

Improving Uniformity of Solution Spacing in Biobjective Evolution

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ABSTRACT

We introduce a new synergistic combination of features, some of which have previously been used individually but not together, to improve uniformity of spacing in evolved non-dominated sets, especially in biobjective problems. On five standard biobjective benchmark tests, these features are shown to enhance performance in distinct and complementary ways.

Categories and Subject Descriptors

G.1.6 [Numerical Analysis]: Optimization – *global optimization*.

Keywords

multiobjective; differential evolution; crowding; uniform spacing.

1. INTRODUCTION

Various methods have been proposed to preserve diversity in non-dominated sets during multiobjective evolution [e.g., 2; 3; 4]. However, when we applied existing methods to a real-valued biobjective problem in watershed management planning [1], we found unacceptable irregularities in solution spacing in this real-world application where stakeholders need to carefully consider the trade-offs between the competing objectives of minimizing cost and minimizing contaminant transport. This motivated us to develop a new version of multiobjective differential evolution that improves the uniformity of solution spacing in the non-dominated front.

2. METHODS

Our method, referred to as USMDE (Uniform Spacing Multiobjective Differential Evolution), comprises a new synergistic combination of features, some of which have been used individually in other methods, along with a newly modified crowding metric designed to explicitly reward for uniformity of spacing in M objectives. The details of this method are fully described in [1] and summarized here. We initialize the population of size N using Latin hypercube sampling, in addition to seeding with extremal solutions. For child creation we use classic differential evolution (DE), known as DE/rand/1/bin, with DE bounce-back [5] and immediately replace dominated solutions to increase selection pressure, as in [6]. Each child in USMDE is created from three randomly selected solution vectors. If all three vectors have equal rank, USMDE chooses the least crowded to be used as the “target” (Parent) vector (we refer to this feature as **P**), using the crowding metric from [2]. This metric penalizes solutions based on their proximity, so including this in parent selection promotes exploration in under-represented areas of the

non-dominated front, similar to the approach to parent selection used in the popular multiobjective genetic algorithm NSGA-II [2]. Otherwise, if two of the vectors have equal rank they are chosen to be the difference vectors for DE mutation, following [3]. In NSGA-II [2], the new generation is created by including all solutions from the least dominated ranks that fit in the new population, and then including as many of the least crowded solutions from the next available rank as needed to achieve population size N . Since crowding is not re-evaluated during this selection process, this can lead to large gaps and ultimately contribute to non-uniformly spaced solutions in the final non-dominated set. In contrast, USMDE prunes out the most-crowded solutions from that same next available rank, but one at a time with immediate **Re**-evaluation of crowding for those solutions that had been adjacent to the most recently pruned solution, until the population size has been reduced back to N (we refer to this feature as **R**). Implementing this with a heap adds $O(M \log N)$ time over pruning without re-evaluation, but does not increase the overall time complexity of the algorithm. For this crowding-based survivor selection, we use a new crowding metric:

$$US_crowding_distance = \sum_{i=1}^M (dist_{1,i}^2 + dist_{1,i} \times dist_{2,i}) \quad (1)$$

where $dist_{1,i}$ and $dist_{2,i}$ are the distances in the i^{th} normalized objective between the solution and its first and second closest neighbors in that objective, respectively. Uniform spacing is achieved when equation (1) is maximized (we refer to the use of $US_crowding_distance$ in survivor selection, as opposed to using the crowding metric of [2] in survivor selection, as **U**).

To demonstrate the synergy of these features, we tested USMDE with and without each of the three features **R**, **P**, and **U**, on five commonly used real-valued biobjective problems: ZDT1 (convex), ZDT2 (concave), ZDT3 (discontinuous), ZDT4 (multimodal), and ZDT6 (nonuniform), corresponding to functions T_1 - T_4 , and T_6 described in [7], using the same parameter settings as in [4] and performing repetitions of each method on the same 50 random initializations for each problem. Four different performance metrics were applied to the resulting non-dominated sets. We assessed uniformity of spacing along the non-dominated front using an improved spacing metric, MST-spacing, which is the standard deviation of all the Euclidean distances along edges in a minimum spanning tree of the graph connecting all non-dominated solutions in the M dimensions. We assessed convergence using generational distance, coverage using inverted generational distance, and spread error with the absolute value of the difference between the maximum spread of the non-dominated solutions and the maximum spread of the true Pareto front, as in [3; 7]. Results of paired replicates were compared using one-tailed paired t -tests.

