Distance-Based Analysis of Crossover Operators for Many-Objective Knapsack Problems

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Abstract. It has been reported for multi-objective knapsack problems that the recombination of similar parents often improves the performance of evolutionary multi-objective optimization (EMO) algorithms. Recently performance improvement was also reported by exchanging only a small number of genes between two parents (i.e., crossover with a very small gene exchange probability) without choosing similar parents. In this paper, we examine these performance improvement schemes through computational experiments where NSGA-II is applied to 500-item knapsack problems with 2-10 objectives. We measure the parent-parent distance and the parent-offspring distance in computational experiments. Clear performance improvement is observed when the parent-offspring distance is small. To further examine this observation, we implement a distance-based crossover operator where the parent-offspring distance is specified as a user-defined parameter. Performance of NSGA-II is examined for various parameter values. Experimental results show that an appropriate parameter value (parent-offspring distance) is surprisingly small. It is also shown that a very small parameter value is beneficial for diversity maintenance.

Keywords: Mating schemes, evolutionary multiobjective optimization (EMO), many-objective optimization, knapsack problems, NSGA-II.

1 Introduction

Evolutionary multi-objective optimization (EMO) has been an active research area in the field of evolutionary computation in the last two decades. A number of multiobjective continuous optimization problems have been proposed as test problems in the EMO community. Whereas continuous problems have been mainly used to evaluate the performance of EMO algorithms, combinatorial test problems such as multiobjective knapsack problems in Zitzler and Thiele [17] have also been used (e.g., see Jaszkiewicz [9], Sato et al. [13], and Zhang and Li [16]).

For multi-objective knapsack problems, it has been reported in some studies [3], [6], [13] that the recombination of similar parents improves the performance of EMO algorithms such as SMS-EMOA [1] and NSGA-II [2]. MOEA/D [16] has an inherent mechanism of recombining similar parents, which is local selection of parents based on a neighborhood structure of solutions. It has been reported in [4] that the removal

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of local selection deteriorates the performance of MOEA/D on multi-objective knapsack problems. Reported results in those studies suggest the existence of a negative effect of recombining totally different parents on the performance of EMO algorithms. Recently Sato et al. [14] demonstrated that the performance of EMO algorithms was improved by exchanging only a small number of genes between two parents (i.e., using a very small gene exchange probability) instead of choosing similar parents.

In this paper, we examine the above-mentioned two schemes for performance improvement of EMO algorithms through computational experiments on 500-item knapsack problems with 2-10 objectives. NSGA-II [2] is used to examine the effect of each scheme. That is, NSGA-II is applied to each test problem under three settings of crossover: Standard uniform crossover, uniform crossover of similar parents, and modified uniform crossover with a very small gene exchange probability. In computational experiments, we measure the parent-parent distance and the parent-offspring distance. Good results are obtained when the parent-offspring distance is small.

To further examine this observation, we implement a distance-based crossover operator where the generated offspring always has a pre-specified distance from its closer parent. That is, the parent-offspring distance is specified as a user-defined parameter. Performance of NSGA-II is measured for various parameter values to examine the relation between the parent-offspring distance and its performance. As performance measures, we calculate the hypervolume of solutions obtained from each run of NSGA-II using two reference points. One is far from and the other is close to the Pareto front. The two reference points are used to examine the effect of the parentoffspring distance on the diversification and convergence properties of NSGA-II.

The rest of this paper is organized as follows. In Section 2, we briefly explain our test problems (i.e., 500-item knapsack problems with 2-10 objectives). In Section 3, we explain the above-mentioned two performance improvement schemes. In Section 4, we report our experimental results where the performance of NSGA-II with each scheme is evaluated. In Section 5, we discuss our experimental results using a distance-based crossover operator. Finally we conclude this paper in Section 6.

