

# Improved Multi-Objective Diversity Control Oriented Genetic Algorithm

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**Abstract.** This paper presents an improved multi-objective diversity control oriented genetic algorithm (MODCGA-II). The improvement includes the introduction of an objective-domain diversity control operator, which is chromosome representation independent, and a solution archive. The performance comparison between the MODCGA-II, a non-dominated sorting genetic algorithm II (NSGA-II) and an improved strength Pareto evolutionary algorithm (SPEA-II) is carried out where different two-objective benchmark problems with specific multi-objective characteristics are utilised. The results indicate that the MODCGA-II solutions are better than the solutions generated by the NSGA-II and SPEA-II in terms of the closeness to the true Pareto optimal solutions and the uniformity of solution distribution along the Pareto front.

## 1 Introduction

It is undeniable that a major factor that contributes to the success of genetic algorithms in the field of optimisation is the parallel search mechanism embedded in the algorithm itself. However, this does not prevent the occurrence of premature convergence in the situation when the similarity among individuals in the population becomes too high. As a result, the prevention of a premature convergence must also be considered during the genetic algorithm design. One of the direct approaches for achieving the necessary prevention is to maintain diversity within the population [1].

Various strategies can be used to maintain or increase the population diversity. Nonetheless, a modification on the selection operation has received much attention. For instance, Mori et al. [2] has introduced a notion of thermodynamical genetic algorithm where the survival of individuals is regulated by means of monitoring the free energy within the population. The modification on the selection operation can also be done in the cross-generational sense [3,4,5]. Whitley [3] has proposed a GENITOR system where offspring generated by standard operators are chosen for replacing parents based upon the ranks of the individuals.

In contrast to Whitley [3], Eshelman [4] recommends the application of mating restriction while Shimodaira [5] suggests the use of variable-rate mutation as a means to create offspring. Then a cross-generational survival selection is carried out using a standard fitness-based selection technique in both cases.

In addition to the early works described above, another genetic algorithm has been specifically developed by Shimodaira [6] to handle the issue of population diversity; this algorithm is called a diversity control oriented genetic algorithm or DCGA. Similar to most genetic algorithms, offspring in the DCGA are generated using standard crossover and mutation operators. However, during the cross-generational survival selection, duplicated individuals in the merged population containing both parent and offspring individuals are first eliminated. Then, the remaining individuals are selected based on either the associate fitness or the consideration on both the fitness and the genomic similarity between the interested individual and the elite individual. The performance of the DCGA has been benchmarked using various test problems [7].

With a minor modification, the DCGA can also be used in multi-objective optimisation. One possible approach for achieving this is to integrate the DCGA with other genetic algorithms that are specifically designed for multi-objective optimisation such as a multi-objective genetic algorithm or MOGA [8]. Such approach has been investigated by Sangkawelert and Chaiyaratana [9] where the inclusion of cross-generational survival selection with the multi-objective genetic algorithm is equivalent to the use of elitism, which is proven to be crucial to the success of various multi-objective algorithms including a non-dominated sorting genetic algorithm II or NSGA-II [10] and an improved strength Pareto evolutionary algorithm or SPEA-II [11]. In addition, the similarity measurement between the non-elite individual and the elite individual required by the diversity control operator is still carried out in the genotypic space. The resulting combined algorithm, which can be uniquely referred to as a multi-objective diversity control oriented genetic algorithm or MODCGA has been successfully tested using a two-objective benchmark suite [12]. Although some insights into the behaviour of the MODCGA have been gained through the benchmark trial by Sangkawelert and Chaiyaratana [9], further studies can be made and are required. In particular, the initial study of the MODCGA is conducted with a similarity measurement between two individuals being carried out in genotypic space. However, in multi-objective optimisation the trade-off surface, which is the direct result from the spread of solutions, is generally defined in objective space. This means that diversity control can also be achieved by considering the similarity between objective vectors of the individuals.

