

# An Active Elitism Mechanism for Multi-objective Evolutionary Algorithms

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## Abstract

Classical (or passive) elitism mechanisms in the MOEA (Multi-objective Evolutionary Algorithm) literature have a holding/sending back structure. In this paper, an active elitism mechanism for multi-objective evolutionary algorithms is proposed. In the active elitism mechanism, a set of elite (or non-dominated) individuals is excited by genetic operators (crossover/mutation) in the archive in the hope of generating better and more diverse individuals than themselves. If a set of excited elites are any better than originals, then archive can be viewed as a place of active solution provider rather than a static storage place. The main motivation behind this approach is that elite individuals are inherently the closest individuals to the solution (of any optimization problem on hand) and exciting those individuals can likely generate more significant outcomes than a far away one. The proposed active elitism mechanism is embedded into well-known multi-objective SPEA and SPEA2 methods (named ACE\_SPEA and ACE\_SPEA2 respectively) and compared to the original methods using four unconstrained test problems. The active elitist versions of SPEA and SPEA2 maintain better spread and convergence properties than the original methods on all test problems. The proposed active elitism mechanism can easily be integrated into existing multi-objective evolutionary algorithms to improve their performance.

**Keywords:** Active Elitism, Evolutionary Algorithms, Multi-objective Optimization, SPEA, SPEA2

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## 1. INTRODUCTION

Multi-objective optimization is with no doubt a very important research topic both for scientists and engineers, not only because of the multi-objective nature of most real world problems but also because there are still many open questions in this area [1]. MOEAs are playing a dominant role in solving problems with multiple conflicting objectives and obtaining a set of non-dominated solutions which are close to the Pareto optimal front. They have a number of advantages such as, obtaining a set of non-dominated solutions in a single run, easy handling of problems with local Pareto fronts and discrete nature due to their population approach and flexible recombination operators [2].

In the literature, there have been a lot of research activities on multi-objective optimization using evolutionary algorithms and a number of well performing MOEAs have been published. MOEAs differ from each other with some mechanisms: fitness assignment, elitism (or archive management) and hybridization to other algorithms. Elitism mechanism has critical role on the performance of a MOEA. Because, elite (or non-dominated) individuals are the best individuals found by an algorithm in a single run. The presence of elitism could improve the performance of MOEAs, but care must be taken to apply it efficiently [2].

Classical sense of elitism in single-objective evolutionary algorithms (SOEAs), the best solution is always copied into the next population. Although the incorporation of elitism in MOEAs is more complex than SOEAs, fundamental practice is similar. There are various ways to incorporate elitism into MOEAs. Most algorithms make use of a second population (or archive) of elite individuals. Though there are great varieties in the implementation of elitism, it can be summarized some important features as follows: First, they require preserving the best solutions

in the population, an archive or sub-population. Second, they require consideration of several strategies, including the elitism strategy, or how the elitist population is updated; the re-insertion strategy, or how elite individuals take part in the production of offspring; and the control flow, or when archiving and re-insertion take place. Unfortunately, particular implementations leave the determination of many parameters to the decision makers. They also inevitably increase the space and time complexity. Nevertheless, the evidence shows that elitism is an important and indispensable factor in EMOO (Evolutionary Multi-objective Optimization) [3].

It has been reported that the elitist versions of two different MOEAs perform equally well [4],[5]. Therefore, elitism makes MOEAs more capable than those which do not employ it. Rudolph has proved that GAs (Genetic Algorithms) converge to the global optimal solution of some test functions in the presence of elitism [6],[7]. Furthermore, the presence of elite individuals enhances the probability of creating better offsprings.

Two major phases in classical elitism mechanism are:

- i) **Holding phase:** *Which individuals are going to be kept in archive?* In this phase, non-dominated solutions (or elites) in parent (primary) population are stored in the archive.
- ii) **Sending back phase:** *Which individuals are going back into the primary population?* One strategy is to copy all elite individuals from current population to next population. Another strategy is to copy only a number of elite individuals to next population [4].

Elitism procedures in the literature are generally similar. Generally, elite individuals are stored in an extra population (or archive). And then, archive is updated by some criterions. Adding new elite individuals to archive and removing dominated elites from archive are named as archive truncation. There are many archive truncation methods used in MOEAs [4],[8],[9],[10],[11]. As a result, common point of all classical (or passive) elitism mechanisms is storing elites in an archive *without any excitation* and passing them into the main population.

In this paper, an active elitism mechanism is proposed. In the active elitism mechanism, a set of elite individuals is excited by genetic operators (crossover/mutation) in archive in the hope of generating better or more diverse individuals than themselves. If a set of excited elites is better than originals, then the archive can be viewed as a place of active solution provider rather than a static storage place.

In this paper, well-known multi-objective SPEA (Strength Pareto Evolutionary Algorithm) and SPEA2 (Strength Pareto Evolutionary Algorithm 2) methods [2],[4],[12] with passive elitism and modified version of them (ACE\_SPEA, ACE\_SPEA2 respectively) with active elitism mechanism are simulated and compared.

The remainder of this paper is organized in five sections. Section 2 describes the basic concepts of MOPs (Multi-objective Problems). Section 3 explains SPEA and SPEA2 algorithms, respectively. Section 4 gives detailed descriptions of the proposed active elitism mechanism. Experimental problem sets and simulation results are given in Section 5. Finally, Section 6 contains the discussion, concluding remarks and future directions.

## 2. MULTI-OBJECTIVE OPTIMIZATION

A multi-objective optimization problem can be stated as follows:

$$\min\{f_1(x), f_2(x), \dots, f_m(x)\} \quad , \quad x \in \Omega \quad (1)$$

where  $x = (x_1, x_2, \dots, x_n)$  is the decision variable vector and  $f_i(x)$  are the objective functions.  $\Omega$  is the decision space. A solution  $x$  is said to dominate solution  $y$  if and only if  $f_i(x) \leq f_i(y)$  for every

$i \in \{1, 2, \dots, m\}$  and  $f_i(x) < f_i(y)$  for at least one index  $j \in \{1, 2, \dots, m\}$ . A point  $x^* \in \Omega$  is Pareto optimal to (1) if there is no point  $x \in \Omega$  such that  $f(x)$  dominates  $f(x^*)$ .  $f(x^*)$  is Pareto-optimal objective vector. The set of all the Pareto-optimal points is called the Pareto Set (PS). The set of all the Pareto-optimal objective vectors is called the Pareto Front (PF).

