LETTER

Improving Proximity and Diversity in Multiobjective Evolutionary Algorithms*

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SUMMARY This paper presents an approach for improving proximity and diversity in multiobjective evolutionary algorithms (MOEAs). The idea is to discover new nondominated solutions in the promising area of search space. It can be achieved by applying mutation only to the most converged and the least crowded individuals. In other words, the proximity and diversity can be improved because new nondominated solutions are found in the vicinity of the individuals highly converged and less crowded. Empirical results on multiobjective knapsack problems (MKPs) demonstrate that the proposed approach discovers a set of nondominated solutions much closer to the global Pareto front while maintaining a better distribution of the solutions.

key words: evolutionary algorithms, multiobjective optimization, nondominated solutions, proximity, diversity, mutation

1. Introduction

Simultaneous optimization of several incommensurable objectives, known as multiobjective optimization, is a major issue in most real-world problems [1], [2]. The objectives conflict with each other since no objective can be improved without compromising the others. Such interdependence leads to a set of alternative, nondominated solutions that cannot be ordered in any natural way [2]. The image of these solutions in the feasible objective space is known as a Pareto (optimal) front. The goal of multiobjective optimization is to discover a set of nondominated solutions closer to the global Pareto front (i.e., higher proximity) while distributing the solutions as uniformly as possible (i.e., better diversity).

Multiobjective evolutionary algorithms (MOEAs) have been perceived to be effective in solving multiobjective optimization problems (MOPs) due to their ability to search for multiple solutions in parallel as well as handle complex features of problems [1]. Most MOEAs have attempted to incorporate elitism and utilize the knowledge about domination and density of individuals. Strength Pareto evolutionary algorithm (SPEA) [2] was developed by employing the elitism with an external population. Its enhanced version, SPEA2 [3], was followed by employing a fine-grained fitness assignment and an archive truncation technique. Non-dominated sorting genetic algorithm (NSGA) [4] was devised by incorporating the nondominated sorting with a niching method. NSGA-II [5] improved upon the previous algorithm by complementing its critical drawbacks such as high computational complexity, lack of elitism, and need of sharing parameters. Rank-density-based genetic algorithm (RDGA) [6] was developed by transforming a multiobjective optimization problem into a biobjective optimization task over the rank-density domain. Although the existing approaches have reported acceptable proximity and diversity, harder problems generally demand more ingenious techniques for discovering better solutions. Thus, this paper presents an efficient approach for improving the proximity and diversity performances in MOEAs.

2. Proposed Approach

2.1 Improving Proximity

In general, elitism plays an important role in drawing the solutions closer to the global Pareto front. A number of MOEAs testified to its availability [2]–[8]. In relation to this, a selection criterion inspired by the elitism is suggested for choosing the most converged individuals from the nondominated set. Proximity can be improved if the chosen candidates act as a wellspring of new nondominated solutions. Note that convex problems are considered in this study. Assume that their objective functions (to be maximized, with or without loss of generality) have nonnegative values. The proposed criterion, called effective quality of solutions (eQoS), for selecting such candidates is defined as the (Euclidean) distance from an individual to a reference in the objective space. Formally, eQoS of the ith nondominated individual, denoted by qi, is defined as follows:

\[ q_i = d_E(f_i, f_{ref}) = \sqrt{\sum_{j=1}^{n}(f_{i,j} - f_{ref,j})^2} \]  

where \( f_{i,j} \) and \( f_{ref,j} \) are the jth objective value of the ith individual and the jth objective value of the reference respectively, and n is the number of objectives. The boundary solutions ** or the origin in the objective space can be taken as the reference for computing eQoS.

**The individuals whose one of the objectives exhibits the best value come under the boundary solutions. Note that \( f_{ref,j} \) is the worst value of the jth objective among them.
Since eQoS is able to effectively indicate which individuals are better among the nondominated solutions, it gives a chance to select the most converged solutions in a wide range of the Pareto front. To this end, the nondominated individuals are first sorted in descending order of their eQoS values. The best \( \tau_1 \cdot N \) nondominated individuals are then chosen. Here, \( N \) denotes the population size and \( \tau_1 \) directly controls the number of selected individuals. When new nondominated offspring are generated in the neighborhood of those selected individuals, the proximity might well increase. However, the probability that such an event occurs is very low because the creation of offspring primarily resorts to crossover in most MOEAs. Although the crossover operator contributes to the exploration of search space, an adverse effect is often invited when it comes to mixing the highly-converged, dissimilar individuals due to the destruction of desirable characteristics. In relation to this, mutation would be a better source for creating new offspring. Further details are described in Sect. 2.3.