The organisation of this paper is as follows. In section 2, the explanation of the original DCGA and how it can be modified to cope with multi-objective optimisation problems is given. In section 3, the multi-objective benchmark problems and performance evaluation criteria are explained. Next, the multi-objective benchmarking results of the improved MODCGA or MODCGA-II are illustrated and discussed in section 4. Finally, the conclusions are drawn in section 5.

## 2 DCGA and Its Extension

The original DCGA developed by Shimodaira [6] can only be used to solve single-objective optimisation problems. However, the algorithm can be easily combined with other genetic algorithms. The extension of the DCGA for use in multi-objective optimisation that will be used throughout this paper involves the integration between the DCGA and MOGA. However, in contrast to the previous work by Sangkawelert and Chaiyaratana [9] where the similarity measurement between individuals is conducted in genotypic space, in this work the measurement will be carried out in objective space. Detailed explanation of the DCGA, MOGA and algorithm integration is given as follows.

### 2.1 Diversity Control Oriented Genetic Algorithm

The diversity control oriented genetic algorithm (DCGA) was first introduced by Shimodaira [6]. Similar to other single-objective steady-state genetic algorithms, the parent population and the offspring population are merged together during the DCGA run where the appropriated individuals are extracted from the merged population. However, instead of selecting the highly fit individuals from the population straightaway, the extraction process in the DCGA starts with the elimination of duplicated individuals in the merged population. The remaining individuals are then sorted according to their fitness values in descending order. Following that the best individual from the remaining individuals is determined and kept for passing onto the next generation. Then either a cross-generational deterministic survival selection (CDSS) method or a cross-generational probabilistic survival selection (CPSS) method is applied in the top-down fashion to the remaining non-elite individuals in the sorted array. In the case of the CDSS, the remaining non-elite individuals with high fitness value will have a higher chance of being selected since they reside in the top part of the array and hence have a higher selection priority than individuals with low fitness values. In contrast, a survival probability value is assigned to each non-elite individual according to its similarity to the best individual in the case of the CPSS. This survival probability ( $p_s$ ) is given by

$$p_s = \{(1 - c)d_h/L + c\}^\alpha \quad (1)$$

where  $d_h$  is the Hamming distance between the interested individual and the best individual,  $L$  is the binary chromosome length,  $c$  is the shape coefficient and  $\alpha$  is the exponent coefficient. With this form of survival probability assignment, if the genomic structure of the individual interested is very close to that of the best individual, the survival probability assigned to this individual will be close to zero. On the other hand, if the chromosome structure of this individual is quite different from that of the best individual, its survival probability will be close to one. Each individual will then be selected according to the assigned survival probability where the survival selection of the sorted non-elite individuals is still carried out in the top-down manner. With the use of sorted

individual array, the selection of non-elite individuals will depend entirely on the assigned fitness in the CDSS scheme. On the other hand, a decision either to select or not to select an individual according to the CPSS scheme depends on both the assigned fitness and the survival probability. Basically, the individual that have a high chance of being selected must possess high fitness and have a genomic structure that is quite different from that of the best individual. This also means that both a highly fit individual that is quite resemble to the best individual and a mediocre individual that is different from the best individual would not have a high chance of being picked. If the total number of all selected individuals including the pre-selected elite individual does not reach the required population size after the survival selection loop, randomly generated individuals will be added to the individual array until the required number is met. A comprehensive description of the DCGA and its benchmarking performance in various continuous test problems can be found in Shimodaira [7].

