Deficiencies of Best-chromosome-wins Dominance in Evolutionary Optimization of Stationary Functions

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ABSTRACT

In evolutionary computation, diploid genotypes (i.e., genotypes with two chromosomes) are traditionally used mostly in the context of optimization of non-stationary problems. Recent research, however, suggested that the use of diploid genotypes with mechanisms such as best-chromosome-wins can improve the performance of evolutionary algorithms even for stationary problems. In this paper we test the effectiveness of diploidy and polyploidy (i.e., genotypes with more than two chromosomes) with best-chromosome-wins on mathematical benchmarks. We verify the effect and the importance of the crossover operator on the behavior of evolutionary algorithms with diploidy and polyploidy. We explore the inner workings of evolutionary algorithms with diploidy and polyploidy in order to better understand their performance. We find that the results reported in previous papers on the best-chromosome-wins dominance for stationary functions may have been overly optimistic, and the use of diploidy with best-chromosome-wins does not enhance the search process for such functions.

CCS CONCEPTS

• **Computing methodologies → Search methodologies**.

KEYWORDS

evolutionary algorithms, diploidy, polyploidy, dominance

1 INTRODUCTION

The use of diploid representations (i.e., genotypes with two chromosomes) in evolutionary algorithms is usually limited to the optimization of non-stationary functions. The reason for this is simple – the nature itself is not stationary, so it only makes sense for something that works well for the optimization of non-stationary problems to be useful for real life, and therefore to be incorporated into the way evolution works in nature. It does not, however, work the other way round – just because a mechanism makes sense in the context of real life evolution does not necessarily need to always enhance evolutionary algorithms, especially in stationary settings.

It doesn't need to – but it just might. Recent papers by Petrovan et al. seem to show promise, as they successfully employ diploid representation in optimization of stationary problems: mathematical benchmarks [8] and the multidimensional two-way number partitioning problem [7]. Paired with the best-chromosome-wins domination mechanism proposed earlier by Shabash and Wiese [9], these results – if confirmed – could shift the currently held haploidy paradigm towards diploidy, or even further – towards polyploidy (i.e., genotypes with more than two chromosomes).

Motivated by this thought, this work evaluates the effect of different levels of ploidy (with the best-chromosome-wins mechanism) under varied probabilities of crossover on the performance of evolutionary algorithms optimizing mathematical benchmarks. We analyze the characteristics of the evolved solutions in order to understand the principles behind the observed performance of different levels of ploidy, and discuss the reasons behind the poor performance of best-chromosome-wins mechanism of dominance.

2 PLOIDY IN EVOLUTIONARY COMPUTATION

In the realm of evolutionary computation, the idea of diploidy was present from the beginning [4], with its main challenge being establishing a proper mechanism of dominance, as arbitrarily selecting one of the alleles to be dominant over the other one could lead to an unfair bias towards one of the alleles. On the other hand, although polyploidy appears to be a natural extension of diploidy, it has been given far less spotlight than its two-chromosomal basis, and has been found to be "*[...] useful in precisely those cases where useful genetic material may otherwise be irretrievably lost*" [2].

Although historically some papers have claimed the benefit of using diploid representations for deceptive, stationary problems [3], in the modern research the diploid representations are usually relegated to optimization of non-stationary problems [1, 5, 10].

Most of the early work on the use of diploidy in evolutionary computation was restricted to GAs, as the structure of genotypes used in other evolutionary algorithms – such as genetic programming, evolutionary design, or optimization of combinatorial problems – does not easily conform to the framework of corresponding genes and alleles. To change that, in 2015 best-chromosome-wins mechanism of dominance was introduced by Shabash and Wiese [9], in which all chromosomes are evaluated independently, and the best of them is expressed in full, so the fitness of the genotype becomes the fitness of the best chromosome. In practice, this allows EA practitioners to use diploidy in tandem with any type of representation, without putting in any extra work.

Later, Petrovan et al. [8] reported that diploidy with the best-chromosome-wins mechanism improves the results of evolutionary optimization not only for non-stationary problems, but also on stationary mathematical benchmarks, compared to a regular haploid representation. Their result was interesting, as historically diploidy was not known to reliably enhance the optimization of stationary problems. Later, they used diploidy with the best-chromosome-wins mechanism in optimization of the multidimensional two-way number partitioning problem [7], showing that the benefits of using a diploid representation on stationary problems are not restricted to mathematical benchmarks.