2.2 Improving Diversity

Recent MOEAs have achieved a good spread of nondominated solutions by means of dynamic, nonparametric crowding methods [3, 5–8]. They tried to rapidly estimate the density information of solutions that surround a particular solution. In NSGA-II [5], the normalized distance of the two nearest neighbors, called crowding distance, has been used as a selection criterion. The crowding distance of the \( i \)th individual is given as the normalized distance between \((i - 1)\)th and \((i + 1)\)th individuals. But the crowding distance only resorts to the local information of each individual. Thus, a new criterion that utilizes both the local and the global information is needed for extracting the least crowded individuals. We define the least crowding concept as the absence of other individuals within a certain area. More specifically, the least crowded individuals can be identified by comparing the crowding distances of individuals with the (threshold) value of \( \epsilon \). In other words, the \( i \)th individual is chosen as one of the least crowded individuals if its crowding distance, denoted by \( d_i \), is greater than \( \epsilon \). Although there might be many different ways to determine the value of \( \epsilon \), it is advisable to utilize the global information collected from the nondominated solutions. The average and the deviation of crowding distances can be available in this regard. The average (crowding) distance is computed by

\[
\mu_d = \frac{1}{|F_1|} \sum_{i=1}^{|F_1|} d_i,
\]

where \( |F_1| \) denotes the first Pareto front (i.e., nondominated front), \( |F_2| \) is the number of nondominated solutions, and \( d_i \) is the crowding distance of the \( i \)th individual. The standard deviation, denoted by \( \sigma_d \), physically indicates the statistical spread of the distance values between neighbors. Thus, the rule for deciding \( \epsilon \) is given by

\[
\epsilon = \mu_d + \lambda \cdot \sigma_d
\]

where \( \lambda \) adjusts the least crowding density by which the number of selected individuals is decided.

In the (offspring) generation phase, the individuals whose crowding distances are greater than \( \epsilon \) are chosen. To emphasize more least crowded individuals, under the condition that \( d_i > \mu_d + \sigma_d \), the selection is performed as follows: if \( d_i \leq \mu_d + 2\sigma_d \), then a single copy (of the \( i \)th individual) is chosen; if \( d_i > \mu_d + 2\sigma_d \), then two copies are selected. Here, the number of selected individuals should not exceed \( \tau_2 \cdot N \). In order to achieve better diversity, new (nondominated) offspring must be created near to the least crowded solutions. If crossover is applied to the chosen individuals, there is a high probability of producing offspring which are far away from their parents. It does not necessarily result in diversity preservation. As a result, mutation would better serve to traverse the surroundings of the chosen individuals. More details are explained in Sect. 2.3.

2.3 Fitting into the Framework of MOEAs

There have been a number of efforts to reinforce platitude (genetic) operators. Examples include the adaptive elitist-population method and the similarity-based mating scheme. From this aspect, the efficient strategies for choosing the most promising individuals have been developed in Sects. 2.1 and 2.2. However, a bridge between those mechanisms and the MOEA framework is still necessary. This task is very straightforward since the directions given in [5] can be simply employed. The reason for choosing NSGA-II as the basic framework is due to its general and representative nature. In this regard, the proposed algorithm, called “modified NSGA-II” (mNSGA-II), is described in Algorithm 1.

Note that the proposed algorithm has the unique features as follows: the rearrangement of nondominated solutions, the selection of the most probable individuals, and the creation of new nondominated offspring (near to the chosen parents). To begin with, the best \( N \) individuals are selected by the usual way as in [5] by which representative solutions highly converged and uniformly distributed are maintained (see Step 6). The best \( \tau_1 \cdot N \) individuals in terms of proximity are then selected, which emphasizes the most converged solutions for the global front (see Step 8). Also, \( \tau_2 \cdot N \) individuals with regard to diversity are selected for stressing the least crowded solutions (see Step 10). In order to discover better solutions (i.e., offspring), mutation is then applied to the chosen individuals without performing crossover (see Steps 9 and 11). At this juncture, any cost-effective local search can be employed; for instance, as regards the feasible solutions, the bit of “0” is flipped over unless it violates any constraint. Further details, however, are beyond the scope of this paper. Although the trade-off relation ex-

\[1\] In the field of EAs, they are known as “building-blocks.”

\[††\] The reason for considering only the two cases is because \( P(d_i > \mu_d + 2\sigma_d) \) is very small if the crowding distance follows a Gaussian distribution.

\[†††\] Different MOEAs can be employed as the basic frameworks, but this issue is beyond the scope of this paper.
The problem is generally specified by a set of items, weights and profits such that the total weight satisfies the given capacity. Multiobjective knapsack problems (MKPs) known to be NP-hard are regarded as a promising test benchmark to evaluate the performance of MOEAs [2], [3], [9]. The aim of MKPs is to find a subset of items, which maximizes the total profit such that the total weight satisfies the given capacity. The problem is generally specified by a set of items, weights and profits of items, and the upper bounds of capacities: \( p_{ij} \) is the profit of the \( j \)th item in the \( i \)th knapsack, \( w_{ij} \) is the weight of the \( j \)th item in the \( i \)th knapsack, \( c_i \) is the capacity of the \( i \)th knapsack.