## 2.2 Multi-Objective Genetic Algorithm

The multi-objective genetic algorithm (MOGA) was first introduced by Fonseca and Fleming [8]. The MOGA functions by seeking to optimise the components of a vector-valued objective function. Unlike single-objective optimisation, the solution to a multi-objective optimisation problem is a family of points known as the Pareto optimal set. Each point in the set is optimal in the sense that no improvement can be achieved in one component of the objective vector that does not lead to degradation in at least one of the remaining components. Given a set of possible solutions, a candidate solution is said to be Pareto optimal if there are no other solutions in the solution set that can dominate the candidate solution. In other words, the candidate solution would be a non-dominated solution. Assuming, without loss of generality, a minimisation problem, an  $m$ -dimensional cost vector  $\mathbf{u}$  is said to be dominating another  $m$ -dimensional cost vector  $\mathbf{v}$  if, and only if,  $\mathbf{u}$  is partially less than  $\mathbf{v}$  ( $\mathbf{u} p < \mathbf{v}$ ), i.e.

$$\mathbf{u} p < \mathbf{v} \leftrightarrow \forall i = 1, \dots, m : u_i \leq v_i \wedge \exists i = 1, \dots, m : u_i < v_i. \quad (2)$$

By identifying the number of solutions in the solution set that dominate the solution of interest, a rank value can be assigned to the solution. In other words, the rank of a candidate solution is given by the number of solutions in the solution set that dominate the candidate solution. After a rank has been assigned to each solution, a fitness value can then be interpolated onto the solution where a genetic algorithm can subsequently be applied in the optimisation procedure. Since the aim of a search by the MOGA is to locate Pareto optimal solutions, in essence the multi-objective optimisation problem has also been treated as a multi-modal problem. Hence, the use of additional genetic operators including the fitness sharing and mating restriction procedures is also required. However, in addition to the usual application of the fitness sharing and mating restriction procedures in the decision variable space, they can also be carried out in the objective space. A comprehensive description of the MOGA, which covers other

advanced topics including goal attainment and priority assignment strategies, can be found in Fonseca and Fleming [8].

### 2.3 Genetic Algorithm Integration

By combining the MOGA and the DCGA together, the resulting algorithm can be referred to as a multi-objective diversity control oriented genetic algorithm or MODCGA. Similar to the MOGA, the rank of each individual will be obtained after comparing it with the remaining individuals. However, the comparison will be made among individuals in the merged population, which is the result from combining parent and offspring populations together. Since the best individuals in the MOGA are the non-dominated individuals, in the case where the CPSS method is used there will be more than one survival probability value that can be assigned to each dominated individual. In this study, the lowest value in the probability value set is chosen for each dominated individual. After the survival selection routine is completed and the fitness values have been interpolated onto the individuals, the standard genetic operations can then be applied to the population in the usual way. In the early work by Sangkawelert and Chaiyaratana [9], a similarity measurement between dominated and non-dominated individuals, which leads to the survival probability assignment, is carried out in genotypic space. In this work, the similarity measurement will be conducted in objective space instead; two advantages are gained through this modification. Firstly, since the aim of multi-objective optimisation is to obtain multiple solutions at which together produce a trade-off objective surface that represents a Pareto front, diversity control in objective space would directly enforce this aim. Secondly, a diversity control operator that is designed for use in objective space would be independent of the chromosome encoding scheme utilised. Recent investigation into multi-objective optimisation using genetic algorithms usually involves problems with large number of decision variables [10,11,12]. The use of a binary representation would lead to an excessively long chromosome and hence degrades the algorithm performance. As a result, real-value chromosome encoding is generally employed instead. With the modification described above, in the case of CPSS scheme the survival probability as given in equation (1) will change to

$$p_s = \{(1 - c)d/d_{max} + c\}^\alpha \quad (3)$$

where  $d$  is the distance between the interested individual and a non-dominated individual in objective space and  $d_{max}$  is the maximum distance between two individuals in the population. In order to distinguish between the early work by Sangkawelert and Chaiyaratana [9] and the present work, the MODCGA where the similarity measurement is done in objective space will be referred throughout this paper as the MODCGA-II. In this investigation, the fitness sharing strategy utilised in the MODCGA-II is similar to the one described in Fonseca and Fleming [8] where the fitness sharing is carried out in objective space.

