A Hybrid Multi-objective Immune Algorithm for Numerical Optimization

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Abstract: With the complexity of real world problems, optimization of these problems often has multiple objectives to be considered simultaneously. Solving this kind of problems is very difficult because there is no unique solution, but rather a set of trade-off solutions. Moreover, evaluating all possible solutions requires tremendous computer resources that normally are not available. Therefore, an efficient optimization algorithm is developed in this paper to guide the search process to the promising areas of the solution space for obtaining the optimal solutions in reasonable time, which can aid the decision makers in arriving at an optimal solution/decision efficiently. In this paper, a hybrid multi-objective immune optimization algorithm based on the concepts of the biological evolution and the biological immune system including clonal selection and expansion, affinity maturation, metadynamics, immune suppression and crossover is developed. Numerical experiments are conducted to assess the performance of the proposed hybrid algorithm using several benchmark problems. Its performance is measured and compared with other well-known multi-objective optimization algorithms. The results show that for most cases the proposed hybrid algorithm outperforms the other benchmarking algorithms especially in terms of solution diversity.

1 INTRODUCTION

In real world, many problems, no matter whether they are in the domain of engineering, business or science, can be formulated into different forms of optimization problems. Most of these problems normally involve multiple objectives rather than one single objective, in which some objectives conflict with others. As such, these problems that require meeting several objectives simultaneously are called multi-objective optimization problems. Solving this kind of problems is never an easy task because objectives of such problems are often found to be at least partly non-commensurable and conflicting. Very often, there is no single best solution to the multi-objectives optimization problems, but rather a set of optimal trade-off solutions which cannot be improved without disadvantaging the optimality of other objectives. During the solution evaluation process, a huge number of alternative solutions are required to be evaluated. However, it is very difficult to evaluate all possible solutions as this requires tremendous computer resources that normally are not available. Thus, an effective and efficient optimization algorithm is needed to guide the search process to the promising areas of the solution space and hence the optimal solutions in reasonable time.

Over the last decades, different metaheuristic algorithms have been developed for solving multi-objective optimization problems. Among the appealing metaheuristic algorithms, Artificial Immune Systems (AIS) based on biological immune system have received special attention among the research community because the immune system provides a rich source of stimulation and inspiration to the research community with their interesting characteristics: distributed nature, self-organization, memory and learning capabilities. Motivated by its great potential for solving multiple-objective optimization problems, the study reported in this paper is to develop a hybrid multi-objective algorithm based on the engineering analogue of the biological immune system – AIS incorporating some ideas from GA for solving multi-objective optimization problems.

The rest of this paper is organized as follows: Section 2 gives an overview of related research

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studies and the basis for the design and development of the proposed algorithm. Section 3 presents the proposed algorithm and its major features. Section 4 assesses the performance of the algorithm through the numerical optimization experiments with results presented and analyzed. Finally, summary and potential research directions are given in Section 5.

2 IMMUNITY-BASED MULTI-OBJECTIVE OPTIMIZATION

2.1 Biological Immune System

The biological immune system consists of diverse sets of specialized cells, molecules, and organs with a collection of defense mechanisms working collaboratively. The interactions among various cells, molecules, and organs result in complicated immunological behaviors for the purposes of provoking suitable immune responses, and defending, recognizing, and memorizing pathogens for protecting a given host against infections, thus keeping the host healthy (Goldsby et al., 2003). Many researchers have successfully developed a number of powerful multi-objective optimization algorithms based on the concepts of the biological immune system. The major inspiration for our proposed algorithm comes from the clonal selection principle and the immune network theory. For a review of immune algorithms, one can refer to Ataser (2013).

2.1.1 Clonal Selection Principle

Clonal selection principle was developed by Burnet (1959). It states that only those B-cells capable of binding with foreign antigens will produce clones having identical receptors to the original B-cells. This process is known as clonal expansion. When the B-cells undergo clonal expansion after binding to foreign antigens with the help of a second signal from accessory cells, their average antibody affinity will increase for the non-self antigens in order to boost the speed and effectiveness of the immune response to secondary encounters. Such a process is known as affinity maturation and results from somatic hypermutation and selection mechanism. The hypermutation can change the specificity of antibodies (cells) by introducing randomness to their genes, hence introducing diversity into the B-cell population. Once this process is completed, the B-cells possessing higher affinity antibodies will be selected to differentiate into a mature form - antibody-producing plasma cells, with each secreting only one type of antibodies. Other than developing into plasma cells, the activated B-cells with high affinity are selected to become long-lived memory B-cells. These cells can be activated by a very low concentration of the antigen that had triggered the primary response so that they can be ready for re-stimulation caused by secondary antigenic stimulus. Meanwhile, the antibodies of self-reactive B-cells are given an opportunity to rearrange their conformation for changing their specificity through the receptor editing process so as to prevent them from apoptosis.

