

Indicator Based Cooperative Coevolution for Multi-objective Optimization

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Abstract—Cooperative coevolutionary algorithms (CCAs) are extensions of traditional Evolutionary Algorithms (EAs) that have a lot of potential in addressing some problems on which EAs tend to perform poorly. They have become an important area of research in the field of evolutionary computation and since the cooperative coevolutionary framework has been extended to multi-objective optimization, a number of approaches have been proposed incorporating the CCA framework to improve the performance of multi-objective EAs. The advantage of cooperative coevolutionary algorithms is the decomposition of the problem they use, which allows us to learn different parts of the problem instead of the whole problem at once. Cooperative coevolution has a symbiotic approach that evolves species populations (each one managing a part of the problem) which are evaluated based on how well they perform together. In order to form a solution, an individual from each species is selected and combined with the other selected individuals. The solution is then evaluated and the individuals that make up the solution are scored based on the fitness of the combined solution. Selection for collaboration is a core issue in cooperative coevolutionary framework. However, the usual approach that has been used in Cooperative Coevolutionary Multi-objective EAs (CCMOEAs) is a method based on Pareto optimality. In this work we present a novel collaboration formation mechanism for CCMOEAs based on the use of the hypervolume indicator. Our preliminary results confirm the impact that the collaboration mechanism has on the performance of CCMOEAs and indicate that the proposed framework clearly improves the results over a CCMOEAs whose selection mechanism for collaboration is based on Pareto optimality.

I. INTRODUCTION

In nature, coevolution is the process of reciprocal genetic change in one species, or group, in response to another. This process has been utilized within Evolutionary Algorithms (EAs) giving rise to the so-called *Coevolutionary Algorithms* (CAs) [1]. The idea of CAs comes from the biological observations which shows that coevolving some number of species defined as collections of phenotypically similar individuals is more realistic than simply evolving a population containing representatives of one species [2]. CAs are then natural extensions of traditional EAs. The main elements of these extensions lay in the adaptive nature of fitness evaluation for the members of coevolutionary systems where individuals are assigned fitness values based on interactions with other individuals from other species (each one representing a piece of a larger problem). It is the task of those populations to

evolve to increasingly fitter pieces for the larger problem. So, instead of evolving a population (global or spatially distributed) of similar individuals representing a global solution, it is more appropriate to coevolve subpopulations of individuals representing specific parts of the global solution. A coevolutionary search then involves the use of multiple species as the representation of a solution to an optimization problem. Each species can either compete or cooperate during the search evolution. For this reason, coevolutionary models have been historically categorized as competitive or cooperative. In this work, our interest is in the second category, the so-called cooperative coevolutionary algorithms (CCAs), which are able to exploit the compositional nature of problems. CCAs use individuals which belong to different species that represent a component of a larger problem and these individuals are rewarded when they work well with other individuals and punished when they perform poorly together [3].

Since the cooperative coevolutionary framework can be extended in a relatively easy way to multi-objective optimization, there has been a growing interest in the application of such framework within Multi-objective Evolutionary Algorithms (MOEAs). Several approaches have been proposed which incorporate it to improve the performance of multi-objective EAs [1], [4]–[6], giving rise to the so-called *Cooperative Coevolutionary MOEAs* (CCMOEAs). A key issue in cooperative coevolution is the way collaborations are done. When applied to Multi-objective Optimization Problems (MOPs), there exist a wide range of possibilities and different ways in which this process can be done. However, most of the existing approaches have not explored many ideas and the usual way is a selection mechanism based on Pareto dominance. The common way to perform the evaluation of each individual is by taking one representative from the other populations that belongs to the best set of non-dominated solutions found so far. Nevertheless, there is a potential problem with this approach; there is no mechanism which awards a ranking based on the contribution of the solution components. Without such a mechanism, potentially good components are lost because they may participate with components in a candidate solution that create new solutions with poor improvements or no improvement at all. In this work, we introduce a novel collaboration formation technique, based on an indicator-based selection mechanism, for Cooperative Coevolutionary MOEAs and present a new algorithm which incorporates it.

We claim that this new mechanism encourages a rewarding of components participating in successful collaborations from each species and improves CCMOEAs performance.

The remainder of this paper is organized as follows. In Section II, we provide some basic concepts related to multi-objective optimization, which are included to make the paper self-contained. The previous related work is discussed in Section III. Section IV is devoted to present our proposed approach and the experiments carried out. Finally, our conclusions and some possible paths for future work are drawn in Section V.

II. THE MULTI-OBJECTIVE OPTIMIZATION PROBLEM

The Multi-objective Optimization Problem (MOP) can be defined as the problem of finding a vector of decision variables which satisfies constraints and optimizes a vector function whose elements represent the objective functions. Hence, the term “optimize” means finding such a solution which would give the values of all the objective functions acceptable to the decision maker [1]. In the following definitions we are assuming, without loss of generality, the minimization of all the objectives. Mathematically, we can write MOPs as:

$$\text{minimize } \vec{f}(\vec{x}) = [f_1(\vec{x}), f_2(\vec{x}), \dots, f_k(\vec{x})]^T \quad (1)$$

subject to:

$$g_i(\vec{x}) \leq 0 \quad i = 1, 2, \dots, m \quad (2)$$

$$h_i(\vec{x}) = 0 \quad i = 1, 2, \dots, p \quad (3)$$

where k is the number of objective functions $f_i : \mathbb{R}^n \rightarrow \mathbb{R}$, $g_i, h_j : \mathbb{R}^n \rightarrow \mathbb{R}$, $i = 1, \dots, m$, $j = 1, \dots, p$ are the constraint functions of the problem and $\vec{x} = [x_1, x_2, \dots, x_n]^T$ the vector of decision variables. We thus wish to determine from the set Ω (where Ω is the feasible region) of all the vectors that satisfy (2) and (3) to the vector $\vec{x}^* = [x_1^*, x_2^*, \dots, x_n^*]^T$ of solutions that are *Pareto optimal*. To describe the concept of optimality that we will adopt, we need to introduce a few additional definitions.

Pareto Optimality: We say that a vector of decision variables $\vec{x}^* \in \Omega$ (where Ω is the feasible region) is **Pareto Optimal** with respect to Ω if and only if $\forall \vec{x} \in \Omega \wedge \forall i \in \{1, \dots, k\}$:

$$f_i(\vec{x}) = f_i(\vec{x}^*) \vee \exists i \in \{1, \dots, k\} : f_i(\vec{x}) < f_i(\vec{x}^*) \quad (4)$$

Pareto Dominance: A vector $\vec{u} = [u_1, \dots, u_k]^T$ is said to **dominate** another vector $\vec{v} = [v_1, \dots, v_k]^T$ (denoted by $\vec{u} \preceq \vec{v}$) if and only if \vec{u} is partially less than \vec{v} , i.e.,:

$$\forall i \in \{1, \dots, k\}, u_i \leq v_i \wedge \exists i \in \{1, \dots, k\} : u_i < v_i \quad (5)$$

Pareto Optimal Set: For a given MOP $\vec{f}(\vec{x})$, the **Pareto Optimal Set** P^* is defined by:

$$P^* := \{\vec{x} \in \Omega \mid \nexists \vec{x}' \in \Omega, \vec{f}(\vec{x}') \preceq \vec{f}(\vec{x})\} \quad (6)$$

Pareto Front: For a given MOP $\vec{f}(\vec{x})$ and its Pareto optimal set P^* , the **Pareto Front** PF^* is defined by:

$$PF^* := \{\vec{f}(\vec{x}) \mid \vec{x} \in P^*\} \quad (7)$$

When plotted in objective space, the non-dominated vectors are collectively known as the **Pareto front**.

III. COOPERATIVE COEVOLUTION

Potter and De Jong pioneered the research on cooperative coevolutionary EAs by developing the first framework of cooperative coevolution (CC) utilized within evolutionary algorithms [7] with their *Cooperative Coevolutionary Genetic Algorithm* (CCGA). Potter’s framework uses a divide-and-conquer approach to split the decision variables into subpopulations of smaller size, so that each of these subpopulations is optimized with a separate EA. The main idea was to decompose a high-dimensional problem into several low-dimensional subcomponents and evolve these subcomponents cooperatively for a predefined number of *cycles*. Each of these components receives a fitness value based on how well it performs in conjunction with individuals from other species. For the problem decomposition, Potter and De Jong took each decision variable of the problem as a subcomponent.

In Potter’s model, each population contains individuals representing a component of a larger solution, and evolution of these populations occurs almost independently, in tandem with one another, interacting only to obtain fitness. Such a process can be static, in the sense that the divisions for the separate components are decided a priori and never altered, or dynamically, in the sense that populations of components may be added or removed as the run progresses [8]. After Potter’s work there were many more *cooperative coevolutionary* approaches, most of them to large scale global optimization, since it showed to be a good framework for solving large scale problems [9]–[13]. The original CC framework can be summarized as follows:

- 1) Decompose the vector of decision variables into m low dimensional subcomponents.
- 2) Set $j = 1$ to start a new cycle.
- 3) Optimize the j -th subcomponent with a certain EA for a predefined number of fitness evaluations (FEs).
- 4) If $j < m$ then $j++$, and go to Step 3.
- 5) Stop if the stopping criteria are satisfied; otherwise go to Step 2 for the next cycle.

The coevolutionary effect in the CCGA is produced by a cooperation among all species.

When extending this cooperative coevolutionary framework to a multi-objective scenario, the MOP is decomposed along the search space of the problem. Each decision variable may be assigned to a number of species populations and a species population may be optimizing more than one decision variable. Therefore, each population contains individuals that represent a particular component (in decision variables space) of the problem, so that one member from each population is needed in order to assemble a complete solution. Evaluation of an individual from a particular population is performed

by joining the individual with collaborating partners from other populations. Then, each of the species populations is optimized with a separate MOEA. Next we describe some of the most representative approaches presented in the specialized literature.

A CCMOEA which integrates cooperative coevolution with Fonseca and Fleming’s MOGA [14] is presented in [4]. The multi-objective cooperative coevolutionary genetic algorithm (MOCCGA) uses a dominance rank for individuals, in which a count of the number of individuals dominating others is the fitness criterion. In MOCCGA, the objectives are evaluated twice for each individual both with the best ranked individuals from each subpopulation, as well as with randomly selected individuals. This follows the approach described by Potter and De Jong, which aims to decrease the premature convergence observed on some test problems adopted with the original CC framework. In MOCCGA, the subcomponents are ranked only within the same subpopulation. It is important to mention that the number of evaluations adopted by the authors is not reported anywhere in the paper. Another approach is presented in [5], where a cooperative coevolutionary algorithm for multi-objective optimization is presented. This algorithm subdivides the decision variable space and determines which portions of the decision variables intervals are being used and discards portions of the intervals that it deems that are not being used by the search process. It also subdivides intervals so that separate sub-populations can operate on the portions of these intervals which contribute to the search. Sub-populations which are not making contributions are eliminated from the search. Parmee and Watson [15] proposed a collaborative multi-objective optimization scheme for the preliminary design of airframes. Here, they use one population to optimize each of the objective functions of the problem. The method utilizes individual genetic algorithms (GAs) for the optimization of each objective in order to reduce the problem to a number of concurrent co-evolutionary tasks specific to the overall design domain. Iorio and Li used NSGA-II [16] to evolve each species in their NSCCGA [17]. This Algorithm uses Potter and De Jong’s scheme [7] where there are as many species as decision variables in the problem and each of them are evolved using NSGA-II. Individuals from each population are evaluated forming collaborations with randomly selected components from the best non-domination levels in the previous generation’s sub-populations. There exist many more examples of the use of cooperative coevolution as a framework [4], [6], [17]–[27], but most of them work in a similar way as the ones we have described in this section.

As evidenced by the approaches we just described, one of the main changes when adopting this framework to solve MOPs consists on how to select individuals from the other populations to assemble a complete solution. Figure 1 depicts the collaboration procedure that a cooperative coevolutionary framework follows. Previous work with the CCA on single objective problems has primarily selected the current *best* components from each species to merge into a collaboration, or performed a tournament with candidate solutions formed

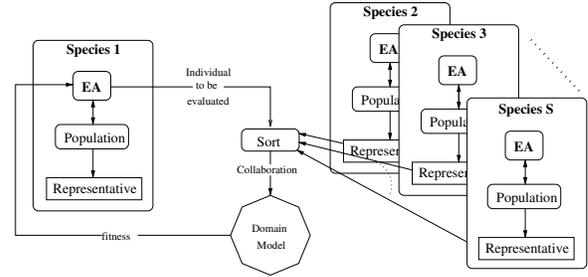


Fig. 1. Cooperative coevolutionary collaboration architecture from the perspective of species number 1. Here, we assume that we have S species, where the representative of each species for collaboration is selected from each subpopulation to evaluate an individual from species 1.

with the current *best* and randomly selected components. In a multi-objective scenario, there may be a number of individuals in each sub-population which are parts of overall solutions that are non-dominated in relation to each other, so the question is: how can we select one over the other? The usual mechanism used by CCMOEA is to select collaborators randomly from the set of non-dominated solutions found so far in each species’ sub-population. However, this way of selecting individuals for collaboration make coevolving populations to be attracted to areas of the search space in which there are many strategies that perform well when combined with individuals from the other populations and this tends to generate individuals that have poor performance in the general context. So far, there is no mechanism which selects an individual to form a collaboration based on the contribution of the solution components and this would be a more suitable way to create collaborations in a multi-objective scenario. In this work we propose to make use of an indicator-based selection scheme to look for better collaborations into the CC framework. With this, we aim to get an improvement on the performance of the CC framework for multi-objective optimization.

IV. OUR PROPOSED APPROACH

Our approach to cooperative coevolution uses the first cooperative coevolution scheme proposed by Potter [7], where each population contains individuals that represent a particular component (in decision variables space) of the problem, so that one member from each population is needed in order to assemble a complete solution. Evaluation of an individual from a particular population is performed by joining the individual with collaborating partners from other populations. As mentioned before, the common way to perform the evaluation of each individual is by taking one representative from the other populations that belongs to the best set of non-dominated solutions found so far. However, there is a potential problem with this approach; there is no mechanism which awards a ranking based on the contribution of the solution components. Without such a mechanism, potentially good solutions are lost because species may participate with individuals which create poor new components in a candidate

solution. Besides, this kind of interaction makes coevolution to only explore narrow regions of the collaboration space, which suggests that evolution is strongly attracted to certain regions of the search space. However, these regions do not necessarily correspond to (fitness-based) optimal solutions, and coevolution often converges to sub-optimal equilibria. Several recent studies have shown that Pareto-based multi-objective evolutionary algorithms (MOEAs) do not perform properly when dealing with problems having more than three objectives [28]. This has motivated the development of new selection schemes from which the use of quality assessment indicators has been the most promising choice [29]. The idea when using indicator-based selection is to maximize a quality assessment indicator that provides a good ordering among sets that represent Pareto approximations. We believe that taking this indicator-based approach into the selection mechanism for collaboration that CCMOEAs use, one can get an improvement on the performance of this sort of algorithms. So we use this idea to develop a new CCMOEA which uses a novel selection mechanism for collaborations, which, instead of looking for best non-dominated solutions, will look for collaborations which take into account the contribution of the solution components over a quality assessment indicator. Our proposed approach is described next.

A. Description of the proposed approach

Our approach works as follows: at the beginning, it divides the vector of decision variables \vec{x} of dimension $D \in \mathbb{N}$ into $S \in \mathbb{N}$ subcomponents, where S is equal to the number of objective functions in the problem. Each subcomponent is created from a random grouping of decision variables in order to increase the probability of grouping interacting variables in non-separable problems. At the same time, S subpopulations (species) are created, each one with NP individuals, and these S subpopulations are assigned their corresponding decision variables in a random way. This means that to each subpopulation, it corresponds a subcomponent from S which had been already created. Thus, every subpopulation will have a total of m decision variables. This is graphically depicted in Figure 2. Once the subpopulations are created, the algorithm does a random initialization of all the individuals across all subpopulations. Aside from evaluation, the populations are evolved independently using independent MOEAs for each species. Then, the algorithm performs the *cycles* in which the evolution of each of the subpopulations is done for a given number of *generations*. This process continues until the stopping condition is reached, and at the end, the solutions that are globally non-dominated (i.e., with respect to all the subpopulations), constitute the outcome of the algorithm.

Collaboration among the subpopulations takes place in the next way: in the first generation, random collaborations are formed and evaluated, obtaining a random individual from each subpopulation and forming a complete set of solutions to be evaluated in their objective functions. Then, the results from the evaluation are assigned back to the individual under evaluation. After the first generation, the resulting child

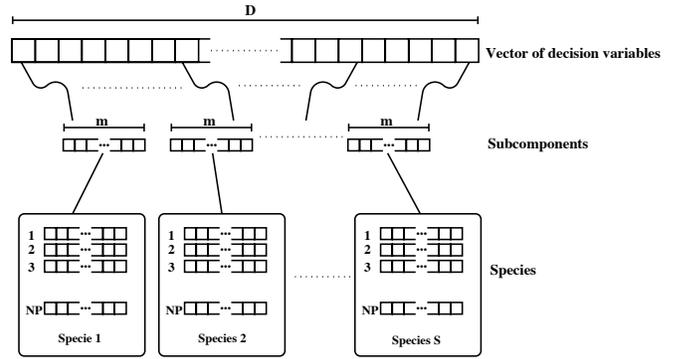


Fig. 2. Graphical representation of the subcomponents (species) creation. Here, we assume a vector of decision variables of dimension D which is divided into S subcomponents of dimension m , created in a random way from the original vector of decision variables and assigned to the S existing species, where $D = m * S$.

subpopulations Q_1 to Q_S will be evaluated by forming collaborations with individuals from the other species which have the best contribution to a quality assessment indicator.

From the several performance indicators currently available, the hypervolume [30] has become the most popular choice for implementing indicator-based MOEAs, mainly because of its good theoretical properties. The hypervolume is the only unary indicator that is known to be Pareto compliant and it has been proved that its maximization is equivalent to finding the Pareto optimal set [31]. The hypervolume indicator has become widely used in recent years [32]. This indicator encapsulates in a single unary value a measure of the spread of the solutions along the Pareto front, as well as the distance of the approximation set from the true Pareto optimal front. Besides, whenever one approximation completely dominates another approximation, the hypervolume of the former will be greater than the hypervolume of the latter. Also, the hypervolume is maximized if, and only if, the set of solutions contains all Pareto optimal points. The hypervolume is defined as the n -dimensional space that is contained by an n -dimensional set of points. When applied to multi-objective optimization, the n -dimensional objective values for solutions are treated as points for the computation of such space. That is, the hypervolume is obtained by computing the volume (in objective function space) of the non-dominated set of solutions Q that minimize a MOP. For every solution $i \in Q$, a hypercube v_i is generated with a reference point W and the solution i as its diagonal corner of the hypercube.

$$S = Vol \left(\bigcup_{i=1}^{|Q|} v_i \right) \quad (8)$$

The hypervolume has important advantages over other set measures [32]:

- It is sensitive to any type of improvements, i.e., whenever an approximation set A dominates another approximation set B , then the hypervolume has a strictly better quality value for the former than for the latter set.

- As a result from the first property, the hypervolume measure guarantees that any approximation set A that achieves the maximally possible quality value for a particular problem contains all Pareto-optimal objective vectors.
- The ranking of the solutions that it generates is invariant to the linear scaling of the objective functions.

The most common way to use the hypervolume as a selection method in MOEAs is through the measure of how much an individual contributes to the hypervolume value of the whole set it belongs to. Then, the solutions that contribute the least to the hypervolume of a front are discarded. The contributing hypervolume of an individual a which belongs to a population P can then be stated in the following way:

$$C_a = \mathcal{S}(\mathcal{P}, y_{ref}) - \mathcal{S}(\mathcal{P} \setminus \{a\}, y_{ref}) \quad (9)$$

The graphical representation of this computation, for a two objective case, can be seen in Figure 3. Within the cooperative coevolutionary framework, we can use this idea to take, as a member for collaboration from each species, the individual which contributes the most on the hypervolume indicator. So, we propose to make collaborations by finding the best individuals according to the hypervolume contribution values of the solutions found so far in each species. A summary of the way in which our approach works is presented in Algorithm 1.

As mentioned before, aside from evaluation, the populations are evolved independently using independent MOEAs for each species. For this sake, we adopted the operators from differential evolution [33] combined with some mechanisms from NSGA-II [16]. Our search engine operates as follows: It starts with a population of random solutions, which becomes the current population. At each generation, an offspring population is created using the differential evolution operators; then, the current population for the next generation is updated using the solutions of both, the offspring and the parent populations. Before proceeding to the next generation, the size of the population is reduced using non-dominated sorting and a pruning technique aimed at diversity preservation, in a similar way as NSGA-II.

B. Experimental Studies

For the purposes of this study, we adopted the Deb-Thiele-Laumanns-Zitzler (DTLZ) test suite [34], with MOPs of three objective functions and 12 decision variables. The main characteristics of these problems are described next: DTLZ1 is a separable and multi-modal problem with a linear Pareto front. DTLZ2 is a separable and uni-modal problem with a concave Pareto front. DTLZ3 is a separable and multi-modal problem with a concave Pareto front. DTLZ4 is a separable and uni-modal problem with a concave Pareto front. DTLZ5 is a uni-modal problem with a degenerated arc Pareto front. DTLZ6 is an uni-modal problem with a degenerated arc front. Finally, DTLZ7 has a disconnected and mixed Pareto front.

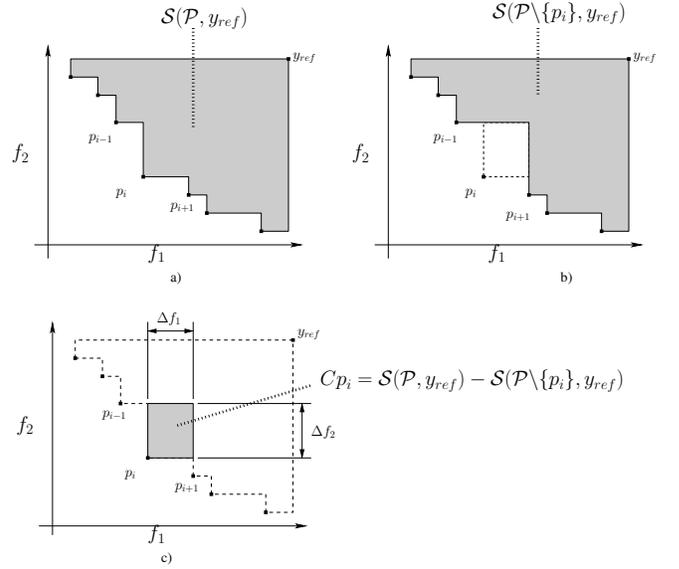


Fig. 3. Contributing hypervolume computation of a solution.

Algorithm 1 CCMOEA

Input: $NP, Cycles, Gmax, NumEsp$

Output: $SolutionSet$

$Pobs \leftarrow Populations(NP, NumEsp)$

$InitializeSpecies(Pobs)$

for $j \leftarrow 1$ **to** $Cycles$ **do**

for $i \leftarrow 1$ **to** $NumEsp$ **do**

for $k \leftarrow 1$ **to** $Gmax$ **do**

$MOEA(Pobs[i])$

end for

end for

end for

$SolutionSet \leftarrow ObtainNonDominatedSet(Pobs)$

return $SolutionSet$

C. Methodology

Since the main objective of this work is to study the impact that our selection mechanism for collaboration has in a CCMOEA and evaluate the performance of our approach, we will analyze our results with respect to those of the new approach we have just described, but adopting the usual selection mechanism for collaboration which takes one representative from the other populations that belongs to the set of non-dominated solutions found so far. We decided to name these versions as Indicator-based CCMOEA (IBCCMOEA) and Pareto-based CCMOEA (PBCCMOEA), respectively. We established a predefined number of function evaluations that the algorithms can use, to analyze how they behave with the same resources. For measuring the results we adopted the hypervolume, but this time as a performance indicator [35]. The hypervolume is obtained by computing the volume (in objective function space) of the non-dominated set of solutions, given as the final result, of each CCMOEA. The aim of this study is to identify which of the CCMOEA's being

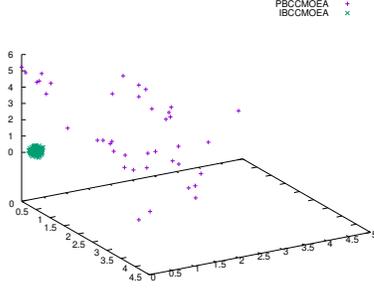


Fig. 4. Plot of CCMOEAs for DTLZ1.

compared is able to get closer to the true Pareto front using the same number of objective function evaluations.

D. Parameterization

The parameters of each CCMOEA used in our study were chosen in such a way that we could do a fair comparison among them. Since both CCMOEAs are of the same nature, we will use the same parameters for both approaches. We used 2 species for each problem with a populations size of 50 individuals for each species population. Each CCMOEA used 50 cycles and just one generation for each species per cycle for both approaches (which means each CCMOEA used 5000 function evaluations in the experiments). Finally, the F and CR values for differential evolution, used by the multi-objective species optimizer, were set to 0.5 and 0.5 respectively. All of this in order to use the same number of function evaluations in both CCMOEAs and to allow for a fair comparison of results.

E. Analysis of results

In our experiments, we obtained the hypervolume value over the 25 independents runs performed. Table I shows the average hypervolume of each of the CCMOEAs being compared for each test problem adopted, as well as the results of the statistical analysis that we made to validate our experiments, for which we used Wilcoxon's rank sum. To ease the analysis of the results in these tables, the cells containing the best hypervolume mean value for each problem have a grey colored background.

From Figures 4 to 10, we plotted the results of the median of the 25 runs. We can observe that, using the same number of function evaluations, our proposed IBCCMOEA is able to get closer than PBCCMOEA to the Pareto front in all the problems. It is clear that our approach has a better performance than the Pareto based approach, in terms of number of function evaluations and according to the Wilcoxon's rank sum test results, the null hypothesis ("medians are equal") can be rejected. Therefore, results confirm that the way selection is done for collaborations in CCMOEAs has an important effect. The new indicator-based approach presented here showed to be very effective in improving performance.

TABLE I

AVERAGE OF THE HYPERVOLUME INDICATOR VALUES OF THE RESULTS OBTAINED FOR THE DTLZ TEST PROBLEMS. WE SHOW AVERAGE (MEAN) VALUES OVER 25 INDEPENDENT RUNS, AS WELL AS THE STANDARD DEVIATION (SD) FOR EACH PROBLEM'S RESULTS. THE CELLS CONTAINING THE BEST HYPERVOLUME VALUE FOR EACH PROBLEM HAVE A GREY COLORED BACKGROUND. THE P(H) COLUMNS SHOW THE RESULTS OF THE STATISTICAL ANALYSIS APPLIED TO OUR EXPERIMENTS USING WILCOXON'S RANK SUM. P IS THE PROBABILITY OF OBSERVING THE GIVEN RESULT (THE NULL HYPOTHESIS IS TRUE). SMALL VALUES OF P CAST DOUBT ON THE VALIDITY OF THE NULL HYPOTHESIS. $H = 0$ INDICATES THAT THE NULL HYPOTHESIS ("MEDIAN ARE EQUAL") CANNOT BE REJECTED AT THE 5% LEVEL. $H = 1$ INDICATES THAT THE NULL HYPOTHESIS CAN BE REJECTED AT THE 5% LEVEL.

Algorithm	IBCCMOEA		PBCCMOEA		IBCC-PBCC
	Mean	SD	Mean	SD	P(H)
Problem	DTLZ1				
	3.3136	0.0295	1.6261	0.5835	0.000000 (1)
Problem	DTLZ2				
	2.5789	0.1207	2.4674	0.0367	0.000275 (1)
Problem	DTLZ3				
	2.6911	0.0105	2.4665	0.0220	0.000000 (1)
Problem	DTLZ4				
	2.6061	0.0984	2.4689	0.1282	0.000117 (1)
Problem	DTLZ5				
	2.0235	0.0076	1.9940	0.0055	0.000000 (1)
Problem	DTLZ6				
	2.0260	0.0109	1.9835	0.0069	0.000000 (1)
Problem	DTLZ7				
	2.2282	0.0442	2.2078	0.0168	0.012087 (1)

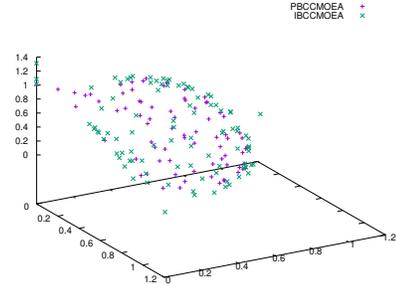


Fig. 5. Plot of CCMOEAs for DTLZ2.

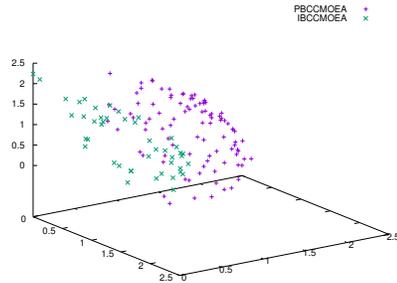


Fig. 6. Plot of CCMOEAs for DTLZ3.

V. CONCLUSIONS AND FUTURE WORK

This paper proposes a new selection mechanism for collaboration in the cooperative coevolutionary framework for solving MOPs, using a novel cooperation strategy based on the hypervolume indicator. With this, we presented a novel cooperative coevolutionary MOEA, called IBMOEA, which was shown to be able to successfully deal with the DTLZ test functions. We have studied the convergence rate of our proposed IBCCMOEA with respect to that of PBCCMOEA, a CCMOEA which follows the same framework as our approach, but with a selection mechanism for collaboration which takes one representative from the other populations that belongs to the set of non-dominated solutions found so far. The results confirmed that our proposed approach outperforms PBCCMOEA and that the collaboration framework has a great impact in CCMOEA's performance. As part of our future work we aim to incorporate other quality assessment indicators to the selection scheme of our algorithm, in order to be able to scale it to more objectives and to study the effect of the different indicators over our proposed selection mechanism. Also, we would like to study the behavior of our approach when solving MOPs with a large number of decision variables.

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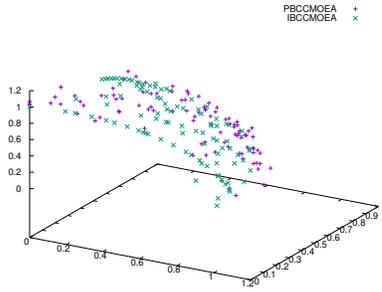


Fig. 7. Plot of CCMOEA for DTLZ4.

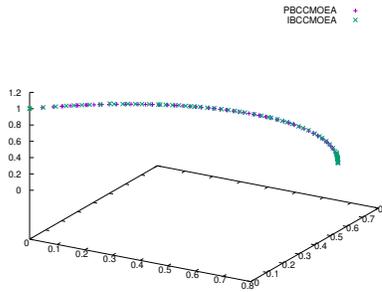


Fig. 8. Plot of CCMOEA for DTLZ5.

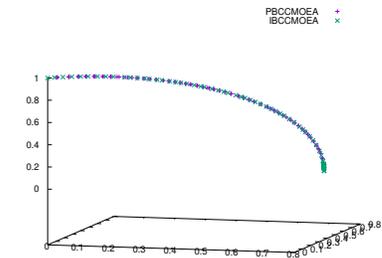


Fig. 9. Plot of CCMOEA for DTLZ6.

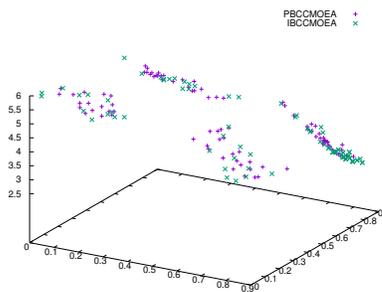


Fig. 10. Plot of CCMOEA for DTLZ7.

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