Overview of Artificial Immune Systems for Multi-objective Optimization

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Abstract. Evolutionary algorithms have become a very popular approach for multiobjective optimization in many fields of engineering. Due to the outstanding performance of such techniques, new approaches are constantly been developed and tested to improve convergence, tackle new problems, and reduce computational cost. Recently, a new class of algorithms, based on ideas from the immune system, have begun to emerge as problem solvers in the evolutionary multiobjective optimization field. Although all these immune algorithms present unique, individual characteristics, there are some trends and common characteristics that, if explored, can lead to a better understanding of the mechanisms governing the behavior of these techniques. In this paper we propose a common framework for the description and analysis of multiobjective immune algorithms.

1 Introduction

Multiobjective problems arise in many engineering and scientific applications, where many conflicting goals have to be achieved simultaneously. In this class of problems, evolutionary algorithms in general have been demonstrated to be an effective and efficient tool for finding the set of trade-off solutions that characterize the Pareto-optimal set. For a good overview of the current state-of-art in multiobjective evolutionary techniques, we refer to some of the main books in the field[21,8,37] and also to the Online EMO Repository [11].

During the last decade [16], a new paradigm based on principles of the immune system has been employed for developing interesting algorithms for both mono and multiobjective optimization (MOO). Artificial immune systems (AIS) [20] have found applications in many fields such as pattern recognition, computer defense, optimization, and others. Since then, many multiobjective AIS algorithms have appeared in a variety of conference proceedings and technical journals, some of them not specialized in evolutionary computation. The main objective of this paper is to present a broad overview of the current MO-AIS techniques available in literature. Performance comparisons, however, are outside of the scope of this work, due to space constraints. This paper proposes a

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common framework for MO-AIS algorithms, presenting a canonical MO-AIS algorithm from which all other MO-AIS algorithms reviewed can be instantiated. This common framework can simplify the comparative analysis of the algorithms, as well as the introduction of new characteristics and the study of their effects. Finally, we discuss the employment of other AIS principles in the improvement of multiobjective techniques, and present a brief overview of other immunological principles that could be employed for the development of new algorithms.

2 Multiobjective Optimization and the Immune System

In multiobjective optimization, we consider the following general problem:

$$\begin{aligned} \mathcal{X}^* &= \arg\min f(x) \\ \text{subject to: } & x \in \mathcal{F} \subseteq \mathcal{X} \end{aligned} \tag{1}$$

in which $x \in \mathcal{X}$ represents the optimization variables. The objective functions are $f : \mathcal{X} \mapsto \mathbb{R}^m$, that is, they map the optimization variables into real values. The set $\mathcal{F}$ represents the feasible set, mathematically defined as:

$$\mathcal{F} = \{x \in \mathcal{X} : g(x) \leq 0\} \tag{2}$$

where $g : \mathcal{X} \mapsto \mathbb{R}^p$ are the constraint functions. If the problem is unconstrained, $\mathcal{F}$ and $\mathcal{X}$ are equivalent.

In the multiobjective context, there is not only one solution, but a set of trade-off or Pareto-optimal solutions defined as:

$$\mathcal{X}^* \triangleq \{x \in \mathcal{F} : \nexists z \in \mathcal{F} | f(z) \leq f(x), f(z) \neq f(x)\} \tag{3}$$

Since $f(z)$ and $f(x)$ are vectors in $\mathbb{R}^m$, we need to define the relational operators $\leq$ and $\neq$:

$$f(z) \leq f(x) \Leftrightarrow f_i(z) \leq f_i(x), \forall i = 1, \ldots, m \tag{4}$$

$$f(z) \neq f(x) \Leftrightarrow \exists i = \{1, \ldots, m\} : f_i(z) \neq f_i(x) \tag{5}$$

The evolutionary multiobjective techniques are designed to find a set of non-dominated solutions that best represents the Pareto-optimal set. The search is performed through the consecutive application of stochastic and heuristic operators, balancing global and local search capabilities, over a population of candidate solutions. For a good overview of evolutionary multiobjective algorithms, see References [21,8].

