Enhanced Distribution and Exploration for Multiobjective Evolutionary Algorithms

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Abstract- The main objectives of multiobjective evolutionary algorithms are to minimize the distance between the solution set and true Pareto front, to distribute the solutions evenly and to maximize the spread of solution set. This paper addresses these issues by presenting two features that enhance the ability of multiobjective evolutionary algorithms. The first feature is a variant of the mutation operator that adapts the mutation rate along the evolution process to maintain a balance between the introduction of diversity and local fine-tuning. In addition, this adaptive mutation operator adopts a new approach to strike a compromise between the preservation and disruption of genetic information. The second feature is a novel enhanced exploration strategy that encourages the exploration towards less populated areas and hence achieves better discovery of gaps in the generated front. This strategy also preserves non-dominated solutions in the evolving population and hence gives good convergence. Comparative studies show that the proposed features are effective.

1 Introduction

Evolutionary algorithms have been recognized to be well suited for multi-objective optimization problems due to their inherent parallelism and their capability to evolve a family of solutions at multiple points along the Pareto optimal frontier simultaneously and efficiently. Many techniques, taking advantage of evolutionary algorithm's capacity to obtain the approximate Pareto Front, had been proposed with varying success (Corne et al, 2000; Deb et al, 2002; Knowles and Corne, 2000; Tan et al, 2001, 2003; Zitzler et al, 2001). The main differences among existing multi-objective evolutionary algorithms are in fitness assignment and diversity maintenance.

The performance of MOEAs is greatly affected by their parameters. Evolutionary algorithms are intrinsically dynamic and adaptive. The adaptation of parameters during the runtime is more consistent to the general evolutionary idea and has shown better performances over constant parameters (Bäck, 1993, 1996; Fogarty, 1989; Ochoa, 1999; Thierens, 2002). Eiben et al. (1999) calssified the types of adaption into dynamic parameter control, adaptive parameter control, and self-adaptive parameter control.

To maintain the diversity of solutions, many researchers put much effort on this issue and several approaches were proposed. The technique of niche sharing is often implemented in MOEAs (Goldberg, 1989; Fonseca and Fleming, 1993, 1995). Knowles and Corne (2000) used a hyper grid scheme in the Pareto archived evolution strategy (PAES). Deb et al. (2002) proposed the crowding distance in the non-dominated sorting genetic algorithm II (NSGAII). Zitzler et al. (2001) used the density estimation in the strength Pareto evolutionary algorithm 2 (SPEA2).

This paper presents two features to address the objectives of MOPs, (1) minimizing the distance between the solution set and true Pareto front, (2) distributing the solutions evenly, and (3) maximizing the spread of solution set. The first feature is an adaptive mutation operator (AMO). The second is an enhanced exploration strategy (EES) which maintains diversity and preserves good solutions in the evolving population while extending more attention to the growth of solutions in less populated areas.

Section 2 explains the AMO and EES. The comparative studies are performed with some well-known mutation operators, diversity operators, and MOEAs in section 3. Conclusions are drawn in section 4.

2 Enhanced Distribution and Exploration

2.1 Adaptive Mutation Operator

In this section, an adaptive mutation operator (AMO) is introduced. The AMO is a variant of the simple bit-flip mutation operator and is unique in two aspects. Firstly, the manner in which the mutation operation is carried out on the chromosome is different. This will be elaborated later in the section. Secondly, the mutation rate of AMO is adapted with time along the entire evolution process. In brief, the AMO is implemented for three objectives: providing the possibility of exploration to produce new structures not previously tested, providing the probability of re-introducing chromosome substructures lost in the selection process, and performing local fine-tuning in the later stage of evolution to achieve better convergence.

For the first objective, consider a minimization problem where m decision variables must be optimized. By using a thirty bit binary representation for each variable, there is a total of 2^{30m} possible binary structures

or chromosomes! Hence, it is difficult if not impossible, for any MOEA with fixed population size to maintain all possible binary bit combinations at any one time. By changing the bit values according to some mutation probability, the mutation operator acts as a potential source of producing the missing structures so that the evolution process is not trapped in any local minimal. With small mutation rates, the individuals produced by mutation will not vary much from the parent in terms of the chromosome structure. Intuitively, it will be very difficult to escape local traps. However, simply increasing the mutation rate cannot solve this problem. With increased mutation rates, the probability of disrupting substructures within the chromosome that are responsible for good candidate solutions, is increased.