In addition to the modification on the diversity control operation, the use of a preserved non-dominated solution archive is included in the MODCGA-II. Basi-

cally, the parent individuals will be picked from a population which includes both individuals obtained after the diversity control and that from the archive. Each time that a new population is created after the diversity control operation, non-dominated solutions within the archive will be updated. If the solution that survives the diversity control operation is neither dominated by any solutions in the archive nor a duplicate of a solution in the archive, then this solution will be added to the archive. At the same time, if the solution that survives the diversity control operation dominates any existing solution in the archive, the dominated solution will be expunged from the archive. In order to maintain the diversity within the preserved non-dominated solution archive,  $k$ -nearest neighbour clustering technique [11] is used to regulate the size of the archive.

### 3 Multi-objective Problems and Performance Criteria

The MODCGA-II will be benchmarked using six optimisation test cases developed by Deb et al. [13]. The problems DTLZ1–DTLZ6 are scalable minimisation problems with  $n$  decision variables and  $m$  objectives. In this paper, two-objective problems with 11 decision variables are investigated. DTLZ1 has a linear Pareto front and contains multiple local fronts. DTLZ2 has a spherical Pareto front. DTLZ3 and DTLZ4 also have spherical Pareto fronts where DTLZ3 contains multiple local fronts while the DTLZ4 solutions are non-uniformly distributed in the search space. DTLZ5 has a curve Pareto front. DTLZ6 also has a curve Pareto front but the problem contains multiple local fronts.

Zitzler et al. [12] suggest that to assess the optimality of non-dominated solutions identified by a multi-objective optimisation algorithm, these solutions should be compared among themselves and with the true Pareto optimal solutions. Two corresponding measurement criteria are considered: the average distance between the non-dominated solutions to the Pareto optimal solutions ( $M_1$ ) and the distribution of the non-dominated solutions ( $M_2$ ). These criteria are calculated from the objective vectors of the solutions obtained. A low  $M_1$  value implies that the solutions are close to the true Pareto optimal solutions. In addition, when two solution sets have similar  $M_1$  indices, the set with a higher  $M_2$  value would have a better distribution.

### 4 Results and Discussions

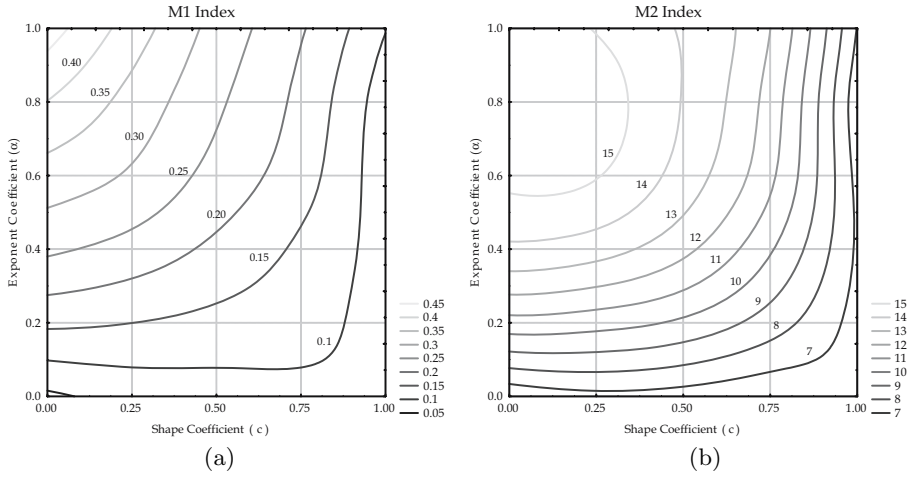
In this section, the results from using the MODCGA-II to solve test problems DTLZ1–DTLZ6 will be presented. The results will be benchmarked against that obtained from the non-dominated sorting genetic algorithm II or NSGA-II [10] and the improved strength Pareto evolutionary algorithm or SPEA-II [11] where the executable codes for the implementation of both algorithms are obtained directly from A Platform and Programming Language Independent Interface for Search Algorithms (PISA) web site (<http://www.tik.ee.ethz.ch/pisa>). Both CDSS and CPSS techniques are utilised in the implementation of the MODCGA-II. The diversity control study will be conducted with other genetic parameters