Figure 1 shows the outline of a general population-based algorithm. This algorithm presents the fundamental ingredients for designing an evolutionary multiobjective technique, with the implementation details of each operator (e.g., whether the initialization procedure is random or deterministic, or the way to implement the Selection) varying from one algorithm to another.

1. Define the search space $\mathcal{X}$, population size N, objective $f(\cdot)$ and constraint $g(\cdot)$ functions;
2. $A(t=0) \leftarrow$ Initialize offline population;
3. $B(t=0) = \left\{b^{(1)}, \ldots, b^{(N)}\right\} \leftarrow$ Initialize online population;
4. **While** ($\neg$ stop criterion) **do**:
   (a) Evaluate population using $f(\cdot)$ and $g(\cdot)$;
   (b) $\Psi(t) = \left\{\psi(b^{(1)}), \ldots, \psi(b^{(N)})\right\} \leftarrow$ Evaluate scalar quality $(B(t))$;
   (c) $C(t) \leftarrow$ Selection $(A(t), B(t), \Psi(t))$;
   (d) $D(t) \leftarrow$ Variation $(C(t))$;
   (e) $A(t+1) \leftarrow$ Update$(A(t), B(t))$;
   (f) $B(t+1) \leftarrow D(t)$;
   (g) $t \leftarrow t+1$;

Fig. 1. Outline of a population-based algorithm

The offline population, also termed memory or archive population, will store the "best solutions" achieved by the algorithm, i.e., the representation of the Pareto-optimal set. The update method for the offline population should consider dominance relations and also a good representation of the Pareto front. Actually, the adoption of an offline population $A(t)$ in multiobjective evolutionary algorithms is nowadays considered as an essential characteristic, being also used as the dividing line between the first and second generation of evolutionary multiobjective techniques [10]. Thus, all algorithms that represent the current state-of-the-art in evolutionary multiobjective optimization employ such explicit elitism method, see References [12,22,41] amongst others. Another important characteristic highlighted in Figure 1 is the calculation of a scalar quantity that measures the quality of the solution in a multiobjective context. Finally, the selection and variation steps represent the heuristic search of the algorithm, responsible for generating the next population based on the current online population $B(t)$.

In general, any population-based technique can be adequately represented by the baseline algorithm above. The fundamental differences in all these algorithms in literature reside basically in: (i) the scalar quality calculation; (ii) the update of the offline population and the mechanism for preserving diversity in $A(t)$; (iii) the selection mechanism; (iv) the variation mechanism, that is, how the next population is generated based on the current one.

Recently, another class of evolutionary techniques have been developed for multiobjective optimization: the multiobjective artificial immune systems (MOAIS) algorithms, motivated by principles and models of the immunology. These algorithms demonstrate that AIS can be effectively employed for improving existing evolutionary techniques or designing new methods under different principles. The next section gives a broad overview of the multiobjective AIS techniques, but first, we discuss the analogies between the immune system and the multiobjective optimization problem in (1).

2.1 The Immune System

In a broad sense, the natural immune system (NIS) can be considered as the sum of the defenses of a given organism against foreign or endogenous threats, such as microorganisms, toxic substances, cancer cells, etc.. These defenses can be in the form of mechanical barriers (e.g., skin), biochemical barriers (body fluids containing destructive enzymes), immune cells (*leukocytes*) or molecular responses (interferons and other cytokines). Together, these defense lines are responsible for most of the body resistance to invasions and malfunctions that would otherwise weaken, damage or kill it.

The immune system is composed by the innate and the adaptive parts. As the name suggests, the innate immune system is born together with the organism, and represents a first-line defense against unknown pathogens. The cells of the innate immune system (*granulocytes* and *macrophages*, two kinds of *leukocytes*) are immediately available to defend the body against a large number of *antigens*, without requiring previous exposure to them and/or infection-specific adaptation. This part of the system plays an essential role on the early immune response against a given intruder, since the evolutionary process of the adaptive immune system has slower dynamics and may take a number of days before starting to function effectively.

In the adaptive immune system, the most important cells are a class of *leukocytes* called *lymphocytes*, which possess the ability to undergo a process of evolutionary adaptation when activated by a strong-binding external *antigens* or another *lymphocytes*' paratope [20]. This ability makes the adaptive NIS far more versatile than the innate immune system.