A simple and effective way to perform exploration while minimizing the disruption of good substructures within the chromosome is to adapt a selective approach to mutate a specific part of the chromosome rather than the entire binary structure. More specifically, each of the decision variable encoded in the chromosome is allocated equal probability of undergoing the mutation operation. During this mutation operation, the bits of selected decision variable will be subjected to bit-flip with probability, $am_rate(n)$. AMO operation for a single chromosome is shown below in figure 1 where *prob* is probability of the decision variable being selected and $am_rate(n)$ is the probability of the bit-flip operation. If *prob* is set as $1/\text{var}_num$ where var_num is the number of decision variables encoded in a single chromosome, on average, the AMO will perform the bit-flip operation on one decision variable for every chromosome. Thus, the AMO allows mutated individual retaining most of the substructures contributing to the chromosomes fitness.

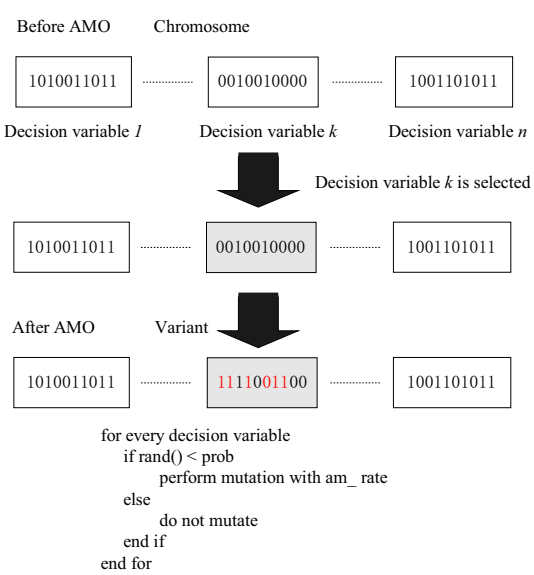

Figure 1. AMO operation

Most recent well-known MOEAs such as SPEAII, PESA, PAES, NSGAII, employ static mutation operators. The AMO adapts the mutation rate to maintain a balance between the introduction of diversity and local fine-tuning. The mutation rate will start off with a high value to produce a diverse set of solutions for an effective genetic search. This value will then decrease as a function of time or generation to fulfill the requirements of local fine-tuning. The mutation rate for this operation is given by

$$am_rate(n) = \begin{cases} a\left(1 - \frac{n}{genNum}\right)^2 + b, & 0 \le n \le \frac{genNum}{4} \\ a\left(0.1 - \frac{n - 4\,genNum}{genNum}\right)^2 + 2b, & otherwise \end{cases} \quad (1)$$

where n is the current generation of the evolution process, *genNum* is the maximal generation number. Figure 2 shows the adaption of mutation rate along the evolution when a is 0.8, and b is 1/(10*30). Two distinct regions can be observed, the exploration region between 0.8~0.753 and the exploitation region between 0.048~0.003. Different from many other adaptive mutation operators where mutation rate decreases gradually along the evolution, AMO pays its attention to searching new strings in the initial stage and then quickly to improving them in the later stage. No time is spent in exploring the immediate region between the exploration and exploitation region while AMO adapts the mutation rate according to a smooth curve inside each region.

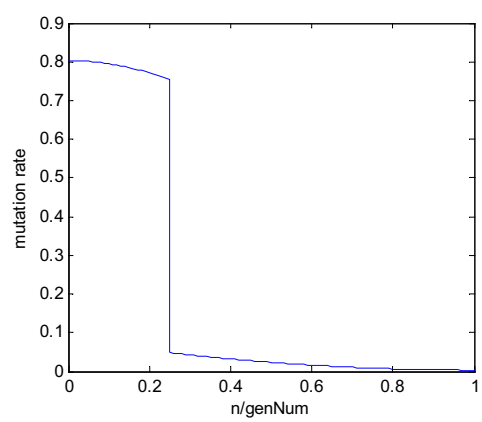

Figure 2. Adaptive mutation rate

2.2 Enhanced Exploration Strategy

In this section, the enhanced exploration strategy (EES) is presented. The EES is an online population distribution scheme that maintains diversity and preserves non-dominated solutions together in the mating population. In addition, it improves solution distribution by encouraging the growth of individuals in less populated areas.