2 Multi-Objective and Many-Objective Knapsack Problems

Multi-objective knapsack problems with 2-4 objectives and 250, 500 and 750 items were used in Zitzler and Thiele [17]. Their two-objective *n*-item problem is written as

Maximize
$$\mathbf{f}(\mathbf{x}) = (f_1(\mathbf{x}), f_2(\mathbf{x})),$$
 (1)

subject to
$$\sum_{j=1}^{n} w_{ij} x_j \le c_i$$
, $i = 1, 2,$ (2)

$$x_j = 0 \text{ or } 1, \ j = 1, 2, ..., n,$$
 (3)

where
$$f_i(\mathbf{x}) = \sum_{j=1}^{n} p_{ij} x_j$$
, $i = 1, 2.$ (4)

In Zitzler and Thiele [17], the profit p_{ij} and the weight w_{ij} of item *j* with respect to knapsack *i* were specified as random integers in the interval [10, 100]. The capacity c_i of knapsack *i* was specified as 50% of the total weight of *n* items for knapsack *i*. Since the number of objectives and the number of items can be arbitrarily specified, multi-objective knapsack problems have been used as many-objective test problems (e.g., [4], [7], [14]). They have also been used as large-scale multi-objective test problems with up to 10000 items [5].

In this paper, we use multi-objective 500-item knapsack problems with 2-10 objectives. Those test problems are generated from the two-objective *n*-item problem in (1)-(4) by specifying *n* as n = 500 and creating additional objectives as follows:

$$f_i(\mathbf{x}) = \sum_{j=1}^n p_{ij} x_j , \quad i = 3, 4, ..., 10 ,$$
 (5)

where the profit p_{ij} of item *j* with respect to knapsack *i* is specified as a random integer in the interval [10, 100] in the same manner as in [17]. We denote the *k*-objective 500-item knapsack problem as the *k*-500 problem. In this paper, we use five test problems with k = 2, 4, 6, 8, 10 (i.e., 2-500, 4-500, 6-500, 8-500, 10-500 problems).

The constraint conditions in (2) and (3) are always used in our test problems independent of the number of objectives. This means that all of our test problems have the same set of feasible solutions. As a result, the same greedy repair method in [17] is used for constraint handling in all test problems in our computational experiments.

3 Two Performance Improvement Schemes

A similarity-based mating scheme was proposed and incorporated into NSGA-II to recombine similar parents in Ishibuchi et al. [6]. In its simplest version, first one parent is selected in the same manner as in NSGA-II (i.e., binary tournament selection with replacement based on non-dominated sorting and crowding distance). Next β candidates are selected by iterating the same parent selection mechanism as NSGA-II β times. Then the closest candidate to the first parent is selected from the β candidates using the Euclidean distance in the objective space. The selected candidate is used as the mate of the first parents. In the mating scheme, β is a user-defined parameter to specify the strength of the selection pressure toward similar parent selection. The larger value of β means the stronger selection pressure toward similar parent selection (i.e., stronger tendency to choose similar parents). When $\beta = 1$, the mating scheme does not change the parent selection mechanism of NSGA-II at all.

Sato et al. [14] proposed an idea of exchanging only a small number of genes between two parents instead of selecting similar parents. They implemented the idea for uniform crossover by using a very small gene exchange probability, which was denoted by α_u in [14]. In the standard uniform crossover, genes of two parents are exchanged at each locus with the probability 0.5. In [14], good results were obtained for multi-objective knapsack problems when α_u was very small (e.g., 0.01).

4 Experimental Results

Three settings of crossover in NSGA-II are examined: Standard uniform crossover, uniform crossover of similar parents, and modified uniform crossover with a small gene exchange probability. One of the two children of crossover is randomly selected and handled as an offspring in NSGA-II in our computational experiments. The following parameter values are examined in the performance improvement schemes:

The number of candidates: $\beta = 1, 5, 10, 20, 30, 40, 50$. Gene exchange probability: $\alpha_u = 0.01, 0.02, 0.03, 0.04, 0.05, 0.10, 0.15, 0.20$.

NSGA-II with each parameter value is applied to each test problem 100 times. The hypervolume of the obtained solutions is calculated using a fast calculation method [15] for each of the 100 runs for two reference points. One is (0, 0, ..., 0) which is far from the Pareto front, and the other is (15000, 15000, ..., 15000) which is close to the Pareto front. Computational experiments are performed under the following settings:

Population: 100 binary strings of length 500 with random initialization, Termination condition: Evaluation of 400,000 solutions,

Crossover probability: 0.8 (One of the three versions of uniform crossover), Mutation probability: 1/500 (Bit-flip mutation).