Each *naïve lymphocyte* (one that has not been involved in an immune response) carries specific receptors on its surface. Since there are millions of lymphocytes circulating through the body at any time, we have a large repertoire of molecular patterns that can be recognized with varying intensities. Once the *lymphocyte* binds to an antigen with a binding strength over a certain threshold, it starts proliferating and producing clones that undergo a process called *affinity maturation*, which is responsible for small variations in the shape of the receptors. Eventually, one of these slightly different clones will present a stronger binding to the *antigen*, and will start dominating the immune response. So, it can be said that the lymphocytes of the adaptive immune system undergo a process in all aspects similar to Darwinian evolution by natural selection, within a given individual.

This evolutionary process, called *Clonal Selection Principle* (CSP), is the basis for most of the multiobjective optimization algorithms based on the immune approach. Another popular theory amongst algorithm designers is the *Idiotypic Network Theory*, sometimes also called *Immune Network Theory*. This theory models the dynamic behavior of the immune system as a network of interacting elements, with the antigens recognizing (and suppressing) not only antigens, but also other antibodies, in a self-regulatory process. Both the CSP and the immune network are described in detail elsewhere [20], and will therefore not be discussed in depth here.

There are a number of other models and theories that are sometimes used in the AIS field. A notable example is the MOIA algorithm, explained later in this paper, which models a large number of biological processes in its iterative process and coding of the candidate solutions. The discussion of these theories is also out of the scope of this paper. Comprehensive reviews on immunology can be found in the main textbooks of this field [1].

2.2 Terminology in AIS Optimization

The antigen recognition by the immune system can be seen as a searching problem since it needs to find the antibody that best binds to a given antigen. In this sense, the problem (1) can be seen as the antigen or, in the case of many objectives and constraints, problem (1) can be seen as a polyvalent antigen.

The candidate solutions in the algorithm are named antibodies. The binding intensity between one antigen and one antibody is called antigen-antibody affinity. The binding intensity between two antibodies is called antibody-antibody affinity. Finally, the affinity degree between a given antibody and a polyvalent antigen is called avidity. In multiobjective optimization, affinity values are represented by the objective and constraint values. The avidity value is a scalar value giving the overall binding intensity between the antigen, represented by problem (1), and the antibody, i.e., the solution $x \in \mathcal{X}$. Hence, the avidity value measures the quality of the solution, and its definition varies among different algorithms. The antibody-antibody affinity can be associated to the similarity degree between the solutions. The calculation of this similarity degree depends of the representation system, for example, either binary or real.

3 Multiobjective AIS Algorithms

3.1 Yoo and Hajela's Algorithm

The first multiobjective technique that employed AIS ideas was Yoo and Hajela's algorithm [39]. They used a genetic algorithm, with normal selection, crossover, and mutation operators, but employing immune-based ideas for modifying the fitness values. In their algorithm, the memory population $A(t)$ containing the nondominated solutions is called antigen population. The online population $B(t)$ is called antibody population. One antigen is randomly selected from $A(t)$ and S antibodies are randomly selected from $B(t)$. The affinity (similarity) between antigen and antibodies is calculated and the one with the highest affinity has his fitness value increased. This process is repeated a given number of times. This approach was tested on a number of structural design problems, including two truss design problems and a I-beam problem. Although Yoo and Hajela's algorithm can not be considered a true MO-AIS, it is pioneer in using AIS ideas in multiobjective optimization.

3.2 I-PAES

Another hybrid approach, the Immune Pareto Archived Evolution Strategy (I-PAES) proposed by Cutello et.al. [13] is based on the PAES algorithm [29], with a local search phase based on the clonal selection principle. The original PAES is a multiobjective (1+1) local search evolution strategy, that proposes a grid-based approach for maintaining diversity in the offline population. I-PAES modifies the variation mechanism in the original PAES(1+1) by using immune inspired operators, specifically cloning and hypermutation [13]. The authors demonstrate the application of I-PAES in protein structure prediction problems.