Niche sharing is achieved using a sharing function. Let d be the distance measure between x and y. The neighbourhood size is defined in term of d and specified by the so-called niche radius ω_{share}. The sharing function is defined as follows:

$$sh(d) = \begin{cases} 1 - d/\omega_{share} & \text{if } d < \omega_{share} \\ 0 & \text{otherwise} \end{cases} \quad (2)$$

And the niche count function is defined with the help of sharing function:

$$nc(x) = \sum_{y} sh(dist(x, y)) \quad (3)$$

The niche radius ω_{share} is a key parameter that affects MOEA's effectiveness. Improper setting of the value will result in bad distribution of the population. In practice, the niche radius is difficult to estimate because there is no *a-priori* knowledge about the shape of the Pareto front for many problems. In this paper, the objective space is normalized and the sharing distance is set as $\omega_{\text{share}} = 1/archive_size$. The niche count will be used in the selection and archive updating.

The flow chart of EES is shown in figure 3. The purpose of the entire process is to promote the growth of solutions in less populated areas. At every generation, a certain number of individuals will be tournament selected from the archive to form the population called $\exp_pop$ and the selection criterion is based purely on the niche count. Simple bit-flip mutation is performed on $\exp_pop$ with mutation probability $P_{\exp}$. Depending on the test problem, $P_{\exp}$ is either $1/chromosome_length$ or $1/bit_number_per_variable$. The number of individuals selected for $\exp_pop$ is dynamic and it is given by,

$$Num_Explore = 4(1 - epr^2) \cdot d \quad (4)$$

where $epr(n)$ is the evolution progress rate. Evolution progress rate is developed from progress ratio (Tan *et al*, 2001). It is defined as the ratio of the number of new non-dominated solutions discovered in generation *n*, $new_nondomSol(n)$, to the total number of non-dominated solutions in generation *n*, $total_nondomSol(n)$.

$$epr(n) = \frac{new_nondomSol(n)}{total_nondomSol(n)} \quad (5)$$

The set of new non-dominated individuals discovered at each generation is basically composed of individuals that dominate the non-dominated individuals of the previous generation and individuals that contribute to the diversity of the solution set.

The rationale behind selecting an adaptive number of individuals for the exploration is intuitive. When $epr(n)$ is low, it means that either the generated Pareto front is approaching the true front or the evolution process is not discovering new solutions and more resources are required to perform exploration in the less populated areas. When $epr(n)$ is high, it means that the new solutions are being discovered and resources to perform exploration can be reduced.

At the same time, individuals are being selected to a mating pool named mat_pop through the tournament selection of the combination of archive and the evolving population $population(n)$. The selection criterion in this case is based on Pareto based rank and the niche count will be used in the event of a tie. The population size of mat_pop is dynamic and it is given by $Pop_size - Num_Explore$ where Pop_size is the population size of the evolving population. The mat_pop will then be subjected to genetic operations such as crossover and mutation. After the genetic operations, $\exp_pop$ and mat_pop are combined to form $population(n+1)$. The settings of c and d in this paper are 10 and 20 respectively.

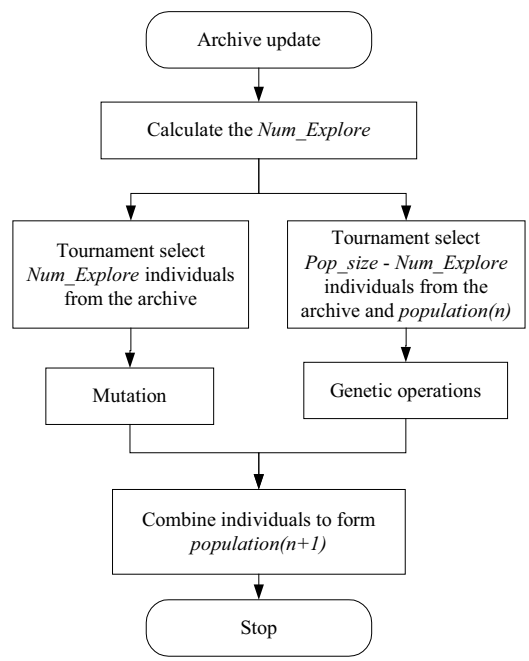

Figure 3. Flowchart for EES operation

3 Case study

In this section, we first describe the test problems used in the comparisons. Next, three performance metrics for multi-objective optimization are described and defined. Then, extensive simulations are performed.