### 3. SPEA and SPEA2

#### 3.1. SPEA (Strength Pareto Evolutionary Algorithm)

SPEA is an elitist evolutionary algorithm method based on Pareto definition [4],[5]. This method was introduced by Zitzler and Thiele. Evolutionary processes of SPEA are managed by two different populations. One of these populations, called regular population is utilized to generate offspring. Other population, called an archive with pre-defined size individuals is employed to preserve the evolutionary information of Pareto front [13]. At each generation, non-dominated individuals are copied to the archive. For each individual in the archive, a strength value is computed.

In SPEA, the fitness of each member of the current population is computed according to the strengths of all external non-dominated solutions that dominate it. Additionally, a clustering technique called “average linkage method” is used to keep diversity.

##### 3.1.1. Fitness Assignment Strategy of SPEA

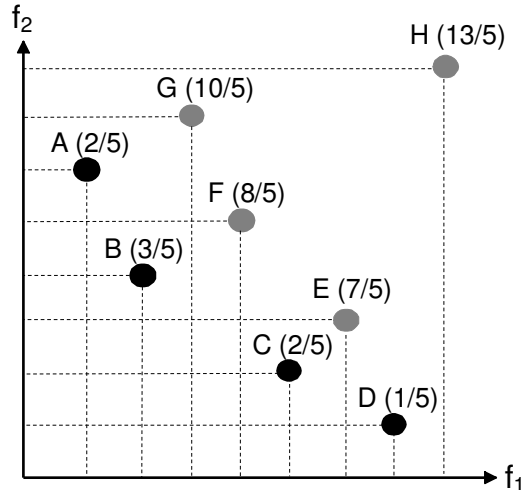
Let  $n$  be the number of individuals dominated by a non-dominated solution and let  $N$  be the total number of dominated individuals (all the individuals except the first Pareto front). Then the fitness (or strength) of the non-dominated solution is defined as:

$$f_i = s_i = \frac{n}{N + 1} \quad (2)$$

The fitness of a dominated solution is calculated by adding the fitness of all the non-dominated individuals that dominate it, plus one:

$$f_j = 1 + \sum s_i \quad (3)$$

For the sake of clarity, the fitness of a non-dominated solution (C) and a dominated solution (E) are numerically given in Figure 1. There are four dominated individuals (E,F,G and H) in the population, so  $N = 4$ . Solution C dominates two individuals (E and H), so the fitness/strength of C is  $2/5$ . Solution E is only dominated by non-dominated C. For this reason the fitness of E is  $(1+(2/5)=7/5)$ , so E(7/5) is assigned.



**FIGURE 1:** Fitness assignment example of SPEA (Non-dominated individuals are shown by black circles, dominated individuals are shown by grey circles).

**3.1.2. Elitism Mechanism of SPEA**

SPEA uses a regular population and an archive. Starting with an initial population and an empty archive, the following steps are performed per iteration. First, all non-dominated population members are copied to the archive; any dominated individuals or duplicates (regarding the objective values) are removed from the archive during this update operation. If the size of the updated archive exceeds a predefined limit, further archive members are deleted by a clustering technique which preserves the characteristics of the non-dominated front. After the mating selection, recombination and mutation phases, the old population is replaced by the resulting offspring population.

**3.2. Strength Pareto Evolutionary Algorithm 2 (SPEA2)**

SPEA2 has three main differences with respect to its predecessor [12]: (i) it incorporates a fine-grained fitness assignment strategy which takes into account for each individual the number of individuals that dominates it and the number of individuals by which it is dominated; (ii) it uses a nearest neighbor density estimation technique which guides the search more efficiently, and (iii) it has an enhanced archive truncation method that guarantees the preservation of boundary solutions.

**3.2.1. Fitness Assignment Strategy of SPEA2**

Each individual  $i$  in the archive  $\bar{P}_t$  and the main population  $P_t$  is assigned a strength value  $S(i)$ , representing the number of individuals it dominates:

$$S(i) = |\{j \mid j \in P_t + \bar{P}_t \wedge i \succ j\}| \tag{4}$$

where  $+$  stands for multiset union and the symbol  $\succ$  corresponds to the Pareto dominance relation. On the basis of the  $S$  values, the raw fitness  $R(i)$  of an individual  $i$  is calculated:

$$R(i) = \sum_{j \in P_t + \bar{P}_t, j \succ i} S(j) \tag{5}$$

That is the raw fitness determined by the strengths of its dominators in both archive and population, as opposed to SPEA where only archive members are considered in this context. The density estimation technique used in SPEA2 is an adaptation of the  $k$ -th nearest neighbor method, where the density at any point is a (decreasing) function of the distance to the  $k$ -th nearest data point. To be more precise, for each individual  $i$  the distances (in objective space) to all individuals  $j$  in archive and population are calculated and stored in a list. After sorting the list in

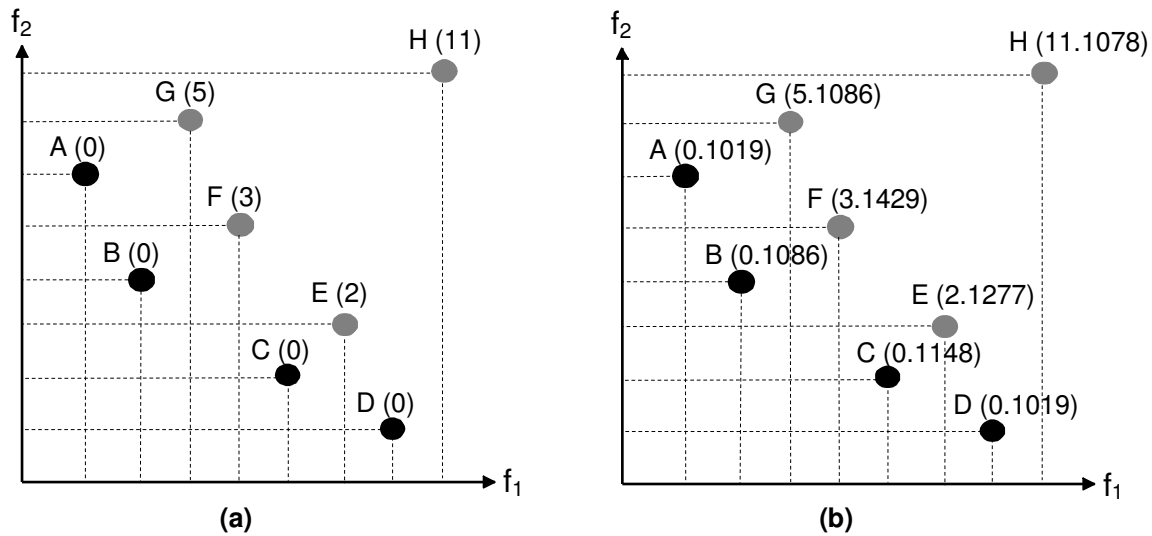
increasing order, the  $k$ -th element gives the distance sought, denoted as  $\sigma_i^k$ . As a common setting, we use  $k$  equal to the square root of the sample size, thus,  $k = \sqrt{N + \bar{N}}$ . ( $N$  : population size,  $\bar{N}$  : archive size). Afterwards, the density  $D(i)$  corresponding to  $i$  is defined by:

