Handling Crossover Bias to Improve Diversity in Multiobjective Evolutionary Optimization

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ABSTRACT

Since the early studies in multiobjective evolutionary optimization, fitness assignment and/or selection have been the main focus of research in the field. In general, many of the methods proposed share the same goals: keep diversity along the Pareto-front and favor convergence towards Pareto-optimality. However, whether in the context of Pareto dominance or hypervolume, many studies have reported difficulties in keeping a good spread of solutions in objective space due to a certain bias that drives the population towards the middle region of the Pareto front. While techniques such niching and crowding (in the context of selection) and restricted mating (in the context of reproduction) have been proposed to circumvent such bias, few is known about its origins. This paper evaluates the influence of crossover in such bias and shows that uniform crossover operators have an intrinsic bias that favors the middle region and deteriorates the effects of diversity preservation mechanisms. Following from that, we propose a simple way to handle the bias of uniform crossover and enable a better synergy with the crowding mechanism of the NSGA2. Results in bi-objective instances of ρMNK-landscapes confirm that such approach enable a better diversity preservation.

Categories and Subject Descriptors

G.1.6 [**Optimization**]: Global Optimization—*Multiobjective Evolutionary Algorithms*

Keywords

crossover bias; diversity preservation; multiobjective

1. INTRODUCTION

Multiobjective Optimization Problems (MOPs) are defined by a set of objective functions that attribute value to decision vectors $\boldsymbol{x} = (x_1, \ldots, x_N) \in \mathcal{S}$, with $\mathcal{S} \subseteq \mathbb{R}^N$. The image of the feasible region $\mathcal{S}$ according to the vector-valued function $\mathbf{f} = (f_1, f_2 \ldots, f_M)$ is the feasible objective region $\mathcal{Z} \subseteq \mathbb{R}^M$,

composed of objective vectors $\boldsymbol{z} = (f_1(\boldsymbol{x}), f_2(\boldsymbol{x}), \ldots, f_M(\boldsymbol{x}))$. In other words, the objective functions map each feasible decision vector $\boldsymbol{x} \in \mathcal{S}$ to objective vectors $\boldsymbol{z} \in \mathcal{Z}$.

$$\max \quad \mathbf{z} = \mathbf{f}(\mathbf{x}), \quad \mathcal{Z} \subseteq \mathbb{R}^N$$
$$\text{subject to} \quad \boldsymbol{x} \in \mathcal{S}, \quad \mathcal{S} \subseteq \mathbb{R}^N \qquad (1)$$

The main goal in solving MOPs is to find of a set of well-diversified (diversity) Pareto-optimal solutions (convergence) from which a target solution can be chosen *a posteriori*.

Since the early studies, selection has been one of the main research focuses in Multiobjective Evolutionary Algorithms (MOEAs). Regarding reproduction operators, the literature is not so abundant. Many methods have been proposed to improve convergence of diversity of the non-dominated solutions found, but few has been said about the specific weaknesses that make traditional crossover operators, like p-uniform and n-point, inappropriate.

We have hypothesized the inherent bias of traditional crossover (uniform, 1-point and 2-point crossover) tends to misguide the population in objective space, favoring biased convergence a prior to diversity. This way, crossover spoil the benefits of diversity preservation mechanisms, decreasing their efficacy in producing a well-spread Pareto-front. We propose and evaluate a crowding-biased uniform crossover which favors the synergy between diversity preservation and crossover in order to produce a better spreading.

2. ORIGINS OF CROSSOVER-BIAS

The p-uniform crossover operator will take two parents $\boldsymbol{x}_1, \boldsymbol{x}_2 \in \mathcal{S}$ and generate one child $\boldsymbol{y}$. Each bit $y_i, \forall i = 1, \ldots, N$ comes from parent $\boldsymbol{x}_1$ with probability p and parent $\boldsymbol{x}_2$ with probability $1 - p$. The number of bits from each parent is a random variable $\mathscr{B}_p$ with expected value:

$$\mathbb{E}(\mathscr{B}_p) = \sum_{i=1}^{N} p = N \cdot p \qquad (2)$$

Therefore, if $p = 0.5$, $\boldsymbol{y}$ is, on average, distant $N/2$ bits from each parent. Now, suppose $\boldsymbol{x}_1$ is a very good solution according to an objective and $\boldsymbol{x}_2$ is a very good solution for a second objective. Therefore, $\boldsymbol{y}$ will have half of the genetic material of each parent and we can expect it to be only half as good as each parent, in this case, $\boldsymbol{z_y}$ is biased towards the center of the objective space. Although Non-dominated Sorting Genetic Algorithm 2 (NSGA2)' crowding may attribute extra fitness to solutions $\boldsymbol{x}_1$ and $\boldsymbol{x}_2$ to favor extreme regions, the region in the middle will be more intensely exploited and extreme solutions are likely to be lost.

3. CROWDING-BIASED CROSSOVER

In order to handle crossover bias and at the same time synchronize the goals of crowding and reproduction, parameter p in uniform crossover must be adapted according to the characteristics of the parents undergoing crossover. In NSGA2, the crowding distance $d(\boldsymbol{x})$ associated with every solution $\boldsymbol{x} \in P(t)$ at generation $t > 0$ describes how isolated the objective vector $\boldsymbol{z_x}$ is in the objective space. Therefore, by defining p according to the crowding distance of parents $\boldsymbol{x}_1$ and $\boldsymbol{x}_2$ (respectively, $d(\boldsymbol{x}_1)$ and $d(\boldsymbol{x}_2)$), we can generate offspring closer to more isolated regions.