3.1 The Test Problems

Three test problems are resorted to validate the performance of AMO and EES. Table 1 summarizes features of these test problems and these problems are defined in table 2. They include important characteristics and are suitable to validate the effectiveness of MOEAs. Knowles and Corne (2000), Corne et al (2000), Deb (2002) Tan et al (2002), and Zitzler et al (1999, 2000, 2001), have used these problems in the validations of their algorithms.

Therefore these problems should be a good test suite for a fair comparison.

Table 1. Features of the test problems

Problem	Features
ZDT4	Pareto front is highly multi-modal and there are 21^9 local Pareto fronts.
ZDT6	The Pareto-optimal solutions are non-uniformly distributed along the global Pareto front. The density of the solutions is lowest near the Pareto-optimal front and highest away from the front.
FON	Pareto front is convex. It has a wide spread.

Table 2. Definitions of the test problems

ZDT4	
Minimize $T(x) = (f_1(x), f_2(x))$, *where*	(6)
$f_1(x) = x_1$	
$f_2(x) = g(x_2,\cdots,x_m)h(f_1(x), g(x_2, \ldots, x_m))$	
$g(x_2,\cdots,x_m) = 1 + 10(m-1) + \sum_{i=2}^{m}(x_i^2 - 10\cos(4\pi x_i))$	
$h(f_1,g) = 1 - \sqrt{f_1/g}$	
subject to $x = (x_1,\cdots,x_m), m = 10, x_1 \in [0,1]$,	
and $x_2,\cdots,x_m \in [-5, 5]$.	
ZDT6	
Minimize $T(x) = (f_1(x), f_2(x))$, *where*	(7)
$f_1(x) = 1 - \exp(-4x_1)\sin^6(6\pi x_1)$	
$f_2(x) = g(x_2,\cdots,x_m)h(f_1(x), g(x_2, \ldots, x_m))$	
$g(x_2,\cdots,x_m) = 1 + 9((\sum_{i=2}^{m} x_i)/(m-1))^{0.25}$	
$h(f_1,g) = 1 - (f_1/g)^2$	
subject to $x = (x_1,\cdots,x_m), m = 10, x_i \in [0,1]$.	
FON	
Minimize $T(x) = (f_1(x), f_2(x))$, *where*	(8)
$f_1(x_1,\ldots,x_8) = 1 - \exp\left(-\sum_{i=1}^{8}(x_i - 1/\sqrt{8})^2\right)$	
$f_2(x_1,\ldots,x_8) = 1 - \exp\left(-\sum_{i=1}^{8}(x_i + 1/\sqrt{8})^2\right)$	
subject to $-4 \le x_i \le 4$, $i = 1,2,\ldots,8$.	

3.2 Metrics of Performance

Three different quantitative performance measures for multi-objective optimization are used in this study. They are referred from (Deb, 2002) and modified slightly by us.

The metric of generational distance is a value representing how "far" the PF_{known} is from PF_{true} and is defined as:

$$GD = \left(\frac{1}{n}\sum_{i=1}^{n} d_i^2\right)^{1/2} \tag{9}$$

where n is the number of members in PF_{known}, d_i is the Euclidean distance (in objective space) between member i in PF_{known} and its nearest member in PF_{true}. The smaller the generational distance is, the closer the PF_{known} is to PF_{true}.

The metric of spacing measures how "evenly" members in PF_{known} distribute. It is defined as:

$$S = \left[\frac{1}{n}\sum_{i=1}^{n}(d_i - \bar{d})^2\right]^{1/2} / \bar{d} \tag{10}$$

where $\bar{d} = \frac{1}{n}\sum_{i=1}^{n} d_i$, n is the number of members in PF_{known}, d_i is the Euclidean distance in objective space between the member i in PF_{known} and its nearest member in PF_{known}. The smaller the spacing is, the more evenly members in PF_{known} distribute.

The metric of maximum spread measures how well the true Pareto front is covered by the discovered Pareto front through the hyper-boxes formed by the extreme function values observed in the true Pareto front and generated Pareto front. In order to normalize the metric, this metric is modified as

$$MS = \sqrt{\frac{1}{M}\sum_{m=1}^{M}\left[(\max_{i=1}^{n} f_m^i - \min_{i=1}^{n} f_m^i)/(F_m^{\max} - F_m^{\min})\right]^2} \tag{11}$$

where n is the number of members in the discovered Pareto front, f_m^i is the m-th objective of member i, $F_m^{\max}$, $F_m^{\min}$ are the maximum and minimum of the m-th objective in the true Pareto front. The greater the maximum spread is, the more area of PF_{true} is covered by the PF_{known}.

