Incorporating Distance Domination in Multiobjective Evolutionary Algorithm

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Abstract. In this article we propose a novel distance domination parameter and describe a multiobjective evolutionary concept called distance domination based multiobjective evolutionary algorithm (DBMEA). The distance parameter drives the algorithm faster in approximating the Pareto optimal front. To ensure proper diversity in the solutions of the non-dominating set, a new method for incorporating diversity is explained. The DBMEA has been compared with the NSGA-II algorithm on different test functions using different performance measures.

1 Introduction

In this article, a new evolutionary multiobjective optimization (MOO) algorithm called “Distance-domination Based Multiobjective Evolutionary Algorithm (DBMEA)” is proposed. DBMEA uses the concept of distance domination parameter which refines the fitness function and helps in better convergence to the true Pareto-front. It incorporates non-dominated sorting and crowded-tournament selection as in NSGA-II [1]. The diversity parameter used here is also novel. DBMEA incorporates the concept of elitism, using archive concept as in SPEA-2 [2]. Comparative results of DBMEA and NSGA-II are provided for different standard test functions in terms of four performance measures.

2 Basic Principles

A general minimization problem of M objectives can be mathematically stated as:

- Minimize : $f(x) = [f_i(x), i = 1, \dots, M]$, subject to :
 $g_j(x) \leq 0$, $j = 1, 2, \dots, J$, and
 $h_k(x) = 0$, $k = 1, 2, \dots, K$, where $f_i(x)$ is the i^{th} objective function, $g_j(x)$ is the j^{th} inequality constraint, and $h_k(x)$ is the k^{th} equality constraint.

The MOO problem then reduces to finding x such that $f(x)$ is optimized. A solution is said to dominate another solution if it is not worse than that solution in all the objectives and is strictly better than that in at least one objective. The solutions over the entire solution space that are not dominated by any other solution are called *Pareto-optimal solutions*.

3 Distance-Domination Based Multiobjective Evolutionary Algorithm (DBMEA)

The basic structure of DBMEA is given in **Algorithm 1**. Different steps are described below in brief.

As is normally done, the parameters of the search space in DBMEA are encoded as string like structures called *chromosomes*. A *fitness* value is assigned to each chromosome that denotes the degree of goodness of the encoded solution. The fitness F_i of the i^{th} chromosome is computed as:

$$F_i = f_{ri} + f_{di} \quad (1)$$

where f_{ri} is the rank parameter as defined in [1] and f_{di} is the distance domination parameter proposed in this article.

- **Rank Parameter (f_{ri}):** The parameter f_{ri} is a measure of a solution's non-dominance. For computing f_{ri} , non-dominated sorting [1] is used to first determine the non-dominated fronts. f_{ri} is then set equal to the front number where i^{th} solution appears [1].
- **Distance Domination Parameter (f_{di}):** This new parameter is calculated as the normalized Euclidean distance of a dominated solution from its nearest non-dominated solution on the first front. The significance of this parameter is to give higher priority to those dominated solutions, that are closer to their dominating solution on the first front. As an example considering two functions minimization in Figure 1(a), the solutions 'g', 'h' and 'j' are dominated by solution 'c' on the first front. Normally, 'g', 'h' and 'j' would have the same status. However, it can be observed that 'h' is much closer to the first front. It is our intuition that 'h' should get higher priority over 'g' and 'j'. The parameter f_{di} (= 'd1' for 'g', 'd2' for 'h' and 'd3' for 'j') takes care of this fact.

The *elitism* concept in DBMEA is similar to that in SPEA-2 [2]. An *archive* of fixed size (equal to the size of the population, N) is maintained, that gets updated at each iteration. After computation of the fitness archive is first filled by non-dominated solutions of the current archive and population, followed by the best (in terms of F_i s) remaining solutions till the archive is full. In case of archive overflow at any stage, the density parameter d_i is used to truncate the archive. The parameter (d_i) (which is similar to crowded-distance [1], with some modification) is computed as the distance of each solution to its immediate next neighbour summed over each of the M objectives. For example in Figure 1(b), 'd1' and 'd2' correspond to the distances along f_1 for solutions 'e' and 'f' respectively. Similarly 'd4' and 'd3' correspond to the distance along f_2 for solutions 'c' and 'b' respectively.