3 METHODS

Mathematical benchmarks. In this work we perform a series of evolutionary optimization experiments on a set of 14 mathematical benchmarks; their full definitions, domains, and global minima can be found in [6]. The set contains the following functions: Schwefel's, Ackley's, Rastrigin's, Griewank's, Alpine N. 1, Sphere, Step, Sum Squares, Quartic, Qing's, Dixon-Price, Exponential, Powell Sum, and Ridge. In the experiments reported in this work, the dimensionality of the problems is set to $D = 25$. We multiply the original minimized fitness functions by -1 and treat them as maximization problems.

Representation. The number of chromosomes in a single genotype is hereafter denoted as P; in the experiments we use haploid ($P = 1$), diploid ($P = 2$), and polyploid ($P > 2$) genotypes. Each chromosome is a vector of real numbers of length D. To evaluate the fitness of a genotype we utilize best-chromosome-wins mechanism of dominance, i.e., the fitness of a genotype is equal to the maximum of fitness values of all its chromosomes.

Genetic operators. The mutation operator is performed separately for each chromosome in a genotype. The mutation adds a random vector, each value of which is drawn at random from the normal distribution $\mathcal{N}(0, \sigma)$, where $\sigma = allowed\_range/(50 \cdot \sqrt{D})$. The crossover operator randomly shuffles the chromosomes from each of the parents, and then proceeds to perform a crossover operation on each of P pairs of chromosomes taken from both parents, producing P offspring chromosomes that constitute a single offspring genotype. Two chromosomes are crossed over uniformly, by swapping the values of their vectors with 50% probability.

Algorithm. In all experiments reported in this paper, a single-population generational evolutionary algorithm with tournament selection is used. Let us denote the population size as N and let k be the size of the tournament. In each generation, based on selected parent individuals from the old population, $p_m \cdot N$ solutions are created with the mutation operator, $p_c \cdot N$ solutions are created with the crossover operator, and the remaining solutions, if needed, are clones. No elitism mechanism is employed. The initial population is filled with randomly generated solutions. The generation of a random solution is performed by drawing a random vector from the uniform distribution over the allowed search range.

Statistics. For all experiments with diploid and polyploid genotypes, at each generation a series of basic statistics of chromosomal fitness (maximum, minimum, average and standard deviation, separately for dominant and recessive chromosomes) is gathered. Additionally, we calculate Pearson correlation coefficient between the fitness of the dominant chromosome of a solution, and the average fitness of all recessive chromosomes of that solution.

Parameters. The parameters of the algorithms used in the experiments are as follows: level of ploidy $P \in \{1, 2, 3, 4\}$; size of a population $N = 2004/P$ (the base size is divisible by each P); tournament size $k \in \{2, 5, 7, 10\}$; number of generations $g = 150$; number of independent repetitions $r = 30$. The population size depends on the level of ploidy employed in the experiment. This way, since a population using P-ploids is smaller by a factor of P, the amount of a genetic information present in the population at any point will be equal independently of the level of ploidy. In the same fashion, the computational time required for the evaluation of all chromosomes should be the same for all levels of ploidy. This allows for a fair comparison between genotypes of varying levels of ploidy.

Scenarios. We test the haploid, diploid and polyploid representations in three scenarios using different probabilities of genetic operators to verify the impact of crossover on the effectiveness of these representations: low crossover ($p_c = 0.3$, $p_m = 0.5$), high crossover ($p_c = 0.85$, $p_m = 0.1$) and full crossover ($p_c = 1.0$, $p_m = 0.1$). In the case of full crossover scenario all new solutions result from crossover, with 10% being additionally mutated.

4 EXPERIMENTS

Fig. 1 compares the performance of different levels of ploidy on the set of mathematical benchmarks. For each combination of the parameters (P, k, low/high/full crossover scenario, benchmark), the average value of the best solution found over r independent runs is calculated. The results for a low crossover scenario are presented on the left, for a high crossover scenario in the middle, and for a full crossover – on the right. Each cell represents the best value obtained by a given level of ploidy P and a specific mathematical benchmark, among all sizes of tournament k. Each row is normalized, so that value 0 (dark) always corresponds to the worst, and value 1 (light) to the best-performing combination of ploidy and scenario.

In all scenarios haploid genotypes manage to reliably find better solutions than diploid and polyploid genotypes. For most of the benchmarks, high crossover scenarios yields better results. When the population size is corrected for the level of ploidy, increasing the level of ploidy always leads to the algorithm finding solutions of lower quality.
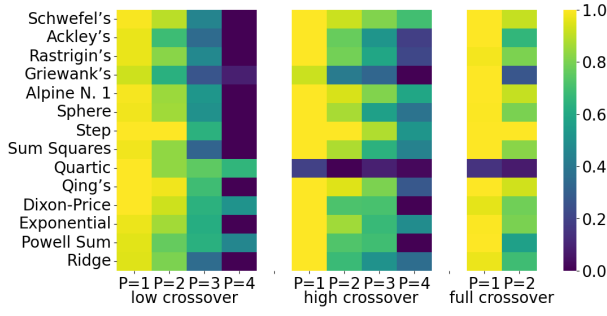
Figure 1: The averaged fitness of the best solutions found by the algorithm, maximized over different tournament sizes $k \in \{2, 5, 7, 10\}$. Results for benchmarks are shown in rows and different levels of ploidy P are shown in columns. Values of each row are normalized with 1.0 (light) representing the best and 0.0 (dark) representing the worst averaged best fitness found for a given benchmark for any tournament size k.

