A Multi-Objective Artificial Immune System based on Hypervolume

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Abstract. This paper presents a new artificial immune system algorithm for solving multi-objective optimization problems, based on the clonal selection principle and the hypervolume contribution. The main aim of this work is to investigate the performance of this class of algorithm with respect to approaches which are representative of the state-of-the-art in multi-objective optimization using metaheuristics. The results obtained by our proposed approach, called multi-objective artificial immune system based on hypervolume (MOAIS-HV) are compared with respect to those of the NSGA-II. Our preliminary results indicate that our proposed approach is very competitive, and can be a viable choice for solving multi-objective optimization problems.

Keywords: Multi Objective Optimization, Artificial Immune System, Hypervolume

1 Introduction

For the last decades, metaheuristics have been widely used to solve multi-objective optimization problems (MOPs). The main advantage of metaheuristics in general, is that at each generation, the algorithm is able to provide solutions (exact or approximate) in a reasonably low amount of time, even if the problem has a highly nonlinear or very large search space. On the other hand, mathematical programming techniques may not work properly under certain conditions (e.g., in some highly nonlinear problems or when the objective function is not available in algebraic form). In spite of their theoretical limitations, metaheuristics tend to generate approximations of the global optimum that are generally sufficiently good to justify their use in a wide variety of practical applications.

From the many metaheuristics in current use, Artificial Immune Systems (AISs) are among the less commonly adopted for numerical optimization, in spite of their good performance in certain domains (see for example [1]). Here, we explore the performance of a multi-objective artificial immune system which incorporates a hypervolume-based selection mechanism (we call it MOAIS-HV). The aim is to show that this sort of approach can be a viable alternative for dealing with complex multi-objective optimization problems, even when facing a high number of objectives.

The remainder of this paper is organized as follows. Section 2 provides the basic concepts required to understand the rest of the paper. In Section 3, we provide a generic outline of multi-objective artificial immune systems (MOAISs). The previous related work is briefly reviewed in Section 4. Our proposed approach is described in detail in Section 5. A comparison of results between our proposed approach and NSGA-II is presented in Section 6. Finally, our conclusions and some possible paths for future research are provided in Section 7.

2   Basic Concepts

We are interested in solving problems of the type[3]:

$$\text{minimize } \boldsymbol{f}(\boldsymbol{x}) := [f_1(\boldsymbol{x}), f_2(\boldsymbol{x}), \dots, f_k(\boldsymbol{x})] \tag{1}$$

subject to:

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

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

where $\boldsymbol{x} = [x_1, x_2, \dots, x_n]^T$ is the vector of decision variables, $f_i : \mathbb{R}^n \to \mathbb{R}$, $i = 1, \dots, k$ are the objective functions and $g_i, h_j : \mathbb{R}^n \to \mathbb{R}$, $i = 1, \dots, m$, $j = 1, \dots, p$ are the constraint functions of the problem.

To describe the concept of optimality in which we are interested, we will introduce next a few definitions.

Definition 1. Given two vectors $\boldsymbol{x}, \boldsymbol{y} \in \mathbb{R}^k$, we say that $\boldsymbol{x} \leq \boldsymbol{y}$ if $x_i \leq y_i$ for $i = 1, \dots, k$, and that $\boldsymbol{x}$ **dominates** $\boldsymbol{y}$ (denoted by $\boldsymbol{x} \prec \boldsymbol{y}$) if $\boldsymbol{x} \leq \boldsymbol{y}$ and $\boldsymbol{x} \neq \boldsymbol{y}$.

Definition 2. We say that a vector of decision variables $\boldsymbol{x} \in \mathcal{X} \subset \mathbb{R}^n$ is **non-dominated** with respect to $\mathcal{X}$, if there does not exist another $\boldsymbol{x}' \in \mathcal{X}$ such that $\boldsymbol{f}(\boldsymbol{x}') \prec \boldsymbol{f}(\boldsymbol{x})$.

Definition 3. We say that a vector of decision variables $\boldsymbol{x}^* \in \mathcal{F} \subset \mathbb{R}^n$ ($\mathcal{F}$ is the feasible region) is **Pareto-optimal** if it is nondominated with respect to $\mathcal{F}$.