3. RESULTS

Complete numerical results can be found in Appendix C of [1], and are summarized here. The means and standard deviations of convergence and spread error of successful trials were very close to zero for all methods on all five benchmark problems, with no significant differences between the means resulting from USMDE with or without **R**, **P**, or **U**, indicating that these features do not impact the ability of the differential evolution to accurately find the optimal front. However, including the feature **R** dramatically improved both MST-spacing (Fig. 1, $p < 1e-42$) and coverage ($p < 1e-35$) in all five biobjective benchmark problems. (We also note that including **R** improved MST-spacing and coverage in three 3D benchmarks tested, although only two of these were statistically significant; see Appendix C of [1] for details).

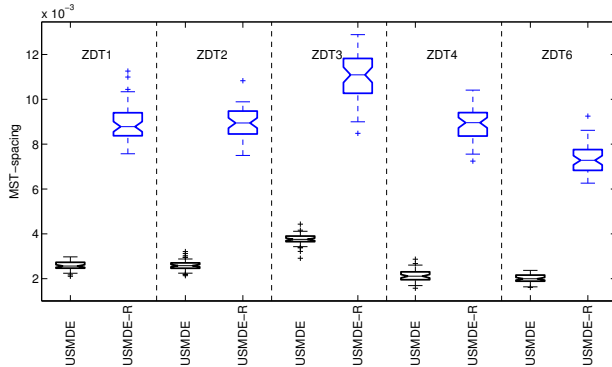


Figure 1. Box plots of MST-spacing from 50 random paired trials of five biobjective problems comparing USMDE to USMDE without R (USMDE-R).

Surprisingly, while excluding either **P** or **U** individually did degrade MST-spacing, these degradations were not statistically significant. However, we found that including both **P** and **U** together prevented occasional pathological collapse of the concave non-dominated front in ZDT2 (which collapsed to a single point in 3 trials without **P** and 2 trials without **U**). The use of **P** helps to counteract this tendency by forcing more intense exploration of the sparser areas, whereas **U** helps to avoid this collapse by explicitly penalizing non-uniformity of spacing rather than just penalizing for gaps. We ran additional tests (not otherwise reported here) without any of **R**, **P**, or **U**, and found that, in general, the relative ordering of these USMDE variants was, from best to worst in terms of MST-spacing: (i) USMDE, (ii) USMDE without **P**, (iii) USMDE without **U**, (iv) USMDE without **R**, **P**, or **U**, and (v) USMDE without **R**. This non-linear ordering suggests there are synergistic interaction effects between **R**, **P**, and **U**.

While we had independently identified the need for **R**, further literature review revealed a similar method had been added to improve GDE3 and was shown to yield better spacing than either NSGA-II or SPEA2 on the same five benchmark problems [5]. Thus, we ran additional tests to compare USMDE to GDE with **R** (downloaded from <http://jmetalcpp.sourceforge.net/>). USMDE showed significantly improved MST-spacing relative to GDE3 for all five biobjective benchmarks ($p < 3e-8$) (and also one of three triobjective benchmarks $p < 3e-3$), indicating that the combination of **R**, **P**, and **U** in USMDE resulted in more uniform spacing than the use of just **R** (but not **P** or **U**) in GDE3. Results of USMDE were not significantly different than GDE3 for convergence or spread (see Appendix C of [1] for details).

Applying USMDE to the watershed application that motivated this study was found to improve MST-spacing by 31%, relative to USMDE without **R**, **P**, or **U**, with a marked increase in uniformity of spacing in the important region near the “knee” of the non-dominated front [1], where stakeholders are most likely to focus.

4. DISCUSSION AND CONCLUSIONS

USMDE uses three complementary features, not previously used together, that synergistically improve uniform spacing of solutions along the non-dominated front: (i) re-evaluation of crowding distance as each solution is pruned during survivor selection (**R**), (ii) use of crowding distance during parent selection (**P**), and (iii) use of a new crowding distance formula that penalizes off-center solutions during survivor selection (**U**). This combination of features was shown to improve uniformity of spacing in all problems tested and to prevent collapse of the non-dominated set in a concave problem. While we did find one prior use of **R** [4] (but in the absence of **P** or **U**), the importance of this feature on uniformity of solution spacing appears to be underappreciated in the evolutionary computation community and has not been incorporated into popular packages such as NSGA-II [2].

5. ACKNOWLEDGMENTS

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