3.3 Luh and Chueh's MOIA

Luh and Chueh's multiobjective Immune Algorithm (MOIA) was first proposed in 2003 [32], and then adapted to deal with constrained multiobjective problems in 2004 [33]. It is a complex algorithm with a strong biological motivation, based on the *Clonal Selection* theory, DNA library building, distinction between heavy and light protein chains in the antibodies, interleukin interactions, and a number of other immunological models that fall out of the scope of this paper (see Reference [6] for further details).

MOIA uses binary representation of the search space, with each variable of the candidate solutions represented by a *heavy chain* part (the most significant bits) and a *light chain* (less significant bits). This distinction is used at a certain stage of the algorithm to implement a local search procedure around the most promising solutions of the population.

After generating a random initial online population, MOIA enters the iterative cycle by evaluating this population over all objectives and constraints, and using these values to calculate the rank of the antibodies. It must be noted that in MOIA the constrained problems are transformed in an unconstrained one by means of a special kind of penalization of the objective functions by the constraint violations [33]. After calculating the rank of each antibody, the non-dominated ones are selected for a local search procedure, implemented through cloning and hypermutation of the *light chains* in the bitstring. The best solutions found by this process are copied to both the offline and online populations. The offline population is then cleaned from dominated or unfeasible solutions, with a few dominated feasible solutions being stored for insertion in the *Germ-line DNA library* in a later step of the algorithm.

After the local search procedure, the *avidity* value is calculated for all antibodies. In MOIA, the *avidity* accounts both for the performance of the solutions and for the similarity between them. The algorithm then assembles the *Germ-line DNA library*, by combining a few antibodies expelled from the offline population (as mentioned above) with ones selected by Tournament from the current population. This *Germ-line DNA library* is then used to generate the next-generation population, by combining fragments of the *donor* solutions into new points in the search space, a procedure similar to the *Crossover* operator used in genetic algorithms.

A last step in this algorithm is to apply a number of diversity generation operators over the next-generation population, according to user-defined probabilities. These operators [33] are responsible for keeping the exploration feature of the algorithm, avoiding the premature convergence to a local Pareto Front. The iterative cycle is repeated until a given number of generations are completed.

MOIA was used to solve some analytical benchmarck problems [32], and the results obtained were superior to those obtained by SPEA, MOGA, NPGA and NSGA. Also, the constrained version of MOIA [33] was used in the design of truss structures.

3.4 MISA

The Multi-objective Immune System Algorithm (MISA) [7,9,14] is an immune algorithm based on the *Clonal Selection Principle* with elitism. The algorithm uses a grid-based random generation of the initial population in the search space, and presents an interesting selection strategy for choosing the antibodies to be cloned, based both on dominance and feasibility. Also, the number of clones each selected antibody receives is regulated by a niching procedure in the objective space, in order to drive the evolution towards a fair sampling of the Pareto front.

The performance of the MISA is tested on various analytical benchmark problems [7], and compared to other state-of-the-art multiobjective optimization algorithms [9], where it has shown a competitive performance when compared to NSGA-2, micro-GA, and PAES.

3.5 MOCSA

The Multi-Objective Clonal Selection Algorithm (MOCSA) [5] combines ideas from CLONALG [18] and opt-AINet [19] in a MO-AIS algorithm for real-valued optimization. In MOCSA, the quality values are calculated using nondominated sorting. The population is sorted based on these values, and the first N_c best solutions are selected for cloning. MOCSA uses real-coding and Gaussian mutation similarly to opt-AINet. The number of clones in the proliferation phase depends on the ranking of the individual in the nondominated fronts.

The mutated clones are evaluated and combined with the original ones. They are sorted again using nondominated sorting and the N_c best solutions are preserved. MOCSA also employs a diversity generation mechanism in such a way that the worst individuals, i.e., those not selected for cloning, are eliminated and substituted by randomly generated individuals.

MOCSA was used to solve an analytical benchmark problem, as well as the problem of designing an electrostatic micromotor [5]. The analytical results were compared to results obtained by MISA, NSGA-2, PAES and micro-GA, with MOCSA producing competitive results according to two standard metrics (*generational distance* and *spacing* [9]). In 2006, an improved version of the MOCSA was employed for the solution of a 3-objective design of a superconducting magnetic energy storage (SMES) system [26].

