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## *Diploidy-based Genetic Algorithm in Nonstationary Environment*

### Introduction

Modern synthesis of adaptive control systems can hardly exist beyond numerical optimization. Not all of the optimization methods, however, are appropriate to develop real-world applications. If we deal with not a toy-problem but a real dynamic object whose characteristics do not usually meet the requirements of Kuhn-Tucker (continuity, differentiability within variable space, etc.), deterministic methods of local search may fail. Lacking in resources to leave the first found extrimum, a local method gets stuck in it and loses the ability to go on with the search.

It is quite obvious that optimization procedure must ensure a global search. Moreover, it should keep this ability in nonstationary enviroment when characteristics of the dynamic object change.

Taking the above-mentioned into account, we have explored Genetic Algorithms (GA) - a most powerful of known so far tools of global optimization. Among numerical methods available to solve inverse problems, GA are denoted for their vizualization and obviousness. However, GA-based optimization techniques require the researcher's ability to interpret mechanisms of biological evolution with respect to technical objects. What we have tried to do is to study a possibility to implement within the framework of canonical principles of GA the concept of diploidy. Diploidy is a perfect form of storing and reproducing genetic information in higher organism populations. Biologists consider diploidy one of the greatest inventions by Nature. GA-community, however, firmly keeps describing individuals as haploid organisms.

Earlier we tested diploidy-based GA in stationary environment [1]. But diploid populations are known to posses a great adaptive potential which allows them to easily follow environment changes. This biological fact urged us on the try to carry the concept of diploidy into simulation of artificial evolution which we consider as adaptation in nonstationary environment.

### Phenomenon of Diploidy and Genetic Algorithms: Historical Survey

Hollstein pioneered the use of the diploid populations in function optimization [2]. He suggested a representation of the chromosome, in which each binary gene was described by two genes, a modifier gene and a functional one. The functional gene took on the normal 0 or 1 values and was decoded to some parameter. The modifier gene took on values of d or r. The evolution of dominance relations was set with Table 1. According to this scheme, 0 allele is dominant when there is at least one d allele present at one of the homologous modifier loci.

Unfortunately, Hollstein did not see a considerable improvement of the search ability of a diploid population as compared with a haploid one.

Table 1.  
Dominance map from Hollstien

	0d	0r	1d	1r
0d	0	0	0	0
0r	0	0	0	1
1d	0	0	1	1
1r	0	1	1	1

Table 2.  
The suggested map

	0d	0r	1d	1r
0d	0*	0	?*	0
0r	0	0**	1	?**
1d	?*	1	1*	1
1r	0	?**	1	1**

\* - The gene belonging to the less fit individual becomes recessive

\*\* - The gene belonging to the less fit individual becomes dominant

The matter is that Hollstein only researched into stationary functions. Later, Goldberg and Smith demonstrated that, when testing GA by means of a nonstationary function, a diploid population had obvious

superiority over a haploid one [3]. To evolve the dominance relations, they used a single-locus triallelic dominance map which contained the same dominance rules as Hollstein's.

Our research is of a bit different kind. Describing an individual, we separate the modifying genes from the functional genes and combine them in an additional haploid chromosome. Trying to simulate the evolution of dominance relations we have used a concept of epigenetic triggers. According to this theory, the contrasting genes in each locus cannot both be either in the dominant or in the recessive state simultaneously. In case the situation does happen we switch the state of the gene which belongs to the gamete of the less fit parent to the opposite one. Thus, we strengthen the influence of the more successful parent on the offspring. Table 2 shows the final representation of the offspring's dominant alleles which are used to decode the genotype into real-value phenotype.

### Reproductive plan and test function

The iteratively repeated part of our reproductive plan modified for a diploid population comprises the following steps:

- (i) random selection of mates;
- (ii) extraction of a gamete from each parent by means of the crossover operator;
- (iii) inversion of the gamete or gene mutation in the gamete;
- (iv) merger of the gametes into zygote;
- (v) reformation of the dominance relations within zygote according to Table 2;
- (vi) replacement of the least fit individuals by new offspring;
- (vii) ranging of the population.

Figure 1 illustrates the different steps of this process.

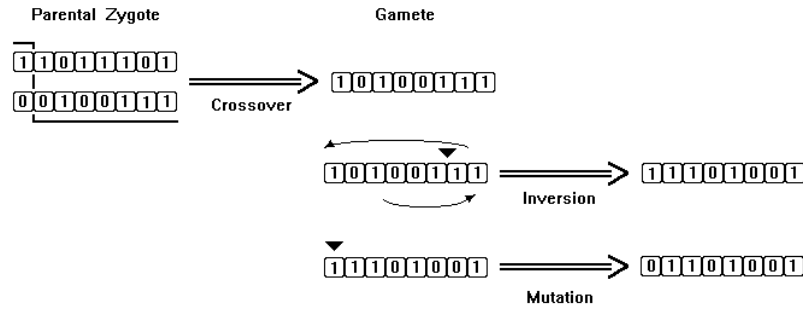


Figure 1. Different genetic operators

To evaluate the ability of the population to track nonstationarities we have taken the well-known objective function and inserted in it a changeable parameter  $\Delta$  which shifts one of the global extremum coordinates in the search space every 100 generations.

$$f(\mathbf{x}) = -(x_1 + \Delta) \sin \sqrt{|x_1 + \Delta|} - \sum_{i=2}^5 x_i \sin \sqrt{|x_i|}, \quad -500 \leq x_i \leq 500$$

$$\Delta = \begin{cases} 0, & \text{if } 200n \leq g < 100(2n+1) \\ 100, & \text{if } 100(2n-1) \leq g < 200n \end{cases} \quad n = 0, 1, 2, 3, 4, \dots$$

Its global minimum is equal to  $f(\bar{x}^o) = -2094.914$ .

### Diploid population versus haploid one: Comparison of test results

The results of the numerical experiments performed over a haploid and a diploid populations of 100 individuals are shown in Figure 2.

As we can see, the diploid population demonstrates the superiority performance. It follows the changes of  $\Delta$  more quickly. Unlike the haploid population which loses genetic diversity, the diploid one saves variability and does not waste time on waiting for necessary genes to appear.

We suppose that describing individuals by means of a double chromosome set permits to utterly solve the problem of losing genetic diversity during long selection. Similar to a haploid population, a diploid one can exhaust in phenotypes but never in genotypes.

Furthermore, the developed algorithm results in the additional parallelism of the search. Every diploid individual would represent a whole subpopulation located at the tops of a hypercube in the search space built on the diagonal which connects the points corresponding to the parent gametes. The top where the individual

actually exists is active, while the others are passive. During the evolution the dominance relations between homologous genes change, thus resulting in switching the active top. We turn out to work not with a population of points but with a population of hypercubes in the search space what helps to explore the space much more precisely.

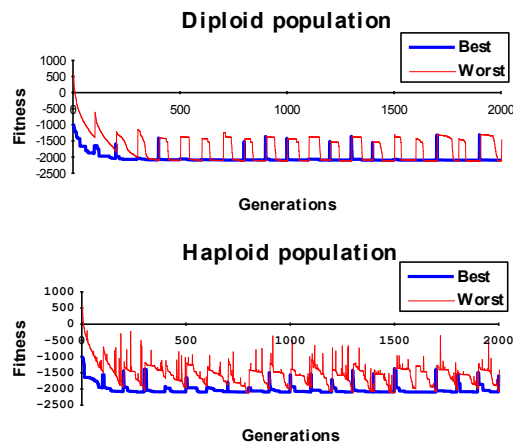


Figure 2. Comparison of the numerical experiment results

### Conclusion

The main problem which makes simulating the evolution of the diploid populations more difficult is the dominance relations between the contrasting genes located in identical loci on homologous chromosomes. The suggested scheme of dominance based on the comparison of the parent fitnesses has proved to be efficient in nonstationary environment as well.

Though describing individuals as diploid organisms makes the algorithm a bit more complicated, this technique allows to decrease the selective pressure on less fit individuals and due to this to increase the search ability of the population in nonstationary environment.

It is difficult to foretell possible trends of further improvement of GA, but in our opinion, advanced technique of individual genotype coding by means of doubled chromosome set can play a noticeable part in future research.

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