The calculated hypervolume value for each run with each parameter specification of β and α_u is normalized using the average result by NSGA-II with the standard uniform crossover for each reference point. It should be noted that the standard uniform crossover corresponds to the setting of $\beta = 1$ and $\alpha_u = 0.5$. In computational experiments, we also calculate the Hamming distance between two parents and between an offspring and its closer parent. The parent-offspring distance is measured after mutation only when crossover is used. Experimental results are summarized in Fig. 1 and Fig. 2 for each performance improvement scheme.

From Fig. 1 (a), we can see that the average normalized hypervolume value for the reference point (0, 0, ..., 0) is improved for all test problems by similar parent recombination from the baseline value 100 by the standard uniform crossover with $\beta = 1$ (the baseline value 100 is also obtained from the setting of $\alpha_u = 0.5$). In Fig. 2 (a), larger performance improvement is achieved for the 6-500, 8-500 and 10-500 problems by small gene exchange probabilities than similar parent recombination in Fig. 1 (a). However, better results are obtained for the 2-500 and 4-500 problems by similar parent recombination in Fig. 1 (a) than small gene exchange probabilities in Fig. 2 (a).

When the hypervolume for the reference point (15000, 15000, ..., 15000) is used as a performance measure in Fig. 1 (b) and Fig. 2 (b), we can observe both positive and negative effects of the performance improvement schemes. In Fig. 1 (b), the average normalized hypervolume value is improved by similar parent recombination for the 2-500 and 4-500 problems. However, the performance is degraded by similar parent recombination for the 6-500, 8-500 and 10-500 problems. In Fig. 2 (b), the use of too small gene exchange probabilities (e.g., $\alpha_u = 0.01$) severely degrades the performance for the 6-500, 8-500 and 10-500 problems. However, when α_u is specified between 0.1 and 0.2, the use of small gene exchange probabilities improves the performance for those test problems.



Fig. 1 (c) and Fig. 2 (c) show the average Hamming distance of two parents while the distance in Fig. 1 (d) and Fig. 2 (d) is measured between an offspring and its closer parent. In Fig. 1 (c), the average Hamming distance between two parents is decreased by increasing the value of β . That is, the similarity of two parents is increased by increasing the value of β . As a result, the parent-offspring distance is decreased by increasing the value of β in Fig. 1 (d). We can also see from Fig. 1 (c) and Fig. 1 (d) that both the parent-parent distance and the parent-offspring distance are increased by increasing the number of objectives.

In Fig. 2 (c), the parent-parent distance is not small. This is because no selection mechanism of similar parents is used in Fig. 2. Thus, the average parent-parent distance in Fig. 2 (c) can be considered as being similar to the average distance between two solutions in a population over all generations (whereas they are not exactly the same). Fig. 2 (c) shows that the average parent-parent distance is increased by very small gene exchange probabilities for all test problems. This observation suggests that the performance improvement in Fig. 2 (a) is achieved by the increase in the diversity of solutions. At the same time, the diversity improvement severely degrades the convergence property, which leads to severe performance deterioration in Fig. 2 (b) by very small gene exchange probabilities for the 6-500, 8-500 and 10-500 problems.

In Fig. 1 (d) and Fig. 2 (d), the parent-offspring distance is decreased by increasing the parameter value of β (i.e., increasing the number of candidates for the second parents) and decreasing the parameter value of α_u (i.e., decreasing the gene exchange probability), respectively. From Fig. 1 (a) and Fig. 1 (d), we can see that good results are obtained in Fig. 1 (a) when the parent-offspring distance is small in Fig. 1 (d). The same observation is also obtained from Fig. 2 (a) and Fig. 2 (d).

5 Further Discussions Using Distance-Based Crossover

In this section, we further discuss the relation between the parent-offspring distance and the performance of NSGA-II. First we explain binary crossover using the concept of geometric crossover, which has been proposed by Moraglio and Poli [10]-[12]. Standard binary crossover (e.g., uniform, one-point, and two-point crossover) is geometric crossover in the sense that the sum of the Hamming distances between an offspring and its two parents is always equal to the Hamming distance between the two parents [8], [10]-[12]. That is, the following relation always holds for an offspring *C* generated by standard binary crossover from its two parents P_1 and P_2 :

$$H(C, P_1) + H(C, P_2) = H(P_1, P_2),$$
(6)

where H(A, B) shows the Hamming distance between binary strings A and B. This relation always holds for all standard binary crossover operators [8], [10]-[12].