Our proposed algorithm mimics the essence of the clonal selection principle to generate a varied, enlarged population of antibodies around their parents based on the corresponding antigenic affinity through the processes of the cloning and mutation. In these processes, antibodies perform local exploitation in different directions along the objective space, while the receptor editing process performs global exploration through the whole search space. At the end of each generation, the population will return to its original size with elitist antibodies having better affinity. This principle ensures the selection pressure is only placed on good individuals evolving towards the optimal solution set with reduced redundant search as well as strikes a balance between exploitation and exploration for assuring the achievement of a good result.

2.1.2 Immune Network Theory

The immune network theory describes the behavior of one of the key working principles of the adaptive immune system, which was mainly developed by Jerne (1974). The theory explains the properties of the immune system including immunological memory and tolerance through the existence of a mutually reinforcing network of B-cells that have variable region, i.e. idiotope and paratope. These variable regions bind not only to antigens, but also to other variable regions in the system. The interactions between B-cells result in stimulation on the B-cells with a paratope that has recognized an antigen. However, suppression can also result from the interactions between B-cells where an anti-idiotypic antibody is involved, hence bringing about a regulatory mechanism.

Our proposed algorithm bases on the immune network theory to introduce a suppression operator to the antibody population after the cloning and mutation processes for avoiding antibody redundancy and maintaining the population diversity

so as to acquire the uniformly distributed Pareto front. To achieve this, the affinity among all antibodies is determined in order to determine whether to retain or discard individual antibody.

2.2 Multi-objective Optimization Algorithms

Finding the solutions to the multi-objective optimization problems has long been a challenge to researchers because both the Pareto optimality and the diversity of the generated solutions must be simultaneously addressed. Unlike solutions in single objective optimization problems, which can easily be compared according to the value of the objective function, solutions in multi-objective problems cannot directly be compared with each other unless employing classical techniques, such as, weighted objective aggregation methods and constraint approaches. As such, the multi-objective optimization problems are simplified and solved by converting the multi-objective problems into the single objective problems. Although these approaches are simple, they have some drawbacks for solving multi-objective problems such as the limited spread of non-dominated solutions, the lack of the ability of capturing the characteristics of all objectives, the lack of the ability of generating concave and nonconvex portions of the Pareto front, and their high dependence on user experiences and preference information.

Due to the complexities of real world problems and the limitations of these classical methods, modern evolutionary optimization algorithms such as GA, ES, AIS, etc. incorporating the concept of Pareto optimality with capability of generating diversified solutions have been proposed and have become popular. The reason of employing the concept of Pareto optimality is that it can facilitate the determination of the relative strength between candidate solutions based on their fitness value without converting the multiple-objective problems into the single objective problems, thus resulting in a set of non-dominated solutions or Pareto optimal solutions. They are said to be globally optimal to multi-objective optimization problems because no improvement in any one objective can be obtained without sacrificing the optimality of other objectives.

During the past few decades, evolutionary algorithms have received great interest and a significant number of publications have been done in multi-objective optimization domain since the first multi-objective evolutionary algorithm has been developed by Schaffer (1985). These algorithms have been proved to be effective ways for solving multi-objective optimization problems by finding the approximated Pareto front, including NSGA-II (Deb et al., 2000), SPEA2 (Zitzler et al., 2001), PESA-II (Corne et al., 2001), micro-GA2 (Pulido and Coello Coello, 2003), omni-aiNet (Coelho and Von Zuben, 2006), NNIA (Gong et al., 2008), omni-AIOS (Zhang, 2011), etc. For a comprehensive review of multi-objective evolutionary algorithms, one can refer to Deb (2001) and Coello Coello (2007).