3.3 Effects of AMO

In the comparisons, we employ a basic MOEA paradigm. It has a population of fixed size, and implements elitism in the form of a fixed sized archive. Fonseca and Fleming's ranking scheme is applied. The niche sharing is used in the tournament selection as well as diversity maintenance in the archive. All runs considered are implemented with the same binary coding, binary tournament selection, uniform crossover, and bit-flip mutation. Table 3 lists other configurations.

Table 3. Parameter setting for different operators

Chromosome	Binary coding. 30 bits per decision variable.
Population	Population size 100; Archive (or secondary population) size 100.
Selection	Binary tournament
Crossover operator	Uniform crossover
Crossover rate	0.8
Ranking	Scheme of Fonseca and Fleming
Diversity technique	Niche sharing with radius 0.01 in the normalized objective space
Generation number	1000

The performance of AMO is compared against three different settings of bit-flip mutation operators and FBLP (Tan et al., 2001) listed in tabel 4.

Table 4. Different cases for AMO evaluation

	Case	Description
1	N1	Bit-flip with mutation rate *PM*/2
2	N2	Bit-flip with mutation rate *PM*
3	N3	Bit-flip with mutation rate *PM*2*
4	FBLP	$ab \mid \lvert PM/2, b \quad PM,$ $\eta \mid bit_num_per_\mathrm{var}iable/2$
5	AMO	a=0.8, $b = PM$

PM is defined as $1/chromosome_length$ for *ZDT4* and *ZDT6* and $1/bit_number_per_\mathrm{var}iable$ for *FON.*

In the experiment, 30 runs are performed for each cases on each test problem so as to study the statistical performance. The median of 30 runs on the three performance metrics is listed in table 5. AMO displays the best generational distance for this problem. AMO is the only operator that enabled the algorithm to converge upon the Pareto front of *ZDT6.* In addition, AMO is competitive in the spread. However, it seemed that the good performances of AMO in the spread and generation distance are achieved at the expense of spacing. This is probably due to AMO's emphasis on exploitation in the later stage of evolution. As a result, the AMO is unable to bridge the gaps between the extreme end solutions discovered during the initial exploratory phase.

Table 5. Median values of generation distance, space and spread for AMO comparison. (The problem *ZDT4, ZDT5*, and *FON* are encoded as 1, 2, 3 respectively in table 5,6,8 and 9.)

		Mutation operator				
		AMO	FBLP	N1	N2	N3
1	GD	0.7681	0.8778	0.7868	0.8142	1.4601
	S	0.6481	0.3541	0.2595	0.7463	0.7831
	MS	0.7444	0.7533	0.7572	0.7408	0.4207
2	GD	4.87e-7	0.8657	0.5471	1.5886	2.8208
	S	2.3443	1.3399	1.7457	1.1108	1.1910
	MS	0.9992	0.7042	0.7545	0.7060	0.7047
3	GD	0.0030	0.0031	0.0031	0.0146	0.0492
	S	2.4625	1.3672	0.9318	0.8072	0.7589
	MS	0.5858	0.4845	0.4791	0.5620	0.6773

The effects of various *prob* settings are examined in table 6. The purpose is to prove that the underlying idea of AMO to maintain a balance between preservation and disruption of chromosomes by selective mutation of decision variables can improve the performance of the algorithm. Similarly, 30 runs are performed for each setting on each test problem.

Table 6. Median values of generation distance, space and spread for different *prob* settings

		Parameter Settings: *prob*			
		$1/\mathrm{var}_num$	0.25	0.5	0.75
1	GD	0.7681	0.7996	0.8080	0.7927
	S	0.6481	0.6627	0.7194	0.7129
	MS	0.7444	0.7158	0.7180	0.7384
2	GD	4.87e-7	4.91e-7	5.02e-7	1.0609
	S	2.3443	2.5039	3.1710	0.9033
	MS	0.9992	0.9992	0.9992	0.7047
3	GD	0.0030	0.0034	0.0208	0.0415
	S	2.4625	2.3488	0.8112	0.7131
	MS	0.5858	0.6064	0.6638	0.6999

Note that as *prob* is increased, the behaviour of AMO will approach that of bit-flip mutation operator albeit the changing mutation rate. It can be observed from table 6 that the metric of generation distance increases with increasing *prob.* This is most probably due to the fact that increasing *prob* would correspond to the disruption of more genes.