3.6 VAIS

The Vector Artificial Immune System (VAIS) [23,25] is a multiobjective version of the opt-AINet algorithm [19]. The immune network theory states that antibodies can recognize other antibodies and this chain of recognition either stimulates or suppresses their proliferation. In the original opt-AINet, the memory population stores the sub-optimal solutions in a single objective optimization problem. A suppression operator is applied to the memory population in order to eliminate redundancy.

In VAIS, the author adapts these ideas for developing a multiobjective algorithm whose memory population now stores the nondominated solutions. VAIS employs real representation of the variables and quality-proportional Gaussian mutation, as in the opt-AINet. In order to evaluate the quality values, VAIS utilizes strength values likewise in SPEA2 [41], but without the use of density values, since the suppression mechanism in the memory population already deals with dense regions. The suppression mechanism is also modified in VAIS. It considers similarity in the objective space, not in the parameter space as in opt-AINet.

VAIS was tested in a number of analytical problems[25], in which VAIS showed similar or better results when compared to NSGA-2. A modified version of the VAIS, called VIS, was presented in 2006 [24], along with several examples of application on analytical constrained and unconstrained benchmark problems.

3.7 IDCMA

The Immune Dominance Clonal Multi-objective Algorithm (IDCMA) [27,34] introduces a new similarity measure between antibodies, based on distances in the objective space: the immune differential degree. Again, this similarity measure is used to reduce the size of the offline population in the update step.

The algorithm also presents a different selection mechanism for cloning. In this mechanism, one antibody is randomly selected from the offline population in the beginning of each iteration. The quality value of each individual in the online population is computed based on the antibody-antibody affinity, that is, similarity in the representation of the solutions. The population is sorted based on these affinity values, and the first N_c ones are selected for cloning. Finally, the solutions in the clone population undergo recombination and mutation to generate the next population.

IDCMA was used to solve a 0/1 Knapsack problem, and the results are compared against those obtained by a number of first-generation algorithms, including NSGA, NPGA and VEGA [34]. It was observed that the solutions found by IDCMA dominated the ones obtained by the other algorithms, and could therefore be qualified as better ones.

3.8 IFMOA

From the same group that proposed IDCMA, the Immune Forgetting Multiobjective Optimization Algorithm (IFMOA) [31,40] is also based on the clonal

selection principle for the variation step. The scalar quality values for the solutions are calculated in the same way as in SPEA2 [41]. The selection for cloning is deterministic and the same number of clones is used for each solution. The immune forgetting operator, proposed in IFMOA, consists of substituting a given number of solutions from the online population, randomly selected, by individuals from the offline population, also randomly selected. However, the authors do not clarify the benefit of this operator to the algorithm.

In order to show the applicability of the IFMOA, a number of comparisons against the SPEA2 and MOGA were performed, for diverse analytical benchmarck problems [31]. It was shown that the Pareto fronts obtained by IFMOA were significantly better than the ones from the other algorithms. IFMOA has been also used for solving problems related to unsupervised feature selection [40].

3.9 ACSAMO

Another multiobjective algorithm based on the Clonal Selection Principle is the Adaptive Clonal Selection Algorithm for Multiobjective Optimization (ACSAMO) [38], proposed in 2006 by Wang and Mahfouf. ACSAMO generates a fixed number of clones for all antibodies and presents an quality-proportional mutation, like in the VAIS. The antibody-antigen affinities are calculated by using a dynamically adjusted weighted approach, in which an evolutionary pressure in the direction of the "best so far" and "best this generation" solutions is applied over the online population. At each generation, the two "best" solutions are found according to a random-weight linear aggregation of objectives, as in (6):

$$\mathrm{WF}_i = \sum_{j=1}^{m} w_j f_j\left(Ab_i\right); \quad \sum_{j=1}^{m} w_j = 1 \tag{6}$$

The "best" solutions are chosen based on the random variation of the weights w_j. The affinity is then calculated as:

$$\mathrm{af}_i = dist\left(Ab_i, Ab_c\right) + dist\left(Ab_i, Ab_g\right) \tag{7}$$

where Ab_c and Ab_g are the "best so far" and the "best this generation" solutions according to the aggregation function (6), respectively.

The selection operator for the offline population is based on the Pareto dominance (nondominated solutions are copied to the offline population); if the maximum size of the offline population is exceeded, a crowding procedure is used for eliminating solutions from the most crowded regions of the Pareto front.