When the similar parent recombination scheme is incorporated into NSGA-II, two parents with a small Hamming distance are recombined as shown in Fig. 1 (c). That is, the right-hand side (i.e., $H(P_1, P_2)$) of (6) is decreased by increasing the value of β in the similar parent recombination scheme. As a result, the two terms in the left-hand side of (6) are decreased as shown in Fig. 1 (d).

When the small gene exchange probability scheme is used, the right-hand side of (6) is not decreased as shown in Fig. 2 (c). However, one of the two terms in the

left-hand side of (6) is decreased as shown in Fig. 2 (d). That is, min{ $H(C, P_1)$, $H(C, P_2)$ } becomes very small when the gene exchange probability α_u is very small.

Geometric crossover with the similar parent recombination scheme is illustrated in Fig. 3 (a) using two parents P_1 , P_2 and its offspring *C*. In Fig. 3 (a), the horizontal and vertical axes show the Hamming distances from Parent P_1 and Parent P_2 , respectively. The short three arrows show the possible moves by mutation of a single gene of *C*. In Fig. 3 (a), $H(C, P_1) + H(C, P_2) = H(P_1, P_2)$ holds since $H(C, P_1) = 2$, $H(C, P_2) = 2$ and $H(P_1, P_2) = 4$. Similar parent recombination means that $H(P_1, P_2)$ is small in Fig. 3 (a).

Fig. 3 (b) illustrates geometric crossover with a small gene exchange probability. Since no mechanism for similar parent recombination is used, two parents have a larger Hamming distance in Fig. 3 (b) than Fig. 3 (a): $H(P_1, P_2) = 10$ in Fig, 3 (b). However, due to a small gene exchange probability, the generated offspring *C* is close to P_1 or P_2 as shown in Fig. 3 (b). In our computational experiments, one of the two offspring is randomly selected for further use in NSGA-II.

In uniform crossover with a very small gene exchange probability α_u , the expected value of min{ $H(C, P_1), H(C, P_2)$ } can be approximated by $\alpha_u H(P_1, P_2)$. For example, when $\alpha_u = 0.2$ and $H(P_1, P_2) = 10$, the expected value of min{ $H(C, P_1), H(C, P_2)$ } is 2. This means that the parent-offspring distance depends on the parent-parent distance, which depends on the number of objectives and the value of α_u as shown in Fig. 2 (c).



Fig. 3. Illustration of the two performance improvement schemes

In order to examine the relation between the parent-offspring distance and the performance of NSGA-II in a more straightforward manner, we implement the following distance-based crossover operator, which is incorporated into NSGA-II:

Distance-Based Crossover Operator:

- 1. The parent-offspring distance is specified as a user-defined parameter. This parameter is denoted by *D*.
- 2. Two parents P_1 and P_2 are selected in the same manner as in NSGA-II.

- 3. If $H(P_1, P_2) < 2D$, we cannot generate an offspring *C* such that min{ $H(C, P_1)$, $H(C, P_2)$ } = *D* by geometric crossover (since $H(C, P_1) + H(C, P_2) < 2D$). In this case, we use standard uniform crossover for P_1 and P_2 . Otherwise (i.e., $H(P_1, P_2)$ $\geq 2D$), *D* loci are randomly selected from $H(P_1, P_2)$ loci with different bit values in P_1 and P_2 . Each of those loci is selected uniformly with the same probability. The genes (i.e., different bit values) in the selected *D* loci are exchanged between P_1 and P_2 . Since the *D* genes are exchanged, min{ $H(C, P_1), H(C, P_2)$ } = *D* holds.
- 4. One of the generated two offspring is randomly selected for further use in NSGA-II (i.e., mutation is applied to the selected offspring in NSGA-II).

In the same manner as in Section 4, we apply NSGA-II with the distance-based crossover to our test problems. We examine the following parameter specifications: D = 1, 2, 3, 4, 5, 10, 15, 20. Experimental results are summarized in Fig. 4.