$$D(i) = \frac{1}{\sigma_i^k + 2} \tag{6}$$

Finally, adding  $D(i)$  to the raw fitness value  $R(i)$  of an individual  $i$  yields its final fitness:

$$F(i) = R(i) + D(i) \tag{7}$$

A fitness assignment example of SPEA2 is shown in Figure 2.



**FIGURE 2.** (a) Raw fitness values assigned by SPEA2. (b) Final fitness values assigned by SPEA2 ( $k=3.1623$ ).

The first step is the determination of strength of an individual. Strength of an individual is defined as the total number of individuals dominated by this individual. For example, A dominates two individuals {G,H}, strength of A or  $S(A) = 2$ , and H dominates no individual, thus  $S(H) = 0$ . The strength of an individual indicates relative domination ability of an individual (in terms of number of dominated individuals).

The second step is the determination of raw fitness. The summation of strength values of a set of individuals that dominates an individual is defined as raw fitness value of the individual. Due to this definition, non-dominated individuals {A,B,C and D} get '0' raw fitness values. For example, raw fitness of A or  $R(A) = 0$ , because A is not dominated by any individual and similarly  $R(H)$  is 11 because all individuals dominate H.

In the third step, density information is added to the raw fitness value according to Eq.7 and the final fitness value is obtained for each individual. Figure 2 depicts the raw and final fitness values of an example population assigned by SPEA2.

### 3.2.2. Elitism Mechanism of SPEA2

The archive update operation in SPEA2 differs from the one in SPEA in two respects: (i) the number of individuals contained in the archive is constant over time, and (ii) the truncation method prevents boundary solutions being removed. The first step is to copy all non-dominated individuals, i.e., those which have a fitness value lower than one, from archive and population to the archive of the next generation ( $P$  - main population,  $\bar{P}$  - archive,  $N$  - population size,  $\bar{N}$  - archive size):

$$\bar{P}_{t+1} = \left\{ i \mid i \in P_t + \bar{P}_t \wedge F(i) < 1 \right\} \quad (8)$$

If the non-dominated front fits exactly into the archive ( $|\bar{P}_{t+1}| = \bar{N}$ ) the environmental selection step is completed. Otherwise, there can be two situations: either the archive is too small ( $|\bar{P}_{t+1}| < \bar{N}$ ) or too large ( $|\bar{P}_{t+1}| > \bar{N}$ ). In the first case, the best  $\bar{N} - |\bar{P}_{t+1}|$  dominated individuals in the previous archive and population are copied to the new archive. This can be implemented by sorting the multiset  $P_t + \bar{P}_t$  according to the fitness values and copy the first  $\bar{N} - |\bar{P}_{t+1}|$  individuals  $i$  with  $F(i) \geq 1$  from the resulting ordered list to  $\bar{P}_{t+1}$ . In the second case, when the size of the current non-dominated set exceeds  $\bar{N}$ , an archive truncation procedure is invoked which iteratively removes individuals from  $\bar{P}_{t+1}$  until  $|\bar{P}_{t+1}| = \bar{N}$ . Here, at each iteration, the individual which has the minimum distance to another individual is chosen for removal; if there are several individuals with minimum distance the tie is broken by considering the second smallest distances and so forth.

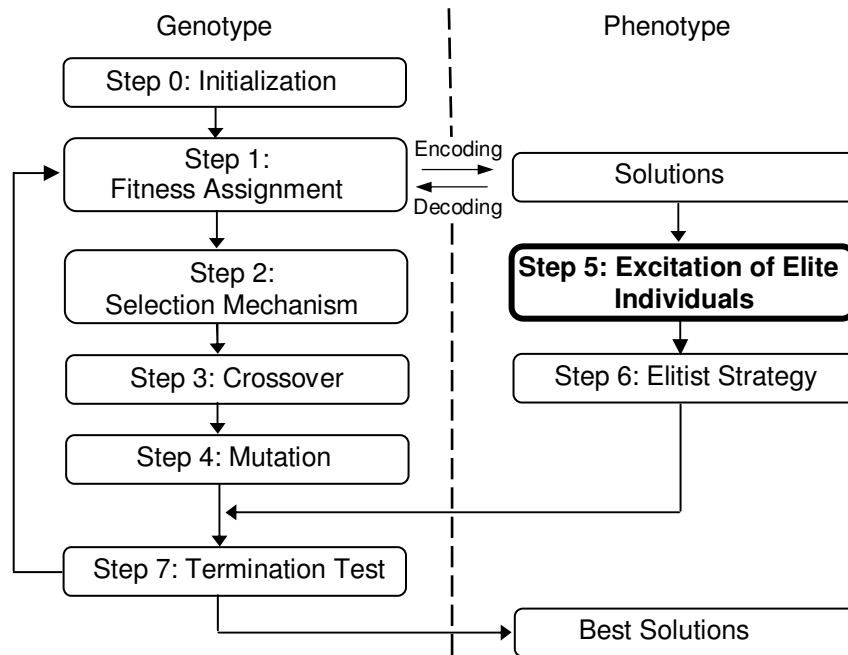
## 4. ACTIVE ELITISM MECHANISM

In the elitism mechanism as stated in [14], a set of elite individuals is excited by genetic operators (crossover/mutation) in archive in the hope of generating better or more diverse individuals than themselves. If a set of excited elites is any better than originals, then the secondary population can be viewed as a place of active solution provider rather than a static storage place. The main motivation behind this approach is that elite individuals are inherently the closest individuals to the solution (of any optimization problem on hand) and exciting those individuals can likely generate more significant outcomes than a far away one. This structure is named as the active elitism mechanism.