Definition 4. The **Pareto Optimal Set** $\mathcal{P}^*$ is defined by:

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[3] Without loss of generality, we will assume only minimization problems.

$$\mathcal{P}^* = \{\boldsymbol{x} \in \mathcal{F} | \boldsymbol{x} \text{ is Pareto-optimal}\}$$

Definition 5. The **Pareto Front** $\mathcal{PF}^*$ is defined by:

$$\mathcal{PF}^* = \{\boldsymbol{f}(\boldsymbol{x}) \in \mathbb{R}^k | \boldsymbol{x} \in \mathcal{P}^*\}$$

We thus wish to determine the Pareto optimal set from the set $\mathcal{F}$ of all the decision variable vectors that satisfy (2) and (3). Note however that in practice, not all the Pareto optimal set is normally desirable (e.g., it may not be desirable to have different solutions that map to the same values in objective function space) or achievable.

When working with multi-objective optimization problems, there are two main aims: to generate solutions as close as possible to the true Pareto front and to have a set of nondominated solutions well distributed along the Pareto front.

3   Multi Objective Artificial Immune Systems

The immune system's role is to defend the body against infections. It has several defenses against outside attacks: the barrier of the skin, mucous membranes, and the passive system defense of cells, but the functioning of antibodies is its main element. Usually, when a foreign element is detected by the immune system, an immediate elimination reaction sets in. This reaction involves phagocytic cells and lymphocytes that circulate continuously throughout the body. This reaction is fast and called non-specific, meaning that the immune system attacks the antigen without knowing its nature.

Depending on the severity of the infection, this rapid and non-specific immune response may not be sufficient to eliminate the intruder. A second reaction, slower and more specific is then set up: it puts into play the recognition of the foreign element by immune cells. Following the recognition, immune cells specifically adapted for the destruction of the foreign agent (lymphocytes) will multiply rapidly. Some of these clones may be corrupt, and a risk of generating autoimmune cells occurs. The immune system is able to suppress self-generated cells (suppression of similar individuals). Subsequently, the organism keeps track of this encounter with the foreign element (thanks to the B cells). There is some form of memory in the immune system. This optimizes the specific immune response, which will be faster at a forthcoming encounter with the same foreign element.

In the design of a multi-objective artificial immune system (MOAIS), two sets of solutions are normally considered: *antibodies* (Ab) and *antigens* (Ag). The differences between them is defined by the designer of the algorithm, but normally one set represents "good" solutions (e.g., nondominated solutions to a multi-objective optimization problem) and the other represents "bad" solutions (e.g., the solutions that are dominated by others). The interactions between the solutions (e.g., Ag-Ab, Ag-Ag, and so on) are defined by an *affinity function.*

It is normally the case that the measures of quality in which we are interested on (e.g., Pareto dominance and the spread of the solutions, in the case of multi-objective optimization) are embedded into the affinity function. Depending on the affinity value, a selection and a cloning process occurs, and then the clones are mutated. Finally, a certain strategy is used to generate the new population and to store the best solutions found so far (normally, an external archive that stores only nondominated solutions is adopted for this sake). Campelo et al. [2], provide a canonical algorithm of a MOAIS (see Algorithm 1).

Algorithm 1: Outline of a canonical MOAIS

1 Define the search space $\mathbb{S}$, objectives functions f_i, constraints g_j, h_k ;
2 $A(t = 0) \longleftarrow$ Initialize offline population;
3 $B(t = 0) \longleftarrow$ Initialize online population with random individuals;
4 while $\neg$ *stop criterion* **do**
5   Evaluate population $B(t)$ using f_i, g_j, h_k;
6 $B_1(t) \longleftarrow$ Define affinities($B(t)$, $[A(t)]$);
7 $B_2(t) \longleftarrow$ Selection for cloning($B_1(t)$, $[A(t)]$);
8 $B_3(t) \longleftarrow$ Proliferation and mutation($B_2(t)$);
9 $B_4(t) \longleftarrow$ Diversification & Suppression;
10 $B(t + 1) \longleftarrow B_3(t) \cup B_4(t)$;
11 $A(t + 1) \longleftarrow$ Update($A(t), B(t + 1)$);
12 $t \longleftarrow t + 1$;
13 end

It is worth noting that the canonical MOAIS of Campelo et al. [2] adopts the clonal selection priciple. The reason is that, most MOAISs currently available in the literature follow this principle.