**Table 1.** Parameter setting for the MODCGA-II, NSGA-II and SPEA-II

Parameter	Value and Setting
Chromosome coding	Real-value representation
Fitness sharing	Triangular sharing function (MODCGA-II only)
Fitness assignment	Linear fitness interpolation (MODCGA-II only)
Selection method	Stochastic universal sampling (MODCGA-II) or tournament selection (NSGA-II and SPEA-II)
Crossover method	SBX recombination with probability = 1.0 [14]
Mutation method	Variable-wise polynomial mutation with probability = $1/\text{number of decision variables}$ [14]
Population size	100
Archive size	100 (MODCGA-II and SPEA-II only)
Number of generations	300 (MODCGA-II) or 600 (NSGA-II and SPEA-II)
Number of repeated runs	30

remain fixed throughout the trial. The parameter setting for the MODCGA-II, NSGA-II and SPEA-II that is used in all problems is displayed in Table 1.

Five values of the shape coefficient ( $c$ )—0.0, 0.25, 0.50, 0.75 and 1.00—and six values of the exponent coefficient ( $\alpha$ )—0.00, 0.20, 0.40, 0.60, 0.80 and 1.00—are used to create 30 different diversity control settings for the MODCGA-II. From equation (3), the settings of  $c = 1.00$  and  $\alpha = 0.00$  are for the implementation of the CDSS technique since the survival probability of each dominated individual is equal to one. For each setting, the MODCGA-II runs for the DTLZ1–DTLZ6 problems with two objectives are repeated 30 times. The  $M_1$  and  $M_2$  performance indices from each run are subsequently obtained and the average values of the two indices calculated from all problems are displayed in the form of contour plots in Fig. 1. The  $M_2$  index is calculated using the neighbourhood parameter  $\sigma = 0.488$  and the  $M_2$  index has been normalised by the maximum attainable number of non-dominated individuals from a single run. From Fig. 1, it is noticeable that a significant performance variation can be detected in the benchmark problems. The region where the  $M_1$  index has a small value coincides with the area where the  $M_2$  index is small. At the same time the region where the  $M_1$  index is high is also in the vicinity of the area where the  $M_2$  index has a large value. In a successful multi-objective search, the  $M_1$  index should be as small as possible. Although a large  $M_2$  index usually signifies a good solution distribution, the interpretation of the  $M_2$  result must always be done while taken the  $M_1$  index into consideration. This is because in the case where the solutions are further away from the true Pareto optimal solutions, the obtained value of the  $M_2$  index is generally high since each solution would also be far apart from one another. In other words, the  $M_2$  index has a lesser priority than the  $M_1$  index and should be considered only when the obtained values of the  $M_1$  index from two different algorithms or algorithm settings are close to one another. Using the above argument, multiple settings of the  $c$  and  $\alpha$  values in Fig. 1 can be used to achieve low  $M_1$  indices. In the current investigation, the setting where



**Fig. 1.** Average values of  $M_1$  and  $M_2$  indices from all multi-objective problems for each diversity control setting (a)  $M_1$  index (b)  $M_2$  index

$c = 0.75$  and  $\alpha = 0.2$  is chosen as the candidate setting that represents the diversity control that leads to a low  $M_1$  value.