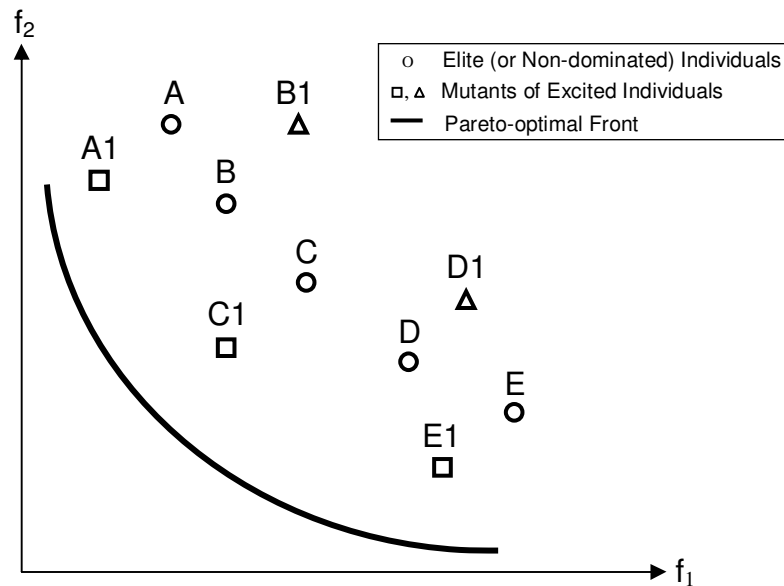
It is not always possible to select all elite individuals and to place them into reproduction process by means of selection mechanism. Unselected elite individuals can't be excited by genetic operators and they can't generate new solutions. However, the active elitism mechanism gives a chance to all elite individuals for generating new solutions. Block diagram of an active elitist MOEA is given in Figure 3.

Active elitism mechanism is applied to MOEAs in two forms:

- i) Excitation of the elite individuals by mutation operator,
- ii) The elite individuals in the current archive are recombined with the elite individuals in the *past* archive ( $n$  step before).



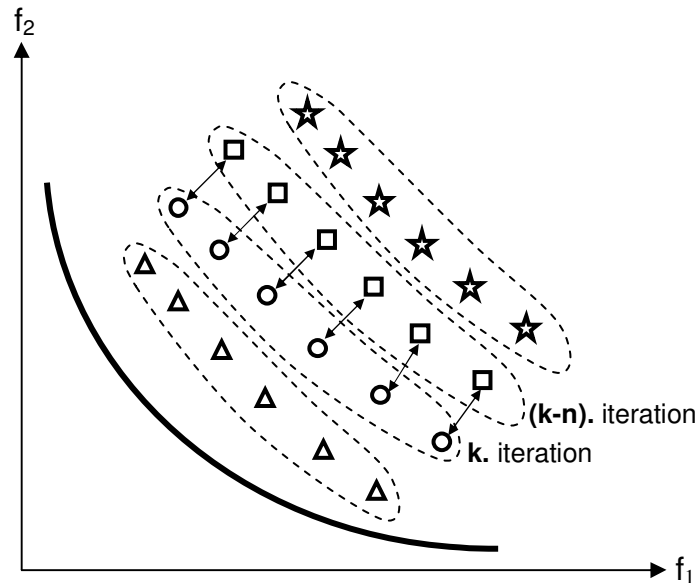
**FIGURE 3.** Block Diagram of an Active Elitist MOEA.



**FIGURE 4.** Excitation of elite (or non-dominated) individuals by mutation operator.

An example of excitation of elite individuals by the mutation operator is shown in Figure 4. Each individual in the archive (or secondary population) is mutated once. A set of mutants depicted by squares (A1,C1,E1) are closer to the Pareto-optimal front (in terms of two objectives) than the original ones depicted by circles (A,C,E). Thus; A, C and E is replaced by A1, C1 and E1 in the archive. Other mutants depicted by triangles (B1 and D1) are farther from the Pareto-optimal front than the original ones (B and D). Therefore; B and D remain unchanged in the archive. Euclidian distance is used to calculation of the distance of the individuals to the Pareto-optimal front.

An example of excitation of elite individuals by the crossover operator is shown in Figure 5. In this phase, elite individuals in  $k$ th iteration are recombined to elite individuals in  $(k-n)$ th iteration. Obtained individuals symbolically depicted by triangles in Figure 5 are better (or closer) than original elites in  $k$ th iteration. So, they are substituted in the archive. Generally speaking, the archive remains unchanged if offspring (generated by excitation of crossover or mutation) is not any better than the original one.



**FIGURE 5.** The current and past elites are recombined with crossover operation. Circles are the elite individuals in  $k$ th iteration, squares are the elite Individuals in  $(k-n)$ th iteration, triangles and stars are offsprings.

## 5. SIMULATION RESULTS

### 5.1. Test Problems

Four continuous test functions (ZDT1, ZDT2, ZDT3 and ZDT6) which have been used in various MOEA studies are experimented. ZDTs are state-of-art test problems for MOEA comparisons [4],[5]. All test problems with their properties are presented in Table 1. All these problems in Table 1 are bi-objective minimization problems. None of these problems have any inequality or equality constraints. Table 1 also shows the number of variables, their bounds, the Pareto-optimal solutions, and the nature of Pareto-optimal front for each problem.