3.4 Effects of EES

The performance of EES is compared against niche sharing (Goldberg, 1989; Fonseca and Fleming, 1993, 1995), hyper grid scheme (Knowles and Corne, 2000), crowding distance (Deb et al., 2002), and density estimation (Zitzler et al., 2001). The niche sharing sums the sharing effects of individuals in a neighbourhood. The hyper grid divides the normalized objective space into hyper boxes and every individual is given an attribute that indicates the number of solutions sharing the same box. The crowding distance is an estimate of the size of the largest cuboid enclosing a solution without any other point. The density estimation is adapted from $k\lceil th$ nearest neighbour method and it is given by the inverse of the $k\lceil th$ distance. In this comparison, all the diversity techniques are conducted in the normalized objective space. Other settings are listed in table 7.

Table 7. Parameter setting for the comparison

Chromosome	Binary coding. 30 bits per decision variable.
Population	Population size 100; Archive (or secondary population) size 100.
Selection	Binary tournament
Crossover operator	Uniform crossover
Crossover rate	0.8
Mutation operator	Bit-flip
Mutation rate	*PM*
Ranking	Scheme of Fonseca and Fleming
Generation number	1000

The median of 30 runs on the three metrics is listed in table 8. With respect to the metric of generation distance, the algorithm incorporated with EES is clearly the best in the test problems. This is particularly evident in the test problem of *ZDT6* and *FON*. *ZDT4* proved to be the most difficult problem for all algorithms. However, EES still produces good performance in all three metrics with respect to the other diversity operators on this problem.

Table 8. Median values of generation distance, space and spread for EES comparison

		Diversity operator				
		EES	Niche	Grid	Crowd	Density
1	GD	0.7652	0.8142	1.0008	0.7832	0.7993
	S	0.3173	0.7463	0.6567	0.2506	1.3513
	MS	0.7610	0.7408	0.7235	0.7366	0.7403
2	GD	5.05e-7	1.5886	1.5984	1.6012	1.6222
	S	0.1734	1.1108	1.1051	1.1444	1.1119
	MS	0.9992	0.7060	0.7051	0.7061	0.7043
3	GD	0.0022	0.0146	0.0141	0.0146	0.0142
	S	0.2252	0.8072	0.9006	0.8077	0.8541
	MS	0.7732	0.7060	0.7051	0.7061	0.7043

It is also obvious that the incorporation of EES improves greatly the distribution and spread of solution along the Pareto front for all test problems. EES is particularly outstanding in the metric of spacing in test problem of *ZDT6* and *FON*. In addition, EES has the best performance in the area of maximum spread for all test problems.

Table 9 shows that the performance of EES with different *d* settings does not vary a lot over the test problems. This observation implies that the EES will be able to perform well against the various diversity operators despite the different settings. More importantly, it also shows that the EES is insensitive to parameter changes.

Table 9. Median values of generation distance, space and spread for different *d* settings

		EES Parameter Settings: *d*			
		20	25	30	40
1	GD	0.7652	0.7712	0.7688	0.7804
	S	0.3173	0.3185	0.3224	0.3167
	MS	0.7610	0.7590	0.7590	0.7557
2	GD	5.05e-7	5.10e-7	5.13e-7	4.94e-7
	S	0.1734	1.4231	0.1660	0.1770
	MS	0.9992	0.9992	0.9992	0.9992
3	GD	0.0022	0.0020	0.0021	0.0021
	S	0.2252	0.2273	0.2379	0.2211
	MS	0.7732	0.8053	0.7857	0.7947

3.5 Effects of AMO+EES

The AMO and EES are incorporated into a general MOEA paradigm that uses binary coding, binary tournament selection, uniform crossover, and Fonseca and Fleming's ranking scheme. This algorithm is called ALG in this paper and will be compared with five recent well-known algorithms to validate the effectiveness of AMO and EES. The indices of the algorithms are listed in table 10. All algorithms are implemented with the same binary coding scheme, binary tournament selection, uniform crossover, Fonseca and Fleming's ranking scheme. Other configutations are listed in table 11.