After the fitness assignment, DBMEA uses *density-based binary tournament selection* on the archive to create the mating pool. This concept is inspired by the *crowded-tournament selection* [1], where crowded-distance has been used in order to overcome the tie in fitness values. Here if we get the solutions with the same F_i values, then we consider d_i and prefer the less crowded solution. The DBMEA uses *single-point crossover* and *bit-wise mutation* operation.

Algorithm 1. $O_f = \text{DBMEA}(P_t, A_t, N, C)$ /* P_t : population at iteration t , A_t : archive at iteration t , N : size of the population and archive, C : maximum number of iterations. O_f : the final output */

1. $t = 0$, randomly initialize P_0 and compute the objectives, $A_0 = \Phi$.
 2. non-dominated sorting on $P_t \cup A_t$.
 3. $\forall i, i \in \{P_t \cup A_t\}$, calculate f_{ri} , f_{di} and d_i .
 $F_i = f_{ri} + f_{di}$
 4. $A_{t+1} \leftarrow$ non-dominated solutions from $P_t \cup A_t$
 - if $\{|A_{t+1}|\} > N$, truncate A_{t+1} to size N using d_i
 - if $\{|A_{t+1}|\} < N$, copy $\{N - |A_{t+1}|\}$ dominated solutions from $P_t \cup A_t$ to A_{t+1} .
 5. If $t \geq C$ or other terminating condition is fulfilled, $O_f \leftarrow A_{t+1}$ and stop.
 6. Genetic Operations:
 - Density-based binary tournament selection on A_{t+1} to get the mating pool.
 - Single-point crossover and bitwise mutation performed on mating pool to get P_{t+1} , compute objectives of P_{t+1} .
- $t \leftarrow t + 1$; goto (2).
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Fig.1. (a): f_{di} parameter (b): diversity parameter

4 Simulation Study

DBMEA and NSGA-II have been compared on ten standard test problems. All the test problems studied in the present article involve minimization of the functions. Though the test problems have real domain, the binary encoded implementation of the algorithms (thus discretizing the domain, in practice) have been studied. The parameters used in these experiments are: *population size: 100, number of iterations: 250, crossover-probability: 0.9, mutation probability: inversely proportional to the chromosome length, chromosome-length: 10 bits per*

variable. Ten runs of the algorithms were executed on each test problem, the mean and variance of the performance measures over these runs are reported.

Test Problems and Performance Measures

The set of test problems used in this article includes SCH1 and SCH2 [3], FON [4], KUR [5], POL [6], ZDT1, ZDT2, ZDT3, ZDT4 and ZDT6 [7]. The performance of DBMEA and NSGA-II is compared with respect to four performance measures: the convergence measure $\mathcal{V}$ [1], diversity measure Δ [1], purity value [8] and minimal-spacing [8]. The larger value of the purity measure and the smaller values of $\mathcal{V}$, Δ and minimal spacing parameters signify the better performance. The details of the measures may be found in the respective references.

Results

Tables 1 and 2 represent the convergence measure and diversity measure, and the purity and minimal spacing measure respectively.

Table 1. Convergence and Diversity measure

Convergence Measure $\mathcal{V}$								
Algorithm	SCH1	SCH2	FON	ZDT1	ZDT2	ZDT3	ZDT4	ZDT6
NSGA-II(Mean)	0.0144	0.0235	0.0032	0.0036	0.0027	0.0023	2.7681	0.0192
(Variance)	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.2939	0.0015
DBMEA(Mean)	0.0132	0.0167	0.0012	0.0050	0.0030	0.0033	1.2338	0.0048
(Variance)	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	1.2069	0.0000
Diversity Measure Δ								
Algorithm	SCH1	SCH2	FON	ZDT1	ZDT2	ZDT3	ZDT4	ZDT6
NSGA-II(Mean)	0.5763	1.4845	0.7713	0.9053	0.8322	0.7037	0.9474	0.9493
(Variance)	0.0068	0.0499	0.0004	0.0067	0.0059	0.0025	0.0011	0.0011
DBMEA (Mean)	0.3639	1.2623	0.7408	0.5758	0.3903	0.7304	0.8075	0.8188
(Variance)	0.0291	0.0795	0.0001	0.0573	0.0014	0.0072	0.0134	0.0023