Problem	n	Variable Bounds	Objectives Functions	Comments
ZDT1	30	$[0,1]^n$	$f_1(x) = x_1$ , $f_2(x) = g(x)[1 - \sqrt{x_1/g(x)}]$ , $g(x) = 1 + 9\left(\sum_{i=2}^n x_i\right)/(n-1)$	Convex
ZDT2	30	$[0,1]^n$	$f_1(x) = x_1$ , $f_2(x) = g(x)[1 - (x_1/g(x))^2]$ $g(x)$ is the same as those of ZDT1	Non-convex
ZDT3	30	$[0,1]^n$	$f_1(x) = x_1$ , $f_2(x) = g(x)\left[1 - \sqrt{x_1/g(x)} - \frac{x_1}{g(x)}\sin(10\pi x_1)\right]$ $g(x)$ is the same as those of ZDT1	Convex, disconnected
ZDT6	30	$[0,1]^n$	$f_1(x) = 1 - \exp(-4x_1)\sin^6(6\pi x_1)$ , $f_2(x) = g(x)[1 - (f_1(x)/g(x))^2]$ $g(x) = 1 + 9\left[\left(\sum_{i=2}^n x_i\right)/(n-1)\right]^{0.25}$	Non-convex, non-uniformly spaced

**TABLE 1:** Test problems used in this paper,  $n$  is the number of decision variables.

### 5.2. Parameter Settings

The parameter settings in the experimental studies are given in Table 2. For ZDT1 and ZDT3, decision variables are coded with 30 bits. For ZDT2 and ZDT6, decision variables are coded with 10 bits. The population size of 100 is selected for making comparisons on the same conditions. For SPEA, a population of size 100 and an archive of size 25 are employed (this 4:1 ratio is suggested by the developers of SPEA to maintain an adequate selection pressure for the elite solutions).

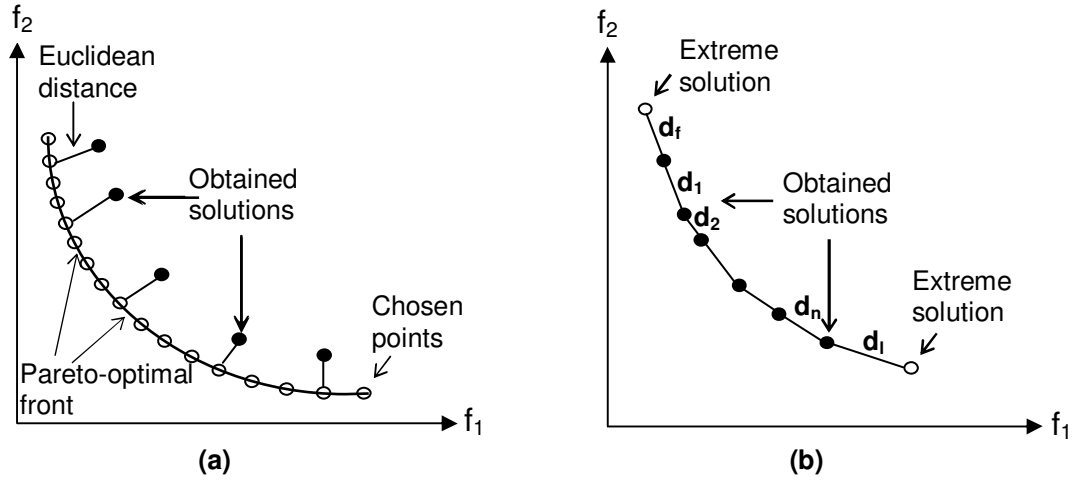
	SPEA / ACE_SPEA	SPEA2 / ACE_SPEA2
The number of decision variables (n)	30	30
The mutation rate ( $p_m$ )	$1/l$ (where $l$ is the string length)	$1/l$
The crossover rate ( $p_c$ )	0.9	0.9
The active mutation rate ( $p_{m\_active}$ )	0.05	0.05
The population size (N)	100	100
The archive size (or the secondary population size) ( $\bar{N}$ )	25	100
Maximal number of generations	100	100
Number of runs	20	20

**TABLE 2:** Parameter Settings for all MOEAs.

### 5.3. Performance Metrics

There are some metrics (or indicators) used for MOEA comparison in the literature. Some of them are C-measure “[4],[5]”, IGD (Inverted generational distance [11], HV (Hypervolume) indicator (S measure in [4], epsilon indicator [15], GD (Generational Distance) and  $\Delta$  “[2],[9]”. GD and  $\Delta$  metrics are used in assessing the performance of the algorithms in the experimental studies. The first metric (GD) measures the extent of convergence to a known set of Pareto-optimal solutions. First, a set of uniformly spaced solutions (500 is used in this paper) from the true Pareto-optimal front in the objective space is found. For each solution obtained with a MOEA, we compute the

minimum Euclidean distance between it and the chosen solutions on the Pareto-optimal front. The average of these distances is used as the convergence metric (GD) [2],[9]. Figure 6(a) shows the calculation procedure of this metric. The smaller the value of this metric, the better the convergence toward the Pareto-optimal front is.



**FIGURE 6.** (a) Convergence Metric (GD). (b) Diversity Metric ( $\Delta$ ).

The second metric ( $\Delta$ ) measures the extent of spread achieved among the obtained solutions. The Euclidean distance  $d_i$  between consecutive solutions in the obtained non-dominated set of solutions is calculated. The average  $\bar{d}$  of these distances is then calculated. Thereafter, from the obtained set of non-dominated solutions, we first calculate the extreme solutions (in the objective space) by fitting a curve parallel to that of the true Pareto-optimal front. Then, the following metric is used to calculate the non-uniformity in the distribution [2],[9]:

$$\Delta = \frac{d_f + d_l + \sum_{i=1}^{N-1} |d_i - \bar{d}|}{d_f + d_l + (N-1)\bar{d}} \quad (9)$$

Here, the parameters  $d_f$  and  $d_l$  are the Euclidean distances between the extreme solutions and the boundary solutions of the obtained non-dominated set, as depicted in Figure 6(b). The values of these two metrics are desired to be small.

#### 5.4. Discussion of the Simulation Results

In this paper, binary tournament is employed as a selection procedure. The single-point crossover and bit-wise mutation are applied. All methods have been run twenty-times on four benchmarks from the literature. Afterwards, mean and variance values of convergence (GD) and diversity ( $\Delta$ ) metrics are calculated. These two metrics are desired to be small.

In ACE\_SPEA (ACtive Elitist SPEA) and ACE\_SPEA2 (ACtive Elitist SPEA 2), the elite individuals are excited by mutation operator up to 31 iterations (it is decided by experimentation), after 31 iterations mutation is being ceased. If the mutants of excited elites better than original elites (Euclidian distance is used), they are substituted in the archive, otherwise original elites remain unchanged. At the same time, the elite individuals in  $k$ th iteration are recombined to the elite individuals in  $(k-n)$ th iteration. For example, the elites in iteration-20 are recombined sequentially to the elites in iteration-10 as depicted in Figure 3. If the excited individuals are better than the elites in iteration-20, then they are substituted in the archive, otherwise original elites remain unchanged.