Table 10. Indices of the different algorithms

Index	Algorithm
1	ALG (AMO+EES)
2	PAES
3	PESA
4	NSGA II
5	SPEA 2
6	IMOEA

Table 11. Configuration of ALG, PAES, PESA, NSGAII, SPEA2, IMOEA.

Chromosome	Binary coding, 30 bits for each variable.
Population	Population size 1 in PAES; population size 100 in PESA, NSGAII, SPEA2; initial population size 20, maximum population size 100 in IMOEA. Secondary population (or archive) size is 100 for all the algorithms.
Crossover operator	Uniform crossover
Crossover rate	0.8
Mutation operator	AMO in ALG; FBLP in IMOEA; bit-flip in others
Mutation rate	$1/chromosome_length$ for *ZDT4* and *ZDT6*; $1/bit_number_per_variable$ for *FON*
Ranking	Scheme of Fonseca and Fleming
Generation number	100,000 in PAES; 1000 in others

The simulation results of the algorithms with respect to the various metrics are summarized in figure 4. The distribution of the simulation data of 30 independent runs is visualized in the box plot format, which has been applied by (Tan et al, 2001, 2002). Each box plot represents the distribution of a sample set where a horizontal line within the box encodes the median, while the upper and lower ends of the box are the upper and lower quartiles. The appendages illustrate the spread and shape of distribution, and dots represent the outside values.

Although the previous investigation of AMO and EES in section 3.3 and section 3.4 show that the individual effects of either feature are not enough to allow the algorithm overcome the local traps of *ZDT4* and the large spread of *FONs'* tradeoff, each have showed their own distinct advantage over their counterpart operators. While AMO have the ability drive the evolution towards the Pareto front and to find points in unexplored regions, it lacks some form of mechanism to guide its operation. This results in the subsequent gaps observed in the discovered Pareto front. The mechanism to guide the exploration of AMO comes in the form of EES. Likewise EES may have shown the ability to locate these gaps, it is unable to escape the local optimum trap of *ZDT4* or maintain a diverse solution set in *FON*. Thus it is not surprising that the ALG produces better performance when these two features are incorporated together.