In Fig. 4 (a), the best results with respect to the hypervolume for the reference point (0, 0, ..., 0) are obtained when the parent-offspring distance is specified as 1 or 2. That is, the best results are obtained when different genes in one or two loci are exchanged between two parents. However, the distance-based crossover operator with such a parameter specification severely degrades the hypervolume for the reference point (15000, 15000, ..., 15000) in Fig. 4 (b). The hypervolume for this reference point for the 8-500 and 10-500 problems are clearly improved when the parent-offspring distance is specified as 10 or 15 in Fig. 4 (b). From Fig. 4 (c), we can see that 10 and 15 are much smaller than the average parent-parent distance.



Fig. 4. Distance-based crossover with the parent-offspring distance D

One may notice that the average parent-offspring distance in Fig. 4 (d) for the 2-500 problem is much smaller than D when D is large. This is because the standard uniform crossover is used when $H(P_1, P_2) < 2D$ (i.e., see Fig. 4 (c) for $H(P_1, P_2)$).

Experimental results in Section 4 and Section 5 are summarized in Table 1 and Table 2 where the best average result by each scheme for each test problem is shown together with the standard deviation and the best parameter value in parentheses. The best result over the three schemes is highlighted by bold for each test problem. From Table 1 and Table 2, we can see that the similar parent recombination does not work well on the 6-500, 8-500 and 10-500 problems whereas it works well on the 2-500 and 4-500 problems. This is because a pair of similar parents is not actually selected (since all solutions in a population are not similar to each other in many-objective optimization). For example, in Fig. 1 (c), the average parent-parent distance is larger than 10 even when the most similar parent is selected from 50 candidates (i.e., $\beta = 50$) for the 10-500 problem. We can also see that the best specification of the parent-offspring distance *D* is surprisingly small in the last column of Table 1.

Table 1. Experimental results for the normalized average hypervolume for the reference point (0, 0, ..., 0). The best result by each scheme is shown for each test problem.

Problem	Similar Parent (SD) (β)	Probability (SD) (α_u)	Distance-Based (SD) (D)
2-500	102.3 (0.4) (20)	100.9 (0.4) (0.03)	101.6 (0.5) (1)
4-500	106.4 (0.9) (20)	104.8 (0.8) (0.02)	106.4 (0.8) (2)
6-500	108.5 (1.0) (20)	109.6 (1.0) (0.02)	112.1 (1.1) (2)
8-500	108.4 (1.5) (20)	113.4 (1.3) (0.02)	116.1 (1.2) (2)
10-500	108.2 (2.1) (20)	116.7 (1.6) (0.02)	119.7 (1.8) (2)

Table 2. Experimental results for the normalized average hypervolume for the reference point (15000, 15000, ..., 15000). The best result by each scheme is shown for each test problem.

Problem	Similar Parent (SD) (β)	Probability (SD) (α_u)	Distance-Based (SD) (D)
2-500	107.4 (1.2) (20)	102.8 (1.4) (0.03)	104.7 (1.5) (1)
4-500	112.9 (4.7) (10)	102.2 (5.1) (0.05)	106.1 (4.9) (3)
6-500	103.0 (14.9) (5)	107.2 (14.3) (0.10)	109.6 (12.5) (5)
8-500	99.5 (31.6) (5)	116.1 (21.9) (0.10)	115.7 (24.8) (15)
10-500	109.9 (50.9) (5)	124.3 (34.1) (0.15)	122.6 (36.6) (15)

6 Conclusions

In this paper, we examined the existing two schemes (i.e., the recombination of similar parents and the exchange of only a small number of genes) for improving the performance of EMO algorithm on multi-objective knapsack problems. For further discussing their effects, we also implemented a distance-based crossover where the distance from an offspring to its closer parent was specified in uniform crossover as a user-defined parameter. The performance of NSGA-II with each scheme was evaluated using the hypervolume values for two reference points. One is far from and the other is close to the Pareto front. For the reference point far from the Pareto front, good results were obtained for all test problems with 2-10 objectives when the parent-offspring distance was very small (i.e., their Hamming distance was 1 for the 2-500 problem and 2 for the other problems). In this case, the diversity of solutions was very large. However, the convergence of solutions was severely deteriorated for many-objective problems. For the reference point close to the Pareto front, good results were obtained for many-objective knapsack problems with 8 and 10 objective when the parent-offspring distance was about 10-15.

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