Table 3 presents the mean and variance of the GD - metric values of the 20 final populations. Table 4 presents the mean and variance of the  $\Delta$  - metric values of the 20 final populations. To make an easy reading, the best results in Table 3 and Table 4 are shown in **bold**.

It is evident from Tables 3 and 4 that ACE\_SPEA significantly outperforms SPEA in terms of both the convergence (GD) and diversity ( $\Delta$ ) metrics on all test problems. Only on ZDT6 test functions, SPEA performs better than ACE\_SPEA in terms of diversity metric.

ACE\_SPEA2 significantly outperforms SPEA2 in terms of both the convergence (GD) and diversity ( $\Delta$ ) metrics on all test problems. Only on ZDT2 test functions, SPEA2 performs better than ACE\_SPEA2 in terms of diversity metric.

	<b>ZDT1</b>	<b>ZDT2</b>	<b>ZDT3</b>	<b>ZDT6</b>
<b>SPEA</b>	0.0627	0.0133	0.0517	1.2824
	2.1822e-4	2.3891e-4	2.5627e-4	0.2391
<b>ACE_SPEA</b>	<b>0.0549</b>	<b>0.0086</b>	<b>0.0488</b>	<b>1.1638</b>
	1.3940e-4	3.3388e-5	8.4167e-5	0.1942
<b>SPEA2</b>	0.0327	0.0044	0.0441	0.7672
	2.5225e-5	5.1226e-6	2.5372e-4	0.0232
<b>ACE_SPEA2</b>	<b>0.0293</b>	<b>0.0031</b>	<b>0.0345</b>	<b>0.7238</b>
	1.7667e-5	2.8834e-6	6.5541e-5	0.0410

**TABLE 3:** Mean (First Rows) and Variance (Second Rows) of the Convergence Metric (GD).

	<b>ZDT1</b>	<b>ZDT2</b>	<b>ZDT3</b>	<b>ZDT6</b>
<b>SPEA</b>	0.6170	0.6189	0.6320	<b>0.8425</b>
	0.0047	0.0032	0.0073	0.0079
<b>ACE_SPEA</b>	<b>0.5945</b>	<b>0.6062</b>	<b>0.6148</b>	0.8761
	0.0055	0.0056	0.0059	0.0070
<b>SPEA2</b>	0.5895	<b>0.6115</b>	0.6080	0.8285
	0.0041	0.0033	0.0112	0.0060
<b>ACE_SPEA2</b>	<b>0.5761</b>	0.6322	<b>0.5874</b>	<b>0.8147</b>
	0.0038	0.0031	0.0095	0.0089

**TABLE 4:** Mean (First Rows) and Variance (Second Rows) of the Diversity Metric ( $\Delta$ ).

To demonstrate some of the cases graphically, SPEA with ACE\_SPEA and SPEA2 with ACE\_SPEA2 are compared on several problems. Figure 7 to 14 shows the non-dominated solutions of all algorithms for arbitrarily chosen single runs of test problems ZDT1 and ZDT2.

The plots of the final solutions in the objective space in the Figure 7,8,9 and 10 also clearly show that the approximations generated by ACE\_SPEA are better than those by SPEA on all test problems. Also, ACE\_SPEA has a better spread than SPEA.

The plots of the final solutions in the objective space in the Figure 11,12,13 and 14 also clearly show that the approximations generated by ACE\_SPEA2 are better than those by SPEA2 on all test problems. Also, ACE\_SPEA2 has a better spread than SPEA2.

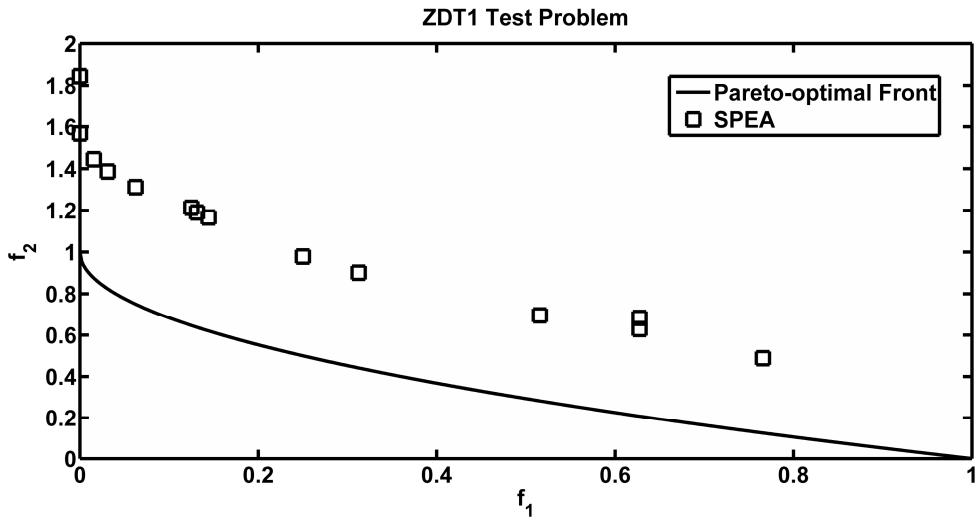


FIGURE 7. Non-dominated solutions of SPEA for a single run of ZDT1.

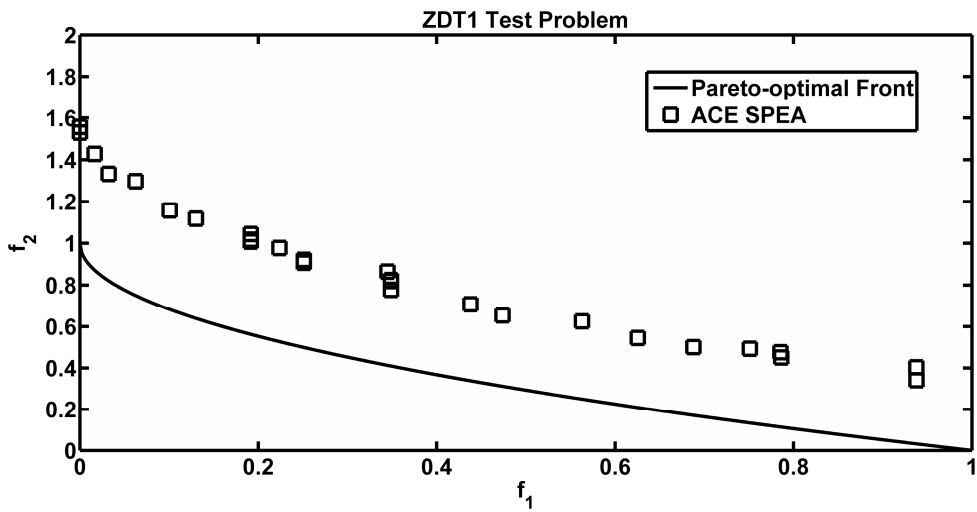


FIGURE 8. Non-dominated solutions of ACE\_SPEA for a single run of ZDT1.