Recently, the hybridization of AIS with other evolutionary algorithms has increasingly become a prevalent trend. For example, Luh et al. (2003) introduced an algorithm called Multi-objective Immune Algorithm (MOIA), which is devised based on the features of the biological immune system and gene evolution for efficiently solving multi-objective optimization problems. Cutello et al. (2006) extended the algorithm called Pareto Archived Evolution Strategy (PAES) (Knowles and Corne, 1999) with a different representation based on immune inspired computing principles in order to devise a modified version of PAES denoted by I-PAES. This algorithm is applied to a multi-objective Protein Structure Prediction (PSP) problem. Wong et al. (2009) developed an immunity-based hybrid EA called Hybrid Artificial Immune Systems (HAIS) for solving constrained multi-objective global container repositioning problems. Qiu and Lau (2014) proposed a new AIS-based hybrid algorithm which hybridizes two AIS theories: clonal selection principle and immune network theory with particle swarm optimization (PSO) theory for solving static job shop scheduling problems with the objective of makespan minimization.

Based on these studies, it is true to point out that complementarily combing the various optimization techniques can usually offer better performance in terms of convergence, computational efficiency, diversity and solution quality than individually employing them by overcoming their own weaknesses. In our proposed multi-objective optimization immune algorithm, other than immune operators, a crossover operator of GAs is adopted to enhance the performance in terms of diversity and convergence (Coello Coello et al., 2007).

3 OPTIMIZATION ALGORITHM DESIGN AND DEVELOPMENT

In this section, an innovative hybrid multi-objective

optimizer – Suppression-controlled Multi-objective Immune Algorithm (SCMIA) based on the clonal selection principle and immune network theory as well as incorporated the ideas from GA is developed. The mapping between the biological immune system and the proposed artificial one is given in Table 1.

Table 1: Mapping between the biological immune system and SCMIA.

Biological Immune System	SCMIA
Antigen (Ag)	Objective function to be optimized
Antibody (Ab)	Candidate solution (a set of decision variables) to be optimized
Ag-Ab affinity	Fitness value of each candidate solution evaluated based on Pareto dominance
Ab-Ab affinity	Crowding-distance working as a measure of population diversity
Immune suppression	Mechanism to control the number of nearby candidate solutions based on similarity among candidate solutions in both the objective space and decision variable space
Memory cell	Current best non-dominated solution

The proposed SCMIA comprises five immune operators: cloning, hypermutation, suppression, selection & receptor editing, and memory updating, and one genetic operator: crossover. Each of them takes responsibility for different tasks for the purpose of finding uniformly distributed Pareto front. The cloning operator generates a number of copies to explore the solution space where better individuals are given more chances for being cloned. The hypermutation operator works on the clones to bring variation to the clone population, hoping for producing better offspring and increasing population diversity. The crossover operator is used to enhance the diversity of the clone population and the convergence of the algorithm by avoiding getting trapped into local optima. The suppression operator works on the whole population including the mutated clones and parent cells to eliminate similar individuals in order to avoid a particular search space being over exploited. The selection & receptor editing operator works like a director to guide the search towards the promising regions of a given fitness landscape by selecting the best antibodies to form the next generation and allowing the genes of the less-fit to be randomly restructured for changing their specificity through the receptor editing process.

The memory updating operator works as an elitist mechanism for helping preserve the best solutions that represent the Pareto front found over the search process. The proposed algorithm is conducted by applying these heuristic and stochastic operators on the antibody population for balancing both the local and global search capabilities. SCMIA is indeed a specific multi-objective algorithm, but its basic structure can be considered a generic framework for multi-objective optimization which can be implemented in different ways according to the problem at hand. Details of the proposed algorithm are discussed below and the block diagram showing the computational steps for the proposed SCMIA is presented in Figure 1.