The search performance of the MODCGA-II with  $c = 0.75$  and  $\alpha = 0.2$  will be compared with that from the NSGA-II and SPEA-II. As stated in Table 1, each algorithm run will be repeated 30 times where the  $M_1$  and normalised  $M_2$  indices are subsequently calculated for each repeated run. After all repeated runs are completed, the individuals from all runs are merged together where the final non-dominated individuals are then extracted. The performance of the MODCGA-II, NSGA-II and SPEA-II in terms of the average and standard deviation of the  $M_1$  and normalised  $M_2$  indices on the two-objective DTLZ1–DTLZ6 problems is summarised in Table 2. In Table 2, the neighbourhood parameter ( $\sigma$ ) for the calculation of  $M_2$  indices for all test problems is also set to 0.488; the parameter is set using the extent of the true Pareto front in the objective space as the guideline.

In terms of the average distance from the non-dominated solutions identified to the true Pareto front or the  $M_1$  criterion, the MODCGA-II possesses the highest performance in all six test problems. Nonetheless, the MODCGA-II is unable to identify the true Pareto optimal solutions in the DTLZ3 and DTLZ6 problems. These two problems are difficult to solve since they contain multiple local Pareto fronts. Although the DTLZ1 problem also contains numerous local Pareto fronts, the majority of results from all 30 MODCGA-II runs indicate that the MODCGA-II is capable of solving this problem. This means that the shape of the Pareto front in two-objective problems can also affect the algorithm performance since the DTLZ1 problem has a linear Pareto front while the DTLZ3 and DTLZ6 problems have spherical and curve Pareto fronts, respectively. The  $M_1$  index also reveals that the performance of NSGA-II and SPEA-II are very similar in all six problems. Since the  $M_1$  indices from both algorithms are quite



**Table 2.** Summary of the MODCGA-II, NSGA-II and SPEA-II performances on the two-objective DTLZ1–DTLZ6 problems

Problem Index		MODCGA-II		NSGA-II		SPEA-II	
		Average	S.D.	Average	S.D.	Average	S.D.
DTLZ1	$M_1$	3.1157	4.7837	11.9186	5.1490	12.9616	5.2649
	$M_2$	0.4326	0.2942	0.6391	0.0474	0.7810	0.0547
DTLZ2	$M_1$	0.0030	0.0008	0.0148	0.0088	0.0190	0.0096
	$M_2$	0.5039	0.0439	0.5672	0.0310	0.5053	0.0494
DTLZ3	$M_1$	22.2335	18.1880	78.6069	24.8055	88.4823	22.4487
	$M_2$	0.5642	0.3941	0.6119	0.0814	0.7463	0.0745
DTLZ4	$M_1$	0.0023	0.0018	0.0238	0.0138	0.0252	0.0104
	$M_2$	0.3353	0.2111	0.2871	0.2353	0.3457	0.2417
DTLZ5	$M_1$	0.0030	0.0006	0.0148	0.0088	0.0175	0.0079
	$M_2$	0.4972	0.0495	0.5672	0.0310	0.5026	0.0501
DTLZ6	$M_1$	1.0199	0.3685	6.4295	0.3509	6.4986	0.3355
	$M_2$	0.8044	0.0603	0.7157	0.0493	0.8946	0.0166

close, a further inspection on the  $M_2$  indices can be easily made. Again, the  $M_2$  indices from the NSGA-II and SPEA-II are also very close to one another. This leads to the conclusion that the capability of both the NSGA-II and SPEA-II is similar.

## 5 Conclusions

In this paper, an improved multi-objective diversity control oriented genetic algorithm or MODCGA-II is presented. The proposed algorithm differs from the MODCGA described in Sangkawelert and Chaiyaratana [9] in the sense that the MODCGA-II performs diversity control via similarity measurement in objective space and the use of a preserved non-dominated solution archive is also included. Six scalable benchmark problems described in Deb et al. [13] are utilised. In addition, the criteria used to assess the algorithm performance include the closeness of non-dominated solutions to the true Pareto front and the distribution of the solutions across the front [12]. The analysis indicates that the MODCGA-II can produce non-dominated solutions that are better than that generated by the NSGA-II [10] and the SPEA-II [11] when the number of objectives in the benchmark problems is limited to two.

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