Algorithm 1 first defines the problem, like all population-based algorithms (line 1). An archive is defined (line 2) in order to store the nondominated solutions found so far. The main (or internal) population is initialized (line 3) containing the solutions from the current generation. The main loop starts and performs the following steps until a stop criterion is met. The algorithm evaluates the online (or main) population (line 5) using the objective functions and constraints of the problem. Depending on the choices made, the solutions of the set B are analyzed and given an affinity value (line 6), the archive A can be used, for example, to define the new affinities between the current solutions and the best solutions found so far. Cloning selection is then triggered following either stochastic or deterministic rules (line 7), and based on affinities values or not. The cloning process is usually done based on the affinity values (proportional cloning), while the mutation of each individual can have several variants (line 8). The two previous steps constitute the so-called *clonal selection principle*. The diversification procedure (line 9) is not mandatory, and its goal is to maintain diversity in the population usually by creating new random individuals. Suppression is not mandatory either and can be applied to delete some individuals

(responsible for autoimmune disorder), particularly to individuals that are not relevant for further optimization. The new population is generated taking into account the best clones (line 10), applying some predefined rules. Eventually, the archive is updated (line 11). At the end of the run, the archive will contain the set of nondominated solutions that constitutes our approximation of the true Pareto front of the problem.

4   Previous Related Work

An overview of MOAISs is provided in [3]. It shows that MISA (Multiobjective Immune System Algorithm), which was originally introduced in 2002 [4] is considered as the first Pareto-based MOAIS reported in the specialized literature[4] [6]. The algorithm is designed to fit the immune system metaphor and it follows the canonical algorithm previously presented. MISA uses Pareto ranking to classify solutions and to determine which of them will be cloned. The number of clones depends on antibody-antibody affinities. The clones are uniformly mutated according to their antigen-antibody affinities whereas other solutions use non-uniform mutation. An adaptive grid is used to ensure diversity in the (fixed size) external archive. Selection to access the archive is determined by some pre-defined rules based on Pareto ranking. The results obtained by MISA showed that the use of AISs for solving multi-objective optimization problems was a viable alternative. Over the years, several other MOAISs were introduced. The approaches that will be discussed here were selected based on the fulfillment of the five following criteria:

1. The approach follows the structure and behavior of a canonical AIS.
2. The approach does not adopt a recombination operator.
3. The approach allows the use of real-numbers encoding (as the approach proposed in this paper).
4. Its authors provide detailed results of the algorithm's performance.
5. The approach is relatively recent (2005 to date).

4.1   Vector Artificial Immune System (VAIS)

This approach was proposed in [7], and it uses a Pareto-based selection, cloning, mutation, suppression and an archiving process. For the nondominated individuals, fitness is determined by the strength defined in SPEA2 [8]. For dominated solutions, fitness corresponds to the number of individuals which dominate them.

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[4] The first direct use of an artificial immune system to solve multi-objective optimization problems reported in the literature is due to Yoo and Hajela [5]. However, this approach uses a linear aggregating function to combine objective function and constraint information into a scalar value that is used as the fitness function of a genetic algorithm. Thus, this approach is really a hybrid algorithm and does not rely on Pareto optimality.

A suppression procedure is used for the archive as well as a diversification procedure by allowing a fixed number of random individuals to enter the archive. Results are compared with respect to the NSGA-II [9]. The authors show that VAIS can outperform NSGA-II in several unconstrained and constrained problems. However, it is worth noting that VAIS was not tested in the Deb-Thiele-Laumanns-Zitzler (DTLZ) test suite [10], which is a standard benchmark for multi-objective evolutionary algorithms (MOEAs).

4.2   Immune Dominance Clonal Multiobjective Algorithm/Nondominated Neighbor Immune Algorithm (IDCMA/NNIA)

The Immune Dominance Clonal Multiobjective Algorithm (IDCMA) was introduced in [11]. However, the difficulties of this algorithm for solving the DTLZ test suite [10], motivated the development of an improved version, which was called Nondominated Neighbor Immune Algorithm (NNIA), which was introduced in [12]. The selection mechanism which is responsible of choosing the set of candidates to be cloned, aims for the nondominated solutions. However, if the nondominated solutions are beyond a certain threshold, then the crowding distance is used. The archiving process uses the same methods to select candidates to enter the archive (i.e., nondominated solutions are always preferred). In NNIA, recombination is adopted. However, the authors also present results without the use of recombination (which is the reason why we selected this approach for this section). Nevertheless, the authors indicate that recombination provides a significant improvement of results for NNIA in some of the DTLZ test problems.