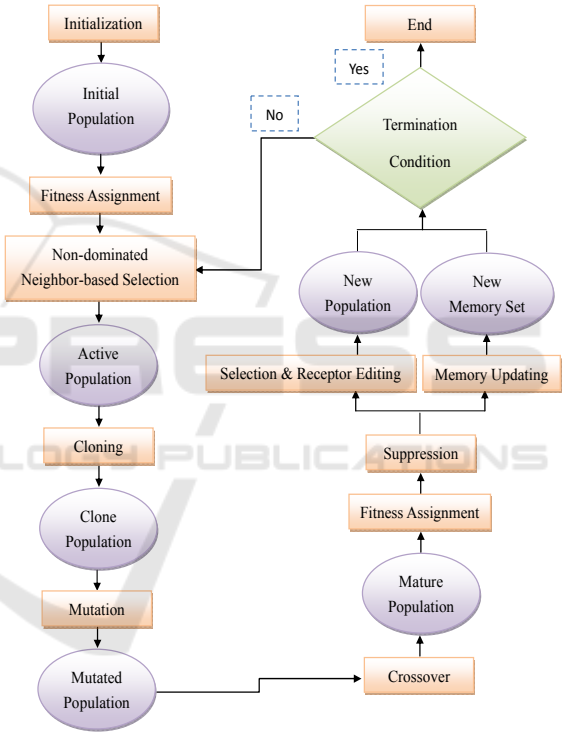

Figure 1: Computational steps for the proposed SCMIA.

Step 1: A random uniformly distributed antibody population $\mathbf{Ab}(t) = \{ab_i: i = 1, 2, \ldots, N\}$ is initially generated, where t is the iteration counter, N is the size of the population, and $ab_i = \{x_j: j = 1, 2, \ldots, m\}$ is a candidate solution containing m decision variables to the fitness function. Other than this online population, an external memory population $\mathbf{P}(t\text{-}1)$ with the size of N_m for storing the non-dominated solutions is also created and initialized to be empty.

Step 2: The values of objective functions of each antibody ab_i are evaluated. In this way, a fitness

array ab(*f*) storing the values of all objective functions for each parent can be determined. And then the Pareto dominance relation of each antibody is determined by comparing their fitness values with respect to each objective. Through this comparison, each of them is assigned an antigenic Ab-Ag affinity called Pareto fitness pf_i. The Pareto fitness of each antibody is computed as follows:

$$pf_i = D_i \tag{1}$$

where D_i is the number of antibodies that dominates the antibody ab_i. It is noted that when the fitness of an antibody *pf* is equal to 0, this antibody is considered a non-dominated solution as it is not dominated by any other antibodies in the population.

Step 3: Based on the idea proposed by Gong in NNIA (Gong et al., 2008), only non-dominated antibodies are selected to form an active parent population $\mathbf{A}(t)$ with the size of N_A for undergoing cloning, crossover and hypermutation. If the number of non-dominated antibodies is smaller than N_A, all non-dominated antibodies are selected to form $\mathbf{A}(t)$. However, if the number of non-dominated antibodies is larger than N_A, an antibody density measure called crowding-distance (Deb et al., 2002) analogous with Ab-Ab affinity in biological immune system is employed. The crowding-distance for a non-dominated antibody is computed as follows:

$$d(ab_i^*) = \sum_{j=1}^{r} \frac{|ab_{i+1}^*(f_j) - ab_{i-1}^*(f_j)|}{ab(f_j^{max}) - ab(f_j^{min})} \tag{2}$$

where $d(ab_i^*)$ is the crowding-distance of the *i*-th non-dominated antibody ab^*, $ab(f_j^{max})$ and $ab(f_j^{min})$ are the maximum and minimum fitness values of the *j*-th objective, $ab_{i+1}^*(f_j)$ and $ab_{i-1}^*(f_j)$ are the fitness values of the nearest neighboring antibodies from both sides in terms of the fitness. With this measure, N_A antibodies with a larger crowding-distance value are selected to form $\mathbf{A}(t)$ in order to enhance the population diversity. It is worth emphasizing that this approach guides the search paying more attention to the less-crowded regions in the current Pareto front at each generation.

Step 4: Cloning operator enlarges the population by generating a number of copies of each antibody in $\mathbf{A}(t)$ and the number of copies is directly proportional to its Ab-Ab affinity, thus forming a clone population $\mathbf{C}(t)$. Hence the size of the population now is $N + N_c$ and N_c is obtained by:

$$\begin{cases} c_i = \text{round}(c_{max} \times d(ab_i^*)) & (3) \\ N_c = \sum c_i & (4) \end{cases}$$

where N_c is the total number of copies produced, c_i is the clone size for the antibody, c_{max} is the pre-defined maximum clone size of each antibody, and round() is an operator for rounding its argument to the closest integer. Clearly, the higher the Ab-Ab affinity an antibody has, the more the number of copies it can generate.