## 5 ANALYSIS OF CHROMOSOMAL FITNESS

To understand the subpar performance of diploid and polyploid genotypes, let us analyze the statistics of chromosomal fitness gathered during the experiments.

The maximum and the minimum values of fitness and standard deviation are found across all recorded population statistics (for all the combinations of parameters and numbers of generations), separately for each benchmark. These values are then used to normalize values of the statistics to a range of $[0, 1]$. After the statistics are normalized, the series containing their values changing during the evolution are averaged across all benchmarks, separately for each combination of parameters (P, k, low/high crossover scenario).

Fig. 2a presents the influence of the parameters on the average fitness values of chromosomes, separately for the dominant and recessive chromosomes. Convergence is faster for dominant chromosomes than it is for the recessive chromosomes. It is especially clear for the case of low crossover, where the recessive chromosomes are significantly worse for most of the time. Since the selective pressure depends only on the quality of the best chromosome, the only way for recessive chromosomes to improve over time is therefore through crossing over with high-quality chromosomes. Although increasing the chance of crossover helps to bridge the fitness gap between the dominant and recessive chromosomes, it is not able to fully close the gap. As the level of ploidy increases, the chance that a chromosome will be crossed over with the dominant chromosome decreases, which explains why the fitness of all chromosomes grows slower when the level of ploidy is higher.

It must be noted that the probability of crossover in our "high crossover" scenario is only $p_c = 0.85$. Increasing it even further may help the recessive chromosomes to fully catch up to the dominant chromosomes and become so similar that they could become dominant themselves through mutation.

Fig. 2b presents the influence of the parameters on the standard deviation of fitness values of chromosomes, separately for the dominant and recessive chromosomes. The standard deviation of fitness tends toward zero as the population converges, independently of
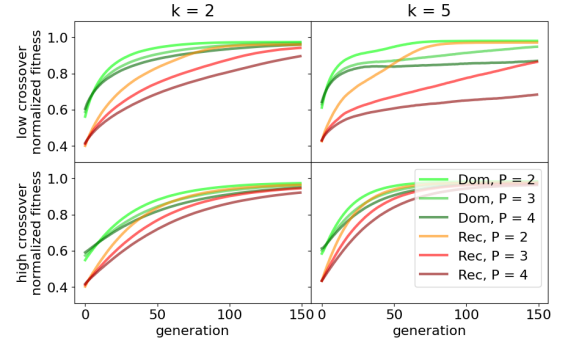
(a) Average fitness of dominant (Dom, green) and recessive (Rec, red) chromosomes.
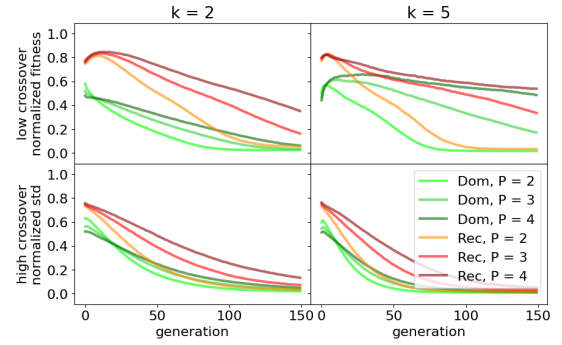
(b) Standard deviation of the fitness of dominant (Dom, green) and recessive (Rec, red) chromosomes.
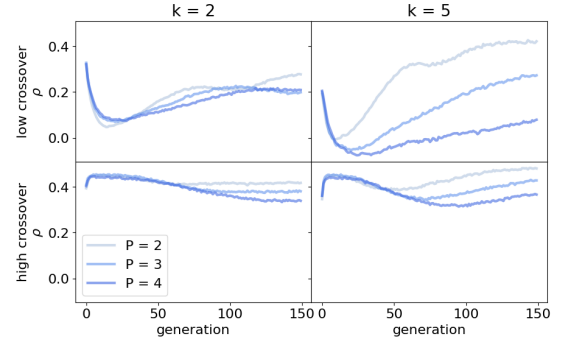
(c) Pearson correlation coefficient ρ between the fitness of dominant and recessive chromosomes.