Let us consider \( l \) variables and \( n \) objectives. Formally, the task of (convex) MKPs is to discover \( x = (x_1, x_2, \cdots, x_l) \in [0, 1]^l \) so as to

\[
\text{maximize } f(x) = (f_1(x), f_2(x), \cdots, f_n(x))
\]

subject to \( \sum_{j=1}^{l} w_{ij} x_j \leq c_i \)  

where each objective function is defined as \( f_i(x) = \sum_{j=1}^{l} p_{ij} x_j \). Uncorrelated profits and weights were used in the experiments; \( p_{ij} \) and \( w_{ij} \) are random integers in the interval [10, 100]. The knapsack capacities are set to half the total weight of the respective knapsack, i.e., \( c_i = 0.5 \sum_{j=1}^{l} w_{ij} \).

To evaluate the quality of nondominated solutions, we employ two performance measures: proximity metric [7] and diversity metric [1], [8]. The proximity metric measures the extent of convergence of the nondominated solutions to the global Pareto front. A smaller value always denotes a higher proximity. The diversity metric measures the distribution of the nondominated solutions. It is able to simultaneously measure the uniformity and the spread of nondominated solutions. A smaller value indicates a better diversity. Meanwhile, there is coverage metric [1], [2]. It directly compares two algorithms by checking the dominance relationship between their nondominated sets. Note that \( C(A, B) = 1 \) if all the nondominated solutions of Algorithm B are dominated by those of Algorithm A; meanwhile, \( C(A, B) = 0 \) for the opposite case.

### 3.2 Experimental Results

Two knapsacks with 250 items and 500 items are chosen as test instances. Moreover, three knapsacks with 100 items and 250 items are considered for higher dimensional tests. The problems are denoted as \( f_{MKP}(X,Y) \) for short, in which \( X \) and \( Y \) are the number of knapsacks and the number of items, respectively. The test data sets used in [2] are employed in the experiments.\(^1\)

The goal of this study is to investigate the effect of the proposed approach on the proximity and diversity of nondominated solutions. It is natural to take NSGA-II as a comparative reference since NSGA-II has been utilized as an underlying framework (see Sect. 2.3). All the algorithms employ pair-wise tournament selection (i.e., the size of the tournament is 2), two-point crossover (with the probability of 1.0), and bit-wise mutation (with the probability of 1/\( l \) where \( l \) is the number of items). The population size \( N \) is set to 100 for all test cases. The allowable number of generations is 500 for \( f_{MKP}(2,250) \), 1000 for \( f_{MKP}(2,500) \), 200 for \( f_{MKP}(3,100) \), and 500 for \( f_{MKP}(3,250) \). Furthermore, the parameters \( \tau_1 \) and \( \tau_2 \) of mNSGA-II are equally set to 0.1.\(^2\) All the results are averaged over 30 runs.

Figure 1 compares the nondominated solutions obtained by NSGA-II and mNSGA-II as applied to a set of MKPs. It is clearly seen that the proximity and the diversity achieved by mNSGA-II are better than those of NSGA-II. The reason is that a number of offspring are generated in the neighborhood of the most converged and the least crowded solutions. In other words, it promotes local search (i.e., mutation) around the highly promising regions, thereby favorably affecting not only the proximity but also the diversity. Table 1 supports the claim that the proposed algorithm improves the proximity and diversity performances in the two dimensional cases. Unfortunately, it is hard to quantify the proximity and the diversity as regards the three dimensional

\(^1\)The test sets can be downloaded from an online server: \url{http://www.tik.ee.ethz.ch/~zitzler/testdata.html}

\(^2\)Although the setting may not be the best, it has been found in the sense of achieving acceptable performances.
Empirical results on the multiobjective knapsack problems have verified that the proposed approach achieves higher proximity and better diversity of nondominated solutions.

There are several paths for future work. Although the proposed approach has exhibited certain advantages over the existing methods, more research on the problems of four or more objectives needs to be carried out. Furthermore, the proposed approach should be tried on other problems (e.g., nonconvex or real-valued problems) for buttressing the claim on its effectiveness.

4. Conclusion

In this paper, we have presented an efficient approach for improving the proximity and diversity performances of multiobjective evolutionary algorithms (MOEAs). The idea was to judiciously manage the most converged and the least crowded solutions as a source of new nondominated offspring. To this end, mutation has only applied to those promising solutions without performing crossover, thereby obtaining a better population in the subsequent generation.

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