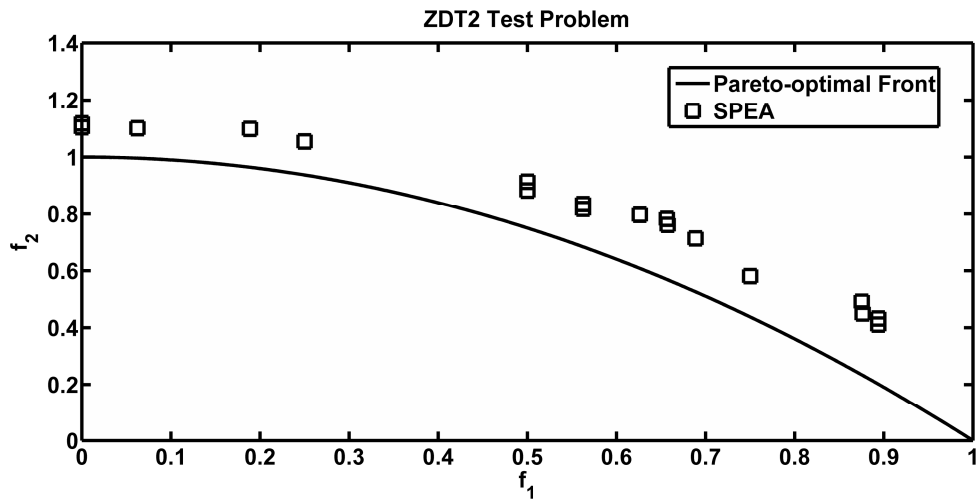


FIGURE 9. Non-dominated solutions of SPEA for a single run of ZDT2.

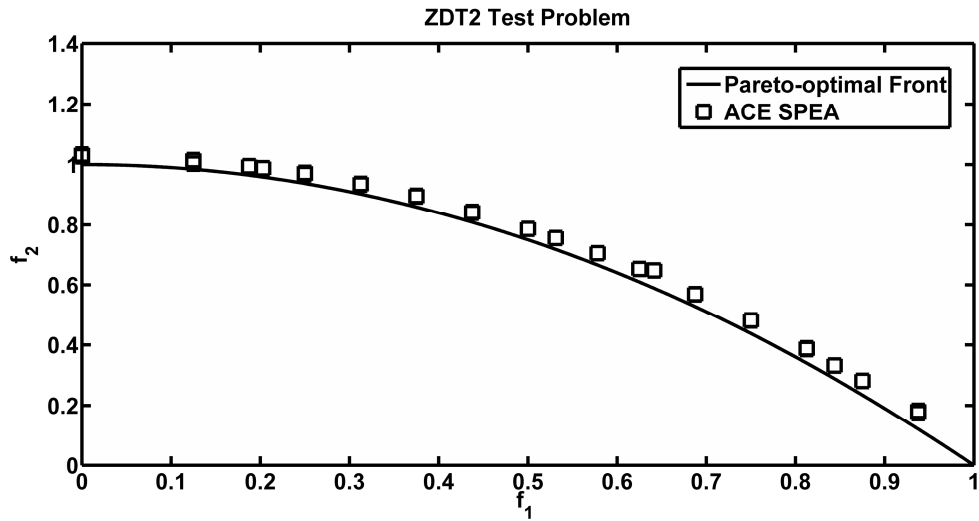


FIGURE 10. Non-dominated solutions of ACE\_SPEA for a single run of ZDT2.

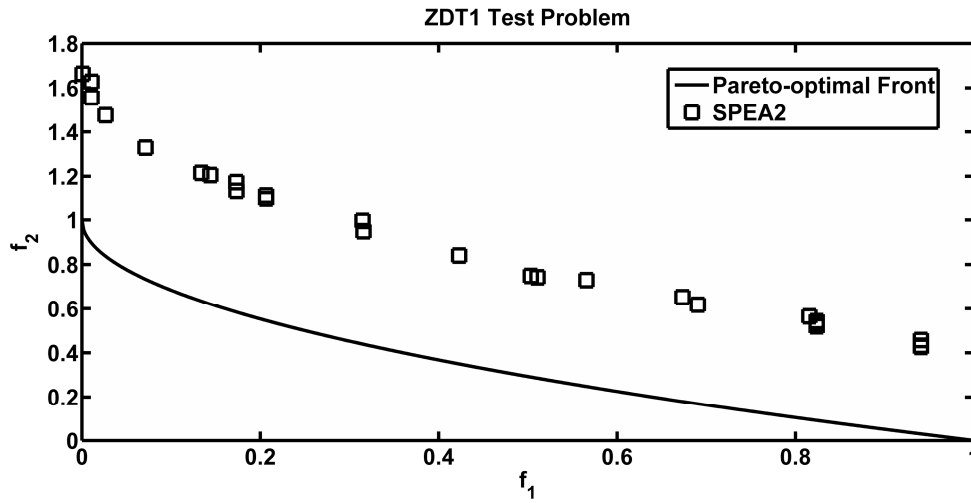


FIGURE 11. Non-dominated solutions of SPEA2 for a single run of ZDT1.