ACSAMO was tested on some analytical benchmark problems, in which it outperformed both SPEA and NSGA-2 [38].

4 A Common Framework for MO-AIS Algorithms

As we can see from the previous section, we have many different ways of implementing a MO-AIS algorithm. Nonetheless, these algorithms share some common

characteristics. Except from the Yoo and Hajela's algorithm, all of them employ the clonal selection principle to a certain extent, including MOIA, that employs clonal proliferation and mutation as a local search procedure for the offline population. This principle is extensively used for designing AIS-based optimization algorithms and it forms a fundamental ingredient in defining the variation step, see Fig. 1, within a MO-AIS technique. In this section, we propose the outline of a canonical MO-AIS, which is shown in Fig. 2.

1. Define the search space $\mathcal{X}$, population size N, objective $f(\cdot)$ and constraint $g(\cdot)$ functions;
2. $A(t=0) \leftarrow$ Initialize offline population;
3. $B(t=0) = \left\{b^{(1)}, \ldots, b^{(N)}\right\} \leftarrow$ Initialize online population;
4. **While** ($\neg$ stop criterion) **do**:
   (a) Evaluate antibody-antigen affinities using $f(\cdot)$ and $g(\cdot)$;
   (b) $\Psi(t) = \left\{\psi(b^{(1)}), \ldots, \psi(b^{(N)})\right\} \leftarrow$ Evaluate avidity $(B(t))$;
   (c) $C(t) = \left\{c^{(1)}, \ldots, c^{(N_c)}\right\} \leftarrow$ Selection for Cloning $(A(t), B(t), \Psi(t))$;
   (d) $D(t) = \left\{d^{(1)}, \ldots, d^{(N_c)}\right\} \leftarrow$ Proliferation and Mutation $(C(t))$;
   (e) $E(t) = \left\{e^{(1)}, \ldots, e^{(N_d)}\right\} \leftarrow$ Diversification;
   (f) $A(t+1) \leftarrow \text{Update}(A(t), B(t))$;
   (g) $B(t+1) \leftarrow D(t) \cup E(t)$;
   (h) $t \leftarrow t+1$;

Fig. 2. Outline of the canonical MO-AIS

This canonical algorithm presents the fundamental ingredients for designing a given MO-AIS. The first important ingredient is the avidity evaluation, i.e., the computation of the scalar quality of the individuals. This can be made using procedures already known for multi-objective evolutionary algorithms and their variations. AIS introduces the additional possibility of using antibody-antibody recognition to define quality, as used in the Yoo and Hajela's algorithm and also in ACSAMO. With these values, we can proceed to the selection for cloning, which can be either deterministic or stochastic. In a deterministic selection the best N_c solutions based on the avidity values are selected. A stochastic selection can use, for instance, a tournament selection based on antibody-antibody affinity, where one antibody from the offline population is randomly selected as reference antibody for the tournament.

Proliferation and hypermutation are important elements in the variation mechanism of MO-AIS. The affinity-proportional mutation rate (likewise in opt-AINet) and the affinity-proportional number of clones (likewise in CLONALG) can be combined together, introducing a very interesting balance between local and global search in the searching process. This is done in MOCSA, for example. The number of clones can be also defined based on the idea of generating more

clones in the best regions, and/or more clones in the less crowded regions of the Pareto front estimative, as proposed in MISA.

The diversification step is another important element in MO-AIS, and it is more related to the global search capability of the algorithm. Not all MO-AIS in literature present such an explicit diversity mechanism. In general, the diversity generation is performed by the introduction of new random solutions, but other implementations are also possible. MOIA's operators for generating the next population from the DNA germinal library can all be seen as a sophisticated diversity mechanism.

Therefore, with the adequate adaptations, all algorithms reviewed in the previous section can be seen as particular instances of this canonical algorithm. In some of them the steps 4.(b) to 4.(e) are not so evident and easily distinguishable. This canonical MO-AIS is useful to identify similarities and differences among the algorithms and make the comparison easier. By delineating these basic ingredients, designers can identify these steps in each algorithm and examine different approaches for implementing the same step in a given MO-AIS algorithm. Moreover, the canonical MO-AIS makes evident the differences between AIS-based algorithms and other multi-objective evolutionary algorithms, mainly in the variation mechanism, by highlighting the specific operators of a truly MO-AIS technique.