Table 2. Purity and Minimal Spacing measure

Test Function	NSGA-II				DBMEA			
	Purity		Minimal Spacing		Purity		Minimal Spacing	
	Mean	Variance	Mean	Variance	Mean	Variance	Mean	Variance
SCH1	0.672	0.0639	0.0104	0.00	0.826	0.0528	0.0044	0.00
SCH2	0.808	0.0107	0.0524	0.00	0.818	0.0213	0.0497	0.00
KUR	0.811	0.0055	0.0897	0.00	0.943	0.0008	0.0877	0.00
POL	0.646	0.0465	0.0705	0.00	0.756	0.0403	0.0699	0.00
FON	0.680	0.0018	0.0084	0.00	0.944	0.0004	0.0005	0.00
ZDT1	0.989	0.0003	0.0113	0.00	0.397	0.0577	0.0069	0.00
ZDT2	0.998	0.0004	0.0142	0.00	0.187	0.0116	0.0114	0.00
ZDT3	0.957	0.0080	0.0358	0.00	0.410	0.0233	0.0369	0.00
ZDT4	0.200	0.1778	0.0164	0.00	0.800	0.1778	0.0064	0.00
ZDT6	1.000	0.0000	0.0146	0.00	1.000	0.0000	0.0087	0.00

Fig. 2. Final Pareto-fronts of (a): DBMEA and (b): NSGA-II on KUR

Fig. 3. Final Pareto-fronts of (a): DBMEA and (b): NSGA-II on ZDT4

As can be seen from Table 1, DBMEA has better convergence on test problems SCH1, SCH2, FON, ZDT4 and ZDT6, whereas NSGA-II has better convergence on functions ZDT1, ZDT2 and ZDT3. However it is interesting to note that except for ZDT3, DBMEA provides a better value of the diversity measure Δ for all other test problems. Again from Table 2, it is evident that DBMEA has better purity value for the test functions SCH1, SCH2, KUR, POL, FON, ZDT4 and ZDT6 compared to NSGA-II. The minimal spacing parameter shows that DBMEA has attained better spread of the solutions on the front for all test functions except ZDT3. Figures 2 and 3 show the final non-dominated fronts obtained by DBMEA and NSGA-II for two of the test functions (results for the others were almost similar). The better performance of DBMEA in terms of convergence and diversity is quite evident from Figure 3. In Figure 2, DBMEA is able to obtain the disjoint Pareto-optimal point ‘o’ at (-20,0) and the third disconnected component ‘c’ of the front, while NSGA-II fails to do that properly. From the results it can be concluded that DBMEA has comparable results with, often better than, NSGA-II in terms of the convergence to the Pareto-optimal front. In terms of the attainment of diversity on the Pareto-optimal front DBMEA is generally better than NSGA-II.

5 Discussion and Conclusions

In the present article, we have introduced a novel concept of measuring fitness function in MOEA by introducing a distance domination factor. A new way of computing density reflecting the diversity is explained that has resulted in much better spread of the solutions on the Pareto-optimal front. The MOEA based on this concept is not only good in approximating Pareto-optimal front, but also performs better in terms of diversity of the solutions on the front. Though the experiments done in this article have considered a good number of test problems with varying characteristics, a theoretical study dealing with the generalised performance of DBMEA is currently under investigation. It may be noted that the notion of distance domination is a general concept that can be used in other MOO algorithms also.

Acknowledgements. The present work has been partially supported by INSA funded project *No.BS/YSP/36/886*.

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