4.3   Immune Forgetting Multiobjective Optimization Algorithm (IFMOA)

This approach was introduced in [13]. In this case, the affinity assignment is based on the Pareto strength from SPEA2 [8]. This approach also adopts an antibody-antibody affinity which is inversely proportional to the sum of the two smallest Euclidean distances between an antibody and the rest of the population. The "immune forget unit" is a set of solutions that do not participate in the clonal proliferation. The results of this approach are compared with respect to MOGA [14] and SPEA2 on six unconstrained problems. The results presented by the authors show a good performance of IFMOA, but none of the test problems adopted is particularly difficult by today's standards in evolutionary multi-objective optimization.

4.4   Omni-aiNet

This approach was introduced in [15] and can be used for both single- and multi-objective optimization. First, all the individuals are cloned N_c times (N_c is a

user-defined parameter). A random variation with rates inversely proportional to the affinity to the antigen is applied to each generated clone. Polynomial mutation is used to apply variations to the clones. Solutions are arranged in classes, so that the better the class, the smaller the variation. The algorithm adopts both suppression and diversification. Unfortunately, the authors provide results only with respect to those of another approach called *DT omni-optimizer*. Additionally, results are presented only in graphical form and for three problems. This does not allow to know how competitive is this approach with respect to state-of-the-art MOEAs.

Based on the previous discussion, it should be clear that most of the current MOAISs still adopt some form of Pareto ranking. Nowadays, however, several efforts have been focused on the development of indicator-based MOEAs. The main motivation for this is to overcome the poor performance exhibited by Pareto-based selection when dealing with problems that have four or more objectives [16]. Although several indicator-based MOEAs have been proposed in the last few years, no indicator-based MOAIS has been proposed so far, to the authors' best knowledge. We believe that the approach introduced in this paper is the first of such indicator-based MOAISs.

It is worth noting that not just any performance indicator can be adopted for selecting solutions. The most commonly adopted is an indicator known as **Hypervolume**.[5] The main advantage of the hypervolume indicator is that it has been proved that its maximization is equivalent to finding the Pareto optimal set [18]. This has been empirically corroborated [19] and, in fact, the maximization of this indicator also leads to sets of solutions whose spread along the Pareto front is maximized (although the distribution of such solutions is not necessarily uniform). Because of its popularity, we decided to adopt hypervolume for the MOAIS reported in this paper.

5 Our Proposed Approach

In this section, our proposed approach, called MOAIS-HV (HV stands for hypervolume) is described in detail. The main goal of the work reported here was to investigate the feasibility of incorporating a hypervolume-based selection into a MOAIS. It is worth noting that our proposed approach follows the main features of an AIS (we do not adopt any recombination operator, unlike most of the hypervolume-based MOEAs in current use).

5.1 Description of the algorithm

The main idea of MOAIS-HV is to maintain an online population of antigens and antibodies. The antigens are considered to be the good solutions, and the antibodies are the bad ones. These two sets form two new subpopulations. The

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[5] The hypervolume (also known as the S metric or the Lebesgue Measure) of a set of solutions measures the size of the portion of objective space that is dominated by those solutions collectively [17].

antigens are cloned (the best antibodies are cloned, too, if the number of antigens is insufficient) and a mutation operator is applied. If only one rank exists, candidates to be cloned are selected from individuals that contribute the most to maximize the hypervolume; otherwise, successive ranks are selected and hypervolume selection is only applied to the last one. The clones and the best antigens found are merged and the size of the main population is maintained by discarding individuals that contribute the least in maximizing the hypervolume. In the algorithm, the following notations will be used: Q, P: the main population and the pool, Ab, Ag: the sets of antibodies and antigens (subsets of Q), n: size of the main population, $m, ngen$: number of objectives and number of generations.