5 Other Immune Principles

From the algorithms reviewed, it is clear that the most common idea used in the development of MO-AIS algorithms is by far the CSP, with some other principles (e.g., immune network, interleukin interactions) also being employed. There are, however, a number of immunological principles that have shown great promise in other areas of engineering, and could theoretically be used either in the development of new tools for multiobjective optimization or in the improvement of the existing algorithms. In this section we introduce two of such principles, along with some general ideas on how they could be applied for MOO.

5.1 Negative Selection

In the natural immune system, negative selection (NS) is responsible for the inhibition/death of a given lymphocyte upon being activated. This principle is used basically to model the elimination of antibodies that react against self-antigens, which could eventually cause auto-immune diseases. In engineering applications, NS-based algorithms have been used for intrusions detection [28], anomaly and fault detection [36,17], among other areas related to pattern recognition. To the knowledge of the authors, however, there has been no use so far of NS-based systems for optimization, either mono or multiobjective.

In general, MO-AIS algorithms present a explicit diversity generation mechanism at some point of the iterative process, which usually involve the insertion of newly generated random individuals in the population. While this unsupervised generation of new individuals has, as intended, the potential to explore

new regions of the search space, it may also generate solutions in regions of the space that have already been explored in previous iterations of the algorithm. This potential waste of valuable function evaluations is particularly aggravated in the later generations of the algorithms, when larger portions of the search space have been covered.

This kind of problem could in theory be reduced by having a NS routine embedded in the diversity-generation operators: during the optimization process, the previously explored regions of the search space would be stored as a "self" set, and new solutions generated by the operator would be created in a way similar to the one used for creating new detectors in NS-based fault detection algorithms [17]. With this, the exploration of new regions by the diversity generation algorithm would be guaranteed, therefore improving the overall algorithm performace.

5.2 Danger Theory

While mainstream immunology supports a view of the NIS classification abilities in terms of *self-nonself* discrimination, there are a number of phenomena that do not fit in this model. For instance, the fact that the immune system does not react against the bacterial flora in the gut, but is triggered by chemicals emmited by stressed *self* cells indicates that some extra mechanism for the recognition of potential threats is present. The Danger Theory (DT) [35] proposes an explanation to these behaviors of the NIS, based not on a *self-nonself* distinction but instead on a measure of the level of threat represented by a given antigen.

In AIS, a number of aplications of the DT have been proposed [2], including intrusion detection systems for computers [3] and anomaly detection. A possible application of this principle in MO-AIS would be to have under-explored regions of the Pareto front sending "danger" signals to the immune algorithm, indicating the need of an "immune response" (i.e., a better exploration of the space) in that direction. Another possibility is the use of DT principles for online decision-making in multiobjective optimization, with some regions of the Pareto emmiting "danger" signals in order to guide the evolution towards specific tradeoffs between the various objectives.

6 Discussion

This paper has presented an overview of current MO-AIS in literature and suggested a common framework for MO-AIS algorithms. The CSP is largely employed in the design of optimization algorithms, especially for defining their variation mechanism. Nevertheless, other principles and theories from AIS have been used in the quality assignment of the population, in the promotion of diversity in the online population, and in the update of the offline population. Moreover, some works have employed AIS ideas for improving constraint handling in evolutionary techniques [15,4] for the multiobjective case.

On the other hand, some AIS theories are not well explored in the field of optimization, such as Negative Selection and Danger Theory. These immune

models have been employed successfully in other fields of engineering, and an investigation of their potential as tools for the improvement of MO-AIS may be an interesting area of research.

From this overview, however, it is apparent that there is probably little need for more new MO-AIS algorithms, but instead an extensive comparison of the available methods and the available implementations of the fundamental steps outlined in Fig.2 should be pursued. The definition of what a MO-AIS algoritmh is and what it must have to be considered as such can help the design of meaningful comparison experiments. This work tries to fill this gap before proceeding to the comparison of methods, which is the logical next step on this research.

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