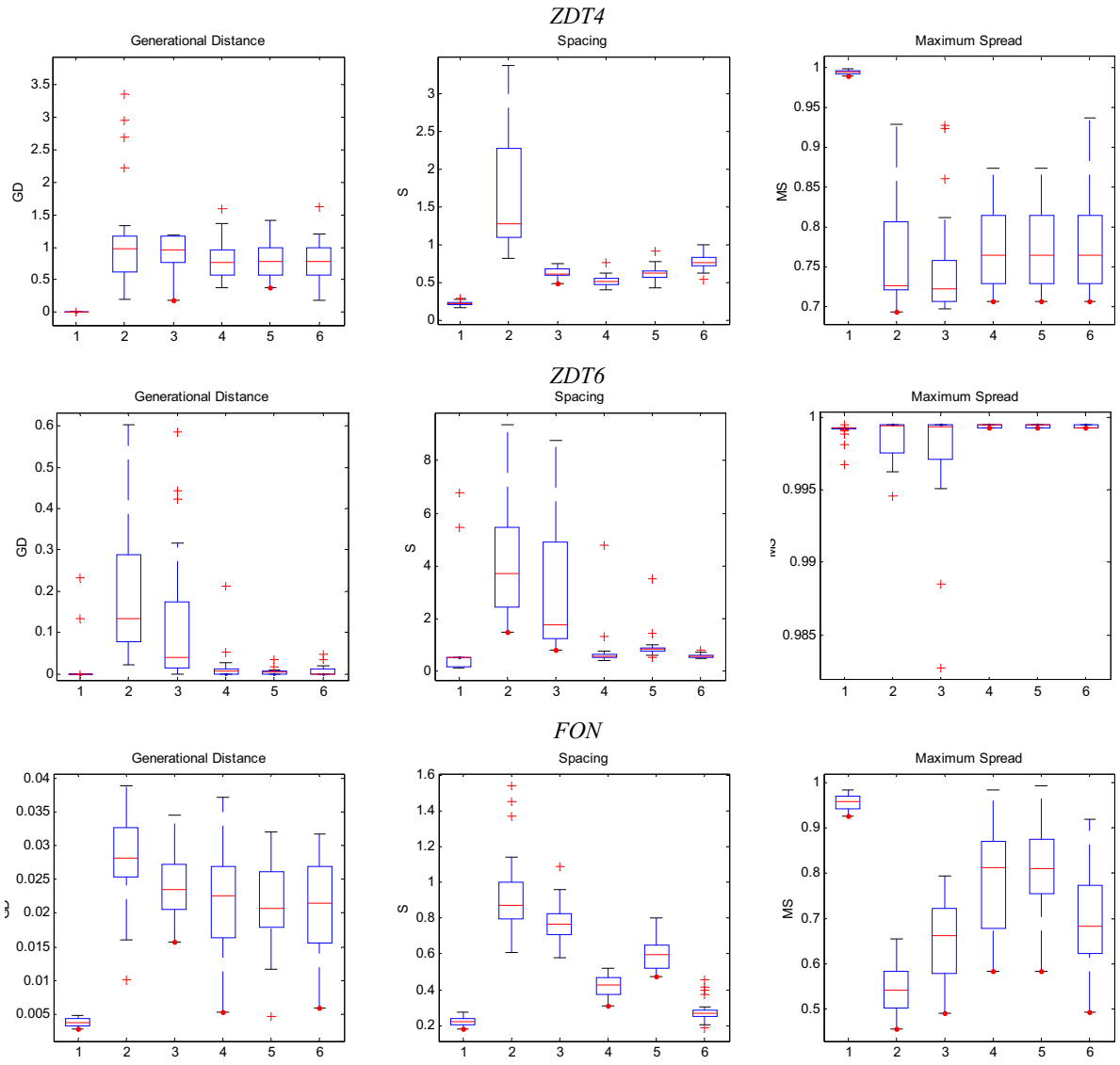

Figure 4. Simulation results for *ZDT4, ZDT6* and *FON*

ZDT4 proves to be the most difficult problem faced by the algorithms since no algorithm, except ALG, is able to deal with multi-modality effectively. This is reflected in the performance metric of generation distance. In addition, the ALG also chalked up outstanding results in the metric of spread and distribution. The biased search space of *ZDT6* is designed to make it difficult for the algorithms to evolve a well-distributed front. In this respect, ALG is still able to give outstanding results in terms of the distribution of results. This is probably because of EES. Otherwise, ALG performance in the aspects of generation distance and spread is well matched by SPEA2 and NSGAII. The challenge of test function, *FON,* is to find and maintain the entire Pareto front uniformly. With the exception of the ALG, the algorithms found it difficult to find a good spread and distribution.

For all test problems, ALG responds well to the challenges of the different difficulties. The ALG performs consistently well in the distribution of solutions along the Pareto front. This is even so for the test problems of *ZDT6* and *FON* that are designed to challenge the algorithm's ability to maintain the Pareto front. The performance of ALG with respect to generational distance is also outstanding in all problems. This demonstrates the ALG's ability to converge upon the Pareto front regardless of problems such as discontinuities, convexities and non-uniformities. It also shows no problems in coping with local traps and this is reflected by its performance in the test problem *ZDT4.* The ALG ability to discover a diverse solution set on the Pareto frontier is demonstrated and this is most evident in the test problem of *FON.*

4. Conclusion

This paper presents a novel enhanced exploration strategy that maintains diversity and non-dominated solutions in the evolving population while encouraging the exploration towards the direction of less populated areas. This achieves better discovery of gaps in the discovered frontier as well as better convergence. An adaptive mutation operator that plays the role of producing new genetic structures is also presented. This AMO adapts the mutation rate to maintain a balance between the introduction of diversity and local fine-tuning.

A comparative study between the proposed features with various well-known multi-objective evolutionary algorithms, diversity operators and mutation operators are carried out on six benchmark problems. Simulations are carried out to examine the effects of AMO and EES with respect to selected mutation and diversity operators respectively. AMO and EES have showed to be competitive if not better than their counterparts and have their own specific contribution. Simulations results also show that the algorithm incorporated with AMO and EES is capable of discovering and distributing non-dominated solutions along the Pareto front. The combined effects of AMO and EES enabled the algorithm to perform well in breaking out of local traps and maintaining diversity in the solution set. The combined effects of these two features allow the algorithm to find a good, well-distributed and diverse solution set along the Pareto front.

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