1. Initializing populations: Initialize population Q (Main population) by generating random individuals.
   $\rightarrow$ fixed size n.
   Initialize Antibodies population Ab to empty.
   $\rightarrow$ fixed size n.
   Initialize Antigens (or Archive) population Ag to empty.
   $\rightarrow$ fixed size n. Store the best individuals found so far.
   Initialize a pool P to empty (to store the clones).
   $\rightarrow$ fixed size $2 * n$.

2. Evaluate all individuals of the population Q.
   $\rightarrow$ Feasibility and objective values
   $\rightarrow$ Fast non-dominated ranking
3. "Split" the population Q into two sets:
   Constrained problems:
   Antigens:
   $\rightarrow$ Feasible and non-dominated
   Antibodies:
   $\rightarrow$ Infeasible and non-dominated
   $\rightarrow$ Feasible and dominated
   $\rightarrow$ Infeasible and dominated
   Unconstrained problems:
   Antigens:
   $\rightarrow$ Non-dominated
   Antibodies:
   $\rightarrow$ Dominated

4. Define Affinity for antibodies and antigens.
   Defining affinity on antibodies:
   For each antibody, select randomly one antigen in Ag. The affinity value of an antibody Ab is defined by its euclidean distance to the selected antigen Ag.
   Defining affinity on antigens:
   For each antigen, the affinity is based on its hypervolume contribution:
   The algorithm that computes the hypervolume contribution is shown in Algorithm 2.
   For both antibodies and antigens, the greater the affinity, the better.

5. **Clonal selection principle**
   Most of the population-based algorithms don't discard dominated individuals when

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Algorithm 2: Algorithm for computing hypervolume contributions

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1 Input: Population Ag ;
2 Initialize Affinities(Ag) to 0.0 ;
3 **for** i *from 1 to m* **do**
4   Sort Ag by obj i;
5   **for** j *from 1 to Ag.size()* **do**
6 $Ag.ind[j].affinity \mathrel{+}= (Ag.ind[j].obj[i] - Ag.ind[j+1].obj[i]);$
7   **end**
8 **end**
9 **for** j *from 1 to Ag.size()* **do**
10 $Ag.ind[j].affinity \mathrel{+}= max_j(Aff(Ab_j));$
11 **end**

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selecting solutions to be cloned or mutated. The main aim in doing this is to keep some diversity in the population. After some experiments, the choice for our algorithm was to select dominated solutions only if necessary (if non-dominated solutions are less than the number of clones). Some previous results have shown that cloning the antibodies gives worse results (convergence metric) than considering the best individuals found so far, the antigens. In order to fit to the immune system metaphor, one can consider here that if the main population already contains a certain number of antigens, it means that the immune system has already recognized some pathogen agents and it will use them to perform the cloning process (the antibody which reached the pathogen agent and is now considered as an antigen). The number of clones is usually defined as about 20% of the population. Nevertheless, a more thorough statistical analysis is still required and for now, we adopt a user-defined parameter to control the number of candidates. In the main population, the antigens and antibodies are classified according to their affinity. The first best NC solutions are chosen and for each of them, a different number of clones is calculated depending on their affinity. Moreover, these candidates are split into two sets $j = 1, 2$: the extreme solutions and the others. For each set, we define their total number of clones. The extreme solutions will be cloned more at the beginning and less at the end.

For each NC solution, the number of clones of each candidate (NCC) is given by:

$$NCC(A_{i,j}) = P_j * \frac{Aff(A_{i,j})}{\sum_{i=0}^{n_j} Aff(A_{i,j})} \quad \forall i,j$$

where: $A_{i,j}$ is the ith antigen or the ith antibody of the set j, P_j is the total number of clones for the set j, n_j is the number of candidates in the set j.

6. **Mutation**

   Regarding mutation, two important choices have to be made:

   – Mutation probability: It controls the probability to mutate one variable of a vector.
   – Mutation step-size: It controls the degree of perturbation given to the variable selected to be mutated.

Concerning the mutation probability, the aim of this study is to simplify the algorithm in order to emphasize the combination MOAIS/Hypervolume and investigate this new idea. Furthermore, since we compare results with respect to NSGA-II, we decided to adopt its same mutation probability. Thus, the mutation probability mp remained fixed in the experiments reported next.

$$mp = \frac{1}{nreal}$$

7. **Hybrid mutation**

   Each time a variable has to be mutated, we compute the following value:

   $$p\_mut\_type = \frac{1.0}{(1.0 + exp(-2.0 * (x + p)))}$$

   where: $x = -6.0 + (t/ngen) * 12.0$, increasing with the number of generations. $p = -4.0 + ls * 8.0$, where ls is a parameter which determines the tradeoff between GL and GG.