Figure 2: Values of different statistics over time for different levels of ploidy $P \in \{2, 3, 4\}$, averaged over 30 repetitions of an EA normalized per benchmark, averaged over all benchmarks.

the parameter values used. This convergence is faster for dominant chromosomes, low levels of ploidy and for the "high crossover" scenario. This matches earlier observations based on Fig. 2a.

An interesting behavior can be observed for the low crossover scenario – at the start of the evolution, diversity of fitness for recessive (for $k = 2$) and dominant (for $k = 5$) chromosomes initially rises before starting to eventually converge. The initial rise

in fitness diversity is caused by the coexistence of recessive chromosomes which have not yet been crossed over with high quality chromosomes, with those that have been crossed over. For the higher selective pressure ($k = 5$), the rise in fitness diversity of dominant chromosomes is caused by only a small portion of the initial population actually improving while the rest stays behind, and is expected when the improvements are fast and the chance of recombination is low.

Fig. 2c presents the influence of the parameters on the Pearson correlation coefficient ρ between the fitness of the dominant and (averaged) recessive chromosomes from the same genotypes. While the values of ρ do not change monotonically throughout the entire evolutionary run, this can be explained in the context of diploidy, with the explanation naturally extending to polyploidy.

Let us first understand why the initial correlations are not close to zero – should this not be the case if the initial population is drawn randomly and uniformly from the entire search space? The answer is negative: while the correlation between two unrelated chromosomes would be 0, by labeling one of the chromosomes as *dominant* we introduce a selection bias, and so the recessive chromosomes of the same genotype must be worse than (or rarely equal to) the dominant one. Therefore, the better the dominant chromosome, the better – on average – are the recessive chromosomes, and so the initial correlation between the fitness of the dominant and the (averaged) recessive chromosomes is actually positive.

Another observation that requires an explanation is the quick initial drop in the values of ρ for the low crossover scenario, which in the case of higher selective pressure $k = 5$ even manages to reverse the sign of ρ. When the probability of crossover is low, the mutation operator itself is not able to bring the fitness of the recessive chromosomes closer to that of the dominant chromosome. As the selection is based on the dominant chromosome, only this chromosome will improve over time, leaving the quality of the recessive chromosomes behind. Since the low quality recessive chromosomes are more plentiful than high quality recessive chromosomes, initially the selective pressure is actually implicitly selecting poor recessive chromosomes. Therefore, if the improvement of the dominant chromosomes is fast and driven primarily by mutation, the initial positive correlation can be reversed, as is the case for low crossover and $k = 5$. It is possible that ρ starts to grow again only once the genetic material of dominant chromosomes starts to spread across the population.

When the crossover probability is high, the correlation between the fitness of the dominant and recessive chromosomes initially grows. Recessive chromosomes may be improved by exchanging the genetic material with the dominant ones, and so if their initial fast improvement is done with crossover rather than mutation, the value of ρ will grow as recombination pulls the recessive chromosomes into more promising areas of the fitness landscape. Such a high correlation is however unsustainable and will eventually decrease in time, unless the selective pressure is high enough to effectively limit genetic diversity of parents and facilitate the "rewriting" of the recessive chromosomes in the image of the dominant chromosome.

Overall, the correlation is lower for the higher levels of ploidy, with the difference between the values of ρ recorded for different levels of ploidy increasing as the evolution progresses. This is caused by lower levels of ploidy being more agile and able to change

the average fitness of the recessive chromosomes more quickly – keep in mind that in crossover, as implemented here , only one of the chromosomes (in particular, recessive ones) has a chance of recombination with the dominant chromosome of another solution.

6 CONCLUSIONS

In this work we have shown that diploid and polyploid genotypes with the best-chromosome-wins dominance are not a good fit for the optimization of stationary problems. We have also performed an in-depth analysis of the reasons behind their poor performance. Recessive chromosomes constitute a dead weight for evolution, with their quality lagging far behind that of the dominant chromosomes which actually perform the search. Although their quality can be brought up to the level of the dominant chromosomes by prevalent crossover, such very frequent crossover decreases the quality of the dominant chromosomes, and in effect the quality of the entire genotype. Therefore, no matter the probability of crossover, the impact the additional chromosomes have on the quality of the final solutions in stationary problems is always negative when the best-chromosome-wins mechanism of dominance is used. While the benefits of having genetic memory in a form of additional chromosomes may outweigh this drawback during the optimization of non-stationary functions, for stationary problems the use of diploidy and polyploidy with the best-chromosome-wins mechanism is only detrimental.

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