We consider ψ a simple linear mapping, with $\min_p = 0.5$, $\max_p = 0.95$ and $\min_d$ and $\max_d$ obtained from the current population and denote as Δ_p and Δ_d, respectively.

$$p = \begin{cases} \min_p + \dfrac{(d(\boldsymbol{x}_1) - \min_d) \cdot \Delta_p}{\Delta_d}, & d(\boldsymbol{x}_1) < \infty \\ \max_p, & d(\boldsymbol{x}_1) = \infty, \end{cases} \quad (3)$$

In words, taking in account the crowding distances of solutions in the current population $P(t)$, for each pair of parents $\boldsymbol{x}_1$ and $\boldsymbol{x}_2$ a p value is defined to bias the offspring towards the more isolated parent. If $\boldsymbol{x}_1$ is an extreme solution, with $d(\boldsymbol{x}_1) = \infty$, the resulting offspring will be composed, in average, by $0.95 \cdot N$ bits from $\boldsymbol{x}_1$. Otherwise, if $d(\boldsymbol{x}_1) = 0$, $\boldsymbol{x}_1$ is in a crowded region (or the crowding distance has not been computed for $\boldsymbol{x}_1$), therefore, the usual $p = 0.5$ is applied. Non-linear mappings could also be applied to control the bias, but we leave this for future works.

## 4. EXPERIMENTS AND RESULTS

4.1 The ρMNK-landscapes Model

The model considers N-dimensional vectors $\boldsymbol{x} \in \{0, 1\}^N$, in which each decision variable x_i interacts with K others $(x_{i_1}, \ldots, x_{i_K})$. As K grows from 0 to $N - 1$, the non-linearity also increases, making the instance harder to solve:

$$\max f_{NK}(\boldsymbol{x}) = \frac{1}{N} \sum_{i=1}^{N} f_i(x_i, x_{i_1}, \ldots, x_{i_K})$$

Vérel et al. [1] proposed and analyzed the fitness landscapes of MNK-landscapes with different degrees of correlation, $\rho = -0.9$, among objective functions (ρMNK-landscapes). Since we want to evaluate the impact of crossover in the diversity of the Pareto-fronts found, we generated negatively correlated instances with the following settings: $M = 2$, $N = 500$, $K = 8$ and $\rho = -0.9$. For each instance, 30 runs were performed, with a limit of $500,000$ fitness evaluations, using the crowding-biased uniform crossover and the usual uniform crossover with $p = 0.1, 0.5$.

4.2 Results and Discussion

Figure 1 shows the comparison of $p = 0.1, 0.5$ uniform crossover and the crowding-biased uniform crossover proposed in Section 3. Uniform crossover, with $0.1 \leq p \leq 0.5$, performed slightly better in the middle region than its crowding biased counterpart. However, as can be noticed by the dark regions, the improvements in spreading reached by the crowding-biased crossover were far more evident. Such simple modification changes the behavior of crossover, decreases its inherent bias and set its goals in agreement with the diversity preservation mechanism of NSGA2 implemented by crowding.
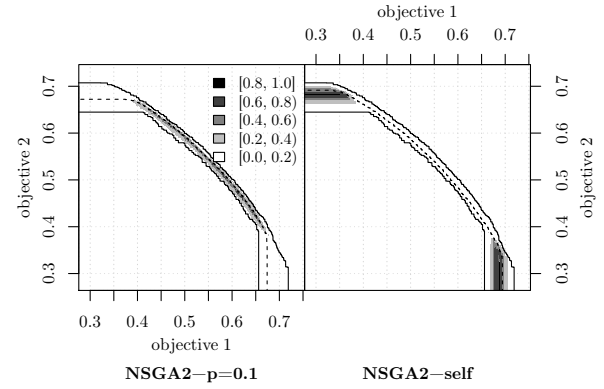
(a) $p = 0.1$ vs crowding-biased uniform crossover
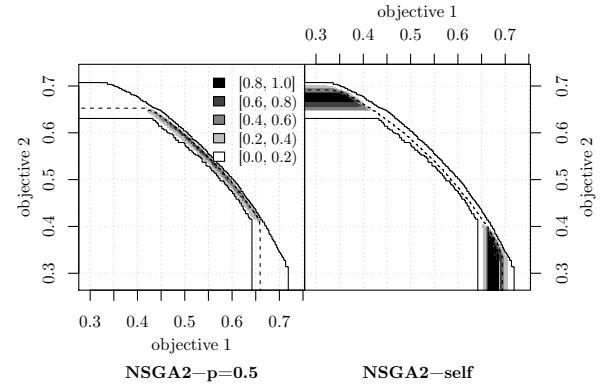
(b) $p = 0.5$ vs crowding-biased uniform crossover

Figure 1: Comparison between crowding-biased uniform crossover (NSGA2-self) and traditional uniform crossover with $p = 0.1, 0.5$ (NSGA2-p=*).

5. CONCLUSIONS

We noticed the incompatibility between the crowding mechanism and crossover results. While the first tries to guarantee a well-distributed front, the second ends up producing more offspring in the middle region. In order to circumvent such incompatibility, we proposed a crowding-biased uniform crossover that, considering two parents, will generate offspring closer to the more isolated one. Experiments with instances of the ρMNK-landscapes model showed the efficacy of this simple approach in increasing diversity and spreading of the Pareto-fronts produced. It would be interesting, to analyze in more practical MOPs.

Acknowledgments

6. REFERENCES

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