   While the algorithm is running, the probability to choose GL will increase and the mutation will perform more local searches. Local Gaussian mutation is performed following the formula:

   $$x_i^* = x_i + (max_i - min_i) * 0.1 * \mathcal{N}(0, st_1)$$

   Global Gaussian mutation is performed following the formula:

   $$x_i^* = x_i + (max_i - min_i) * 0.1 * \mathcal{N}(0, st_2)$$

   where: max_i, min_i are the bounds of each decision variable, x_i is the variable to be mutated, $\mathcal{N}(0, x)$ is the Normal distribution with mean 0 and standard deviation x, $st_1 \in [0.1, 0.5]$, parameter which controls the local Gaussian mutation step, $st_2 \in [0.5, 1.5]$, parameter which controls the global Gaussian mutation step.

8. Evaluate the pool: Objectives, feasibility.
9. Add the Antigens into the pool P
10. Non-dominated sorting in the pool P
11. Update the main population Q

    The archiving process is quite simple but some choices have to be made when the archive is full and the candidates that aim to enter are non-dominated individuals. The main aim of the archive is to increase the value of the whole hypervolume at each generation. In order to achieve this, new individuals are added to the archive only if they dominate a previous individual. An archiving method is presented in [20] but the complexity is, once again, exponential with the number of objectives. Here, the hypervolume maximization of the archive will be ensured by only accepting individuals that dominate previous individuals. One drawback of this method is that we assume that the previous generation has a good spread to ensure that all the solutions of the Pareto front are reachable (relatively, because of the bounded size of the archive) - this is not so in most cases. The following method is adopted in order to find a good spread of solutions before accepting only individuals that will maximize the hypervolume:

12. Fill the main population with successive ranks from the pool P.
13. Split the population (Antigens & Antibodies)
14. Go to step 4 if the stop criterion is not met.

15. Return the antigen population as the approximation of the Pareto front obtained by the algorithm.

A MOAIS algorithm can be considered as a MOEA whose features are changed for selection, proliferation, mutation and archiving. In order to keep the comparison with NSGA-II as fair as possible, the implementation of the new algorithm is based on the data structures used in [9]. Other data structures used are simply arrays and the code is easily understandable and maintainable for further work (we adopted the code provided by Kalyanmoy Deb in `http://www.iitk.ac.in/kangal/codes.shtml`.

A competitive complexity is always hard to achieve when dealing with hypervolume, because of the high computational cost associated to it. Nevertheless, the complexity of the algorithm presented here is $\mathcal{O}(mn^3)$ and $\mathcal{O}(mn^2 log n)$ on average. This low complexity makes the algorithm suitable for real-world problems.

6   Comparison of Results

The aim of this document is to compare the results obtained by our proposed MOAIS-HV with respect to those of NSGA-II [9]. In order to allow a fair comparison, the same number of function evaluations was adopted for both algorithms. The same population size and the same number of generations were adopted for both algorithms.

We adopted both the Zitzler-Deb-Thiele (ZDT) test suite [21] (which contains bi-objective problems) and the DTLZ test suite [10] (which contains scalable problems that were implemented with 3 objectives, except for DTLZ4-4, which has 4 objectives). Due to space limitations, we only provide a summary of our results in Table 1. The performance measures adopted were hypervolume [17], inverted generational distance (IGD) [6] (which measures convergence) and spread [9] (which measures uniform distribution along the Pareto front).

As expected, MOAIS-HV performs better with respect to the hypervolume in all the test problems adopted, except for ZDT4, which is multi-frontal (i.e., it has several false Pareto fronts), which seems to produce some problems to our selection mechanism, although we still manage to produce a reasonably good final result. It is remarkable, however, that MOAIS-HV can produce good results in ZDT3, which has a disconnected Pareto front that normally produces problems to MOAISs (e.g., in [12] the authors have to rely on the use of recombination to properly solve this problem).