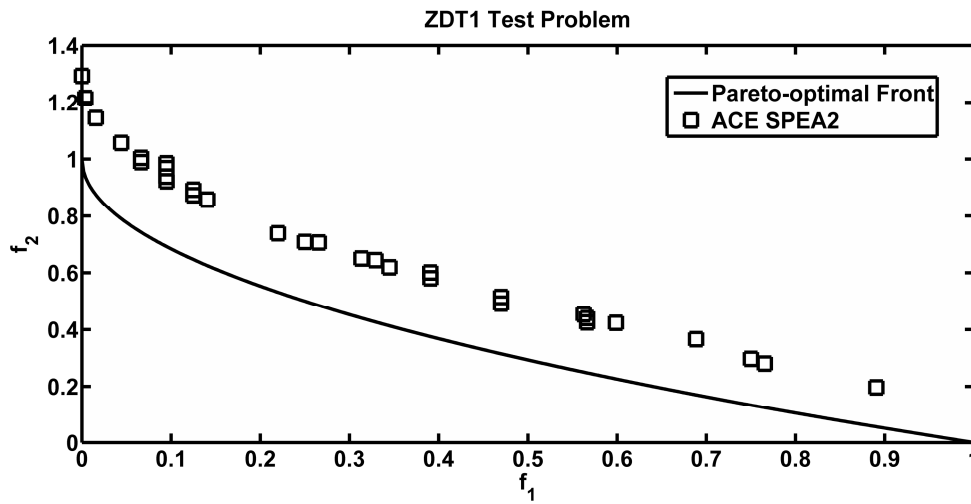


FIGURE 12. Non-dominated solutions of ACE\_SPEA2 for a single run of ZDT1.

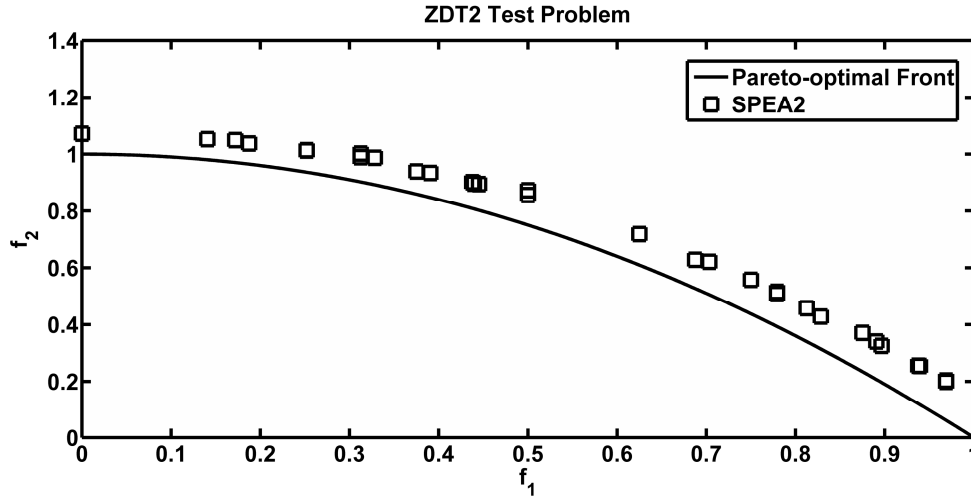


FIGURE 13. Non-dominated solutions of SPEA2 for a single run of ZDT2.

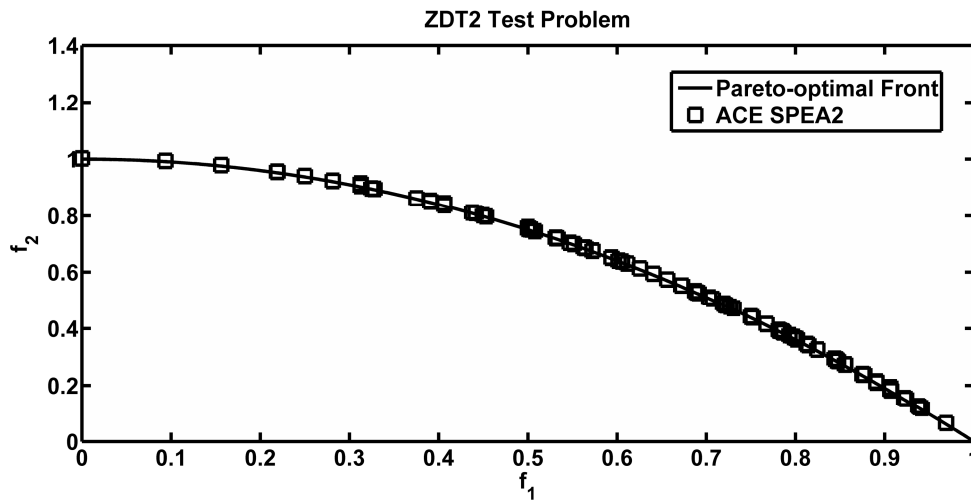


FIGURE 14. Non-dominated solutions of ACE\_SPEA2 for a single run of ZDT2.

## 6. CONCLUSION

In this paper, an active elitism mechanism for multi-objective evolutionary algorithms is proposed. Passive elitism mechanism has been replaced by the proposed active elitism mechanism. The elite individuals are the best individuals and also the nearest individuals to the solution in the current population. Therefore, excitement of a set of elites in the archive with crossover/mutation operator forces them to generate likely better and more diverse than the original elites. In this regards, classical *holding/sending back* passive elitism structure has been improved and evolved into an active elitism structure of *holding/exciting and sending back*. It means that, primary and also secondary populations (or archives) can generate solutions in the active elitism.

Well-known SPEA and SPEA2 methods equipped with passive elitism and proposed ACE\_SPEA and ACE\_SPEA2 methods equipped with active elitism have been simulated and compared on four continuous problems taken from the literature (including ZDT1, ZDT2, ZDT3 and ZDT6). It is found that ACE\_SPEA significantly outperforms SPEA on all test problems. Only exception of this is that SPEA generates a slightly better spread on ZDT6 than ACE\_SPEA. ACE\_SPEA2 is superior to SPEA2 in terms of both the convergence (GD) and diversity ( $\Delta$ ) metrics on all test problems. Only exception of this is that SPEA2 generates a slightly better spread on ZDT2 than ACE\_SPEA2.

Simulation results show that the active elitism is especially beneficial to improve the performance of MOEAs and that the use of the active elitism mechanism speeds up convergence to the Pareto-optimal front. In addition to that, proposed active elitism mechanism can easily be integrated into existing MOEAs in the literature to improve their performance without changing their entire computational structures.

In the future work, the active elitism will be embedded to the other MOEAs in the literature. Furthermore, it is planned to speed up the active elitism algorithm.

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