Step 5: The hypermutation operator induces multi-point mutations to the clones. The mutation depends on the Ab-Ab affinity of their active parents. The reason to take account of the Ab-Ab affinity is to maintain the population diversity and prevent the crowding of antibodies. The clones are mutated proportionally as follows:

$$\begin{cases} \alpha = e^{-p \times d(ab^*)} & (5) \\ \mathbf{C}^m(t) = \mathbf{C}(t) + \alpha \times R & (6) \end{cases}$$

where α represents the mutation rate inversely proportional to the Ab-Ab affinity $d(ab^*)$, p is an exponential coefficient controlling the decay of α, $R \in [-1, 1]$ is a m-dimensional random vector obtained with uniform distribution, and $\mathbf{C}^m(t)$ is the mutated clone population.

Step 6: A modified single point crossover operator works on the mutated clone population to generate a mature clone population $\mathbf{C}^c(t)$ with the size of N_c. With this crossover operator, each offspring is generated by randomly selecting a single crossover point on a clone and then swapping its content beyond that point with that of an active parent antibody randomly selected from $\mathbf{A}(t)$. The diversity can be further enhanced through the crossover operation while the quick convergence can be ensured because some good genes from the active parent can be passed to the offspring.

Step 7: Objective functions of each mature clone are evaluated. And then a combined population is formed by combining both the parent cells and their mature clones for fitness assignment. For each cell in the active parent population and mature clone population, the Pareto dominance relation is determined and the Pareto fitness value pf_i' is assigned. As such, the Pareto fitness being assigned to each cell is dependent on the performance of all other cells in the combined population.

Step 8: **S**uppression operator is introduced and works on each cell in the combined population $\mathbf{A}(t) \cup \mathbf{C}^c(t)$ to avoid antibody redundancy and maintain the population diversity so as to acquire the uniformly distributed Pareto front based on the idea of immune network theory (Jerne, 1974). To achieve this, the antibody similarity among all antibodies has to be determined. Different from other AIS-based multi-objective optimization algorithms, the

similarity among antibodies in this algorithm is determined in terms of both the objective space and the decision variable space so as to determine whether to retain or discard individual antibody. The suppression operation has two phases: in 1st phase, the suppression will be applied to all antibodies and the similarity between two antibodies is defined as follows:

$$\mathrm{dO}(ab_a, ab_b)_j = \left|ab_a(f_j) - ab_b(f_j)\right| \leq \delta_j \qquad (7)$$

where $\mathrm{dO}(ab_a, ab_b)_j$ is the distance between antibodies ab_a and ab_b in terms of j-th objective and δ_j refers to the threshold value for j-th objective. In this phase, if the distances for all objectives between two cells are smaller than the thresholds, the two cells are said to be similar and hence the cell with poorer Pareto fitness will be suppressed and eliminated from the population. This procedure is repeated until all antibodies in the combined population are compared in order to ensure the population diversity.

In 2nd phase, the suppression will only be applied to the similarity between non-dominated cells and dominated cells and the similarity between two antibodies is defined as follows:

$$\mathrm{dV}(ab_a, ab_b) = \sqrt{\sum_{j=1}^{m}[ab_a(x_j) - ab_b(x_j)]^2} \leq \varepsilon \qquad (8)$$

where $\mathrm{dV}(ab_a, ab_b)$ is the Euclidean distance in decision variable space between the two antibodies ab_a (dominated cell) and ab_b (non-dominated cell) and ε refers to the threshold value for the decision space. In this phase, if the distance between two antibodies is smaller than the thresholds in decision variable space, they are said to be similar and hence the dominated cell will be suppressed and eliminated from the population. This procedure is repeated until all antibodies between non-dominated and dominated are compared in order to avoid redundant search. Eventually, surviving populations $\mathbf{A}^s(t) \cup \mathbf{C}^s(t)$ are obtained and then enter into the selection & receptor editing process and memory updating process simultaneously.

To enhance the population diversity and facilitate the search of uniformly distributed non-dominated solutions along the Pareto front of a given problem, the threshold values for the decision variable space and the objective space are dynamically calculated according to the maximum and minimum values found so far, hence adapting to the new values that appear in the population.

Step 9A: An evolutionary selection operator is used to select all non-dominated antibodies with respect to the Pareto fitness from the surviving populations to form a new population $\mathbf{Ab}(t+1)$ with the size of