightarrow \Gamma. \quad (12)$$

is defined. According to the above remark the transition operator $T(t)$ is linked with the above matrix by the dependence

$$T(t) = \mathbf{T}^t. \quad (13)$$

If $u \in \Gamma$, then $T(t)u = ((T(t)u)_1, \dots, (T(t)u)_M)$ is the probability distribution for M populations in the step number t , if we have begun our implementation of SGA given by \mathcal{G} (10) from the probability distribution $u = (u_1, \dots, u_M) \in \Gamma$, by t -application of this method. The number $(T(t)u)_k$ for $k \in \{1, \dots, M\}$ denotes the probability of appearance of the population w^k in the step of number t . By the definition $\mathcal{G}(p)$ in (10),(11), and the remarks made at the end of the previous section, the transition operator $T(t)$ is linear for all natural t .

Notice that though the formula (11) determining individual entries (components) of the matrix \mathbf{T} is a population dependent, and hence nonlinear, the transition operator $T(t)$ is linear thanks to the order relation introduced in the set W of all M populations. The multi-index l, k of the component p_{lk} kills, in some sense, this nonlinearity, since it tells (is responsible) for a pair of populations between which the transition takes place. The matrix \mathbf{T} is a Markovian matrix. This fact permits us to apply Theory of Markov operators to analyze the convergence of genetic algorithms [1,6,9,10].

Notice that the action of the matrix \mathbf{T} can be seen as follows. In the space of the all possible populations there is a walking point, which attains its next random position numbered by $1, 2, \dots, M$, as an action of SGA on the actual population, with probabilities u_1, u_2, \dots, u_M . We know that if at the moment t (in the generation number t) we had population p with the position k on our list, i.e. the population w^k , then the probability that at the moment $t+1$ (in the generation number $t+1$) it will attain population q with the position l , on our list, i.e. the population w^l , is p_{lk} , and this probability is independent of the number of steps in which it is realized. With this denotation the probability p_{lk} is given by the formula (11).

Let $e_k \in \Gamma$ be a vector which at the k -th position has one and zeroes at the other positions. Then e_k describes the probability distribution in which the population w^k is attained with the probability 1.

By the notation $T(t)w^k$ we will understand

$$T(t)w^k = T(t)e_k \quad (14)$$

which means that we begin the GA at the specific population w^k .

Further on we will assume $U_{jj} > 0$ for $j \in \{0, \dots, s-1\}$. Notice that in the case of binary mutation (8) this condition will be satisfied if $0 \leq \mu < 1$.

Definition 2. We will say that the model is asymptotically stable if there exists $u^* \in \Gamma$ such that:

$$T(t)u^* = u^* \quad \text{for } t = 0, 1, \dots \quad (15)$$

$$\lim_{t \rightarrow \infty} \|T(t)u - u^*\| = 0 \quad \text{for all } u \in \Gamma . \quad (16)$$

Since for $k \in \{1, \dots, M\}$ we have

$$|(T(t)u)_k - u_k^*| \leq \|T(t)u - u^*\| , \quad (17)$$

then (16) will gives

$$\lim_{t \rightarrow \infty} (T(t)u)_k = u_k^* . \quad (18)$$

It means that probability of appearance of the population w^k in the step number t converges to a certain fixed number u_k^* independently of the initial distribution u . It is realized in some special case, when our implementation begun at one specific population $p = w^j$.

We shall say that from the chromosome z_a it is possible to obtain z_b in one mutation step with a positive probability if $U_{ba} > 0$. We shall say that from the chromosome z_a it is possible to get the chromosome z_b with positive probability in n -step mutation if there exists a sequence of chromosomes z_{i_0}, \dots, z_{i_n} , such that $z_{i_0} = z_a$, $z_{i_n} = z_b$ and any z_{i_j} for $j = 1, \dots, n$ is possible to attain from $z_{i_{j-1}}$ in one step with a positive probability.

Definition 3. Model is pointwise asymptotically stable if there exists such a population w^j that

$$\lim_{t \rightarrow \infty} (T(t)u)_j = 1 \quad \text{for } u \in \Gamma . \quad (19)$$

Condition (19) denotes that in successive steps the probability of appearance of another population than w^j tends to zero. It is a special case of the asymptotic stability for which

$$u^* = e_j .$$

Theorem 1. Model is pointwise asymptotically stable if and only if there exists exactly one chromosome z_a with such a property that it is possible to attain it from any chromosome in a finite number of steps with a positive probability. In this situation the population w^j is exclusively composed of the chromosomes z_a and

$$T(t)w^j = w^j \quad (20)$$

holds. Moreover, the probability of appearance of other population than w^j tends to zero in the step number t with a geometrical rate, i.e. there exists $\lambda \in (0, 1)$, $D \in \mathbb{R}_+$ that

$$\sum_{\substack{i=1 \\ i \neq j}}^M (T(t)u)_i \leq D \cdot \lambda^t . \triangle \quad (21)$$

The proofs of our theorems and auxiliary lemmas are stated in original articles [12,13].

Numbers λ and D could be determined for a specific model. It will be the subject of the next articles.

Theorem 1 states that the convergence to one population could occur only under specific assumptions. This justifies the investigation of asymptotic stability that in Definition 2.

Definition 4. By an attainable chromosome we denote $z_a \in Z$ such that it is possible to attain it from any other chromosome in a finite number of steps with a positive probability. Let us denote by Z^* the set of all z_a with this property.

Theorem 2. Model is asymptotically stable if and only if $Z^* \neq \emptyset$. △

Theorem 3. Let us assume that the model is asymptotically stable. Then the next relationship holds:

(war) $u_k^* > 0$ if and only if the population w^k is exclusively composed of chromosomes belonging to the set Z^* . △

7 Conclusions

Here we set the summary of our results obtained here and in our other papers [11,12,13]:

1. If $Z^* = \emptyset$ then there is a lack of asymptotic stability.
2. If $Z^* \neq \emptyset$ then asymptotic stability holds but:
3. If cardinality $(Z^*) = 1$ then pointwise asymptotic stability (in some sense convergence to one population) holds.
4. If cardinality $(Z^*) > 1$ then asymptotic stability holds, but there is no pointwise asymptotic stability.
5. If $Z^* = Z$ then $u_k^* > 0$ for all $k \in \{1, \dots, M\}$.

REMARK. In SGA with a positive mutation probability, it is possible to attain any individual (chromosome) from any other individual. Then there is more than one chromosome which is possible to attain from any other in a finite number of steps with a positive probability. Hence, by Theorem 1, it is impossible to get the population composed exclusively of one type of chromosome.

The last conclusion means that if any chromosome is possible to attain from any other in a finite number of steps with a positive probability then in the limit (probability distribution) of infinite number of generations each population (has a positive probability) may be reached with a positive probability.

Acknowledgement The research work on the paper was partially done by W.K and S.K. in the framework of the KBN Project (State Committee for Scientific Research) No. 3 T11 C007 28. Authors thanks Professor Zbigniew Michalewicz for the inspiration and discussions.

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