

Some Remarks on Dynamics of Binary Chromosomes Population

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Population is the fundamental basis of any evolution (Novak, 2006). This statement is true both in biological and artificial evolutionary systems. Population dynamics studies short and long-term changes of the certain population features, and is a branch of life sciences. Here, we discuss new properties of population of binary chromosomes evolved by genetic algorithm (GA), which is one of the possible implementations of artificial evolutionary systems. In particular, we introduce a theorem (Theorem 3) allowing us to determine the minimal number of simple operations necessary to restore the entire space to explore. The work is partly based on Pliszka and Unold (2011, 2012).

The discipline of GAs (and broadly Evolutionary Computation EC) is still focused more on the empirical aspects of algorithms than theoretical studies. Methods, which are currently in use in theoretical studies of these algorithms, could be classified into one of the following groups: schema theory, Markov chains theory, dimensional analysis, order statistics, quantitative genetics, orthogonal functions analysis, quadratical dynamical systems, and statistical physics. Simplistic assumptions have frequently been adopted in the theoretical analyses and these have deformed the analyzed algorithms in such a way that they question the real connection between the results obtained and the investigated algorithms.

The essential step in GA/EC is to determine the representation of computational population (Hu and Banzhaf, 2010). Another one is to define the method of gene duplication. Most of GAs use linear binary representations, and the most standard one is an array of bits. Due to fixed size of such representations, their parts are easily aligned. This facilitates simple crossover operation.

In our approach binary chromosomes are represented as binary, fixed-length chromosomes, using an alternative to zero-one decoding technique, called Hadamard representation. The search space $\{0, 1\}^n$ was replaced by $\{-1, 1\}^n$. Thanks to use a new binary model the requirement of orthogonal columns pairs is omitted. Subject of this study is the following set:

$$H^n = \{(h_{s,n}, h_{s,n-1}, \dots, h_{s,2}, h_{s,1}) : \\ \forall s \in \{0, 1, \dots, 2^n - 1\} \\ \forall i \in \{1, 2, \dots, n\} \\ h_{s,i} \in \{-1, 1\}\}$$

Its elements represent all possible binary chromosomes of equal length n , where n is a natural number higher than 1. Note that the Hadamard representation is in fact a transformed Hamming space. The proposed representation has one, apparently insignificant property, which distinguishes it from the binary representation: a square of each coordinates is equalled 1. This fact draws two subsequent conclusions: the sum of the squares of coordinate of each element of the H^n space is constant and equals this space dimension, and there is no element with zero coordinates. The collection of these simple facts allows for the formulation of rules for phenotypes (indices) and development of automate methods of moving frame H^n , as well as determination of the distance (level of differentiation) between the elements of this space (Pliszka and Unold, 2011).

The use of Hadamard representation allows us to give theoretical proof for epistatic properties as well as exploration possibilities of a crossover operator. We say that the population is ancestral, if all its elements can be obtained from a primary (initial) population as a result of the assembling only crossing-overs.

Theorem 1. The whole space H^n is the ancestral population if and only if there are the elements in the primary population P , which have the following properties: for each locus, we have two elements from P having different (in terms of dual opposing) values (the proof in Pliszka and Unold (2011)).

As a conclusion of the above Theorem 1 we have convenient

Theorem 2. If a primary population $P \subseteq H^n$ contains the pair of polar chromosomes, then the whole space H^n is an ancestral population, where two points h_t and h_k in H^n are called polar chromosomes if and only if for each coordinate these points have opposite values.

For example, having two polar chromosomes h_0 and h_7

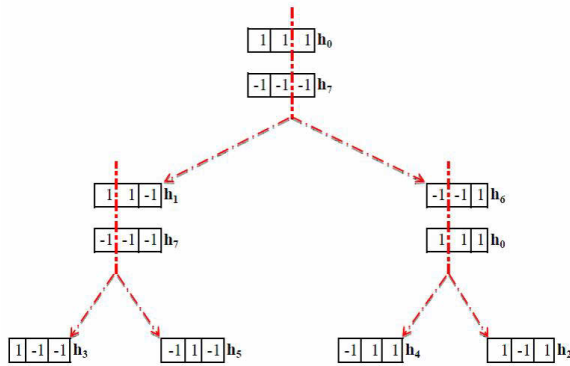


Figure 1: Exemplary ancestral binary population in Hadamard encoding with the primary population h_0 and h_7 .

as a primary population from H^3 we are able after three crossovers obtain all 8 chromosomes from the space in question, according to Theorem 2 (see Figure 1). What is interesting is that more crossover operations are needed when using natural selection and random points of crossing.

Theorem 2 allows us to determine the number of necessary and sufficient one-point crossovers, we need to recover the entire space H^n from the two polar chromosomes.

Theorem 3. Any algorithm established to restore the entire space H^n from two polar chromosomes with a one-point crossover operator needs at least $2^{n-1} - 1$ operations (the proof is omitted).

Moreover, it is possible to construct such an algorithm, which reconstructs the whole binary space exactly in $2^{n-1} - 1$ steps.

Note that introduced representation allow us to distinct and classify different populations, what is more to penetrate into the potential future directions of their evolution regardless of the selected crossover algorithms, selection of parents, or the elimination of individuals. Having Theorem 3 we are able to compare GAs in terms of efficiency and optimization.

References

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