Something interesting is that the other convergence measure adopted (inverted generational distance) seems to contradict the hypervolume (which also measures convergence). The differences, however, are negligible in most cases, since both algorithms produce values close to zero in all cases. It is also interesting to note that the results obtained by our approach with respect to spread are quite competitive, although the hypervolume does not really emphasize uniform distribution of nondominated solutions.

Table 1. Comparison of the average results obtained by NSGA-II and our proposed MOAIS-HV for the ZDT and DTLZ test problems. The reference point adopted to compute the hypervolume is provided in the last column.

Test problem	Spread		IGD		Hypervolume		
	NSGA-II	MOAIS-HV	NSGA-II	MOAIS-HV	NSGA-II	AIS-HV	Ref. point
ZDT1	2.54e-01	**1.91e-01**	1.98e-04	**1.67e-04**	8.88e-01	**8.92e-01**	(1.1, 1.1)
ZDT2	2.51e-01	**1.77e-01**	1.96e-04	**1.63e-04**	5.67e-01	**5.71e-01**	(1.1, 1.1)
ZDT3	**4.42e-01**	5.27e-01	**2.61e-04**	3.66e-04	1.115	**1.119**	(0.935,1.1)
ZDT4	**3.02e-01**	4.64e-01	**6.79e-04**	1.28e-03	**8.54e-01**	7.34e-01	(1.1, 1.1)
ZDT6	2.45e-01	**1.68e-01**	4.90e-04	**1.10e-04**	3.47e-01	**3.66e-01**	(0.935,1.1)
DTLZ1	**3.51e-01**	4.16e-01	**1.21e-03**	1.99e-03	**1.425**	1.422	(1.1, 1.1, 1.1)
DTLZ2	2.56e-01	**2.05e-01**	**1.23e-03**	1.25e-03	1.14	**1.16**	(1.1, 1.1, 1.1)
DTLZ2-4	**0.56**	0.69	**1.2e-02**	1.8e-02	4.60e-01	**4.65e-01**	(1,1,1,1)
DTLZ3	**3.52e-01**	8.58e-01	**1.28e-03**	8.14e-03	3.1002	**3.1003**	(5.0, 5.0, 5.0)
DTLZ4	2.74e-01	**1.92e-01**	**1.19e-03**	3.28e-03	**9.23e-01**	9.17e-01	(1.1, 1.1, 1.1)
DTLZ7	5.60e-01	**5.15e-01**	**1.25e-03**	1.33e-03	2.04	**2.05**	(1.1, 1.1, 7.0)

Our results indicate that MOAIS-HV can produce very competitive results in both bi-objective and three-objective problems. This is remarkable if we consider that no recombination operator was adopted. It is also worth noting that we did not include comparisons with respect to other MOAISs because most of them did not adopt the DTLZ test problems in their experiments.

Additionally, we included one example with four objectives (DTLZ2-4). Although the differences are marginal, it can be seen that our MOAIS-HV still provides better results than NSGA-II with respect to hypervolume. In fact, if we increase more the number of objectives, it is expected that the difference will become more significant very quickly, because of the fast degradation of Pareto-based selection.

7   Conclusions and Future Work

We have presented here what we believe to be the first indicator-based MOAIS. The aim of this work was to investigate the suitability of using hypervolume for designing a MOAIS that can be competitive with respect to state-of-the-art MOEAs.

Our preliminary results indicate that our proposed approach provides a competitive performance with respect to a state-of-the-art MOEA (NSGA-II) in a variety of difficult test problems that had not been used (in full) before for assessing performance of a MOAIS. It is also worth remarking that the hypervolume contribution discard process was simplified with the purpose of lowering the complexity of the algorithm. This was done, however, at the expense of decreasing the quality of the results. However, as part of our future work, we are interested in exploring the use of a faster algorithm for computing the hypervolume that

was recently introduced in [22]. With this new algorithm we expect to produce a more competitive MOAIS, that has a lower computational complexity.

As part of our future work, we are also interested in adding new methods taken from the immune system metaphor for improving our results. For example, implementing an immune system memory seems to be relevant in order to avoid cloning candidates in bad regions of the objective space. Another interesting idea is to use a diversity function to add some random elements "between" two good solutions. These solutions would be nondominated solutions that were suppressed previously by the hypervolume discard process. Such a mechanism should improve the uniform distribution of solutions along the Pareto front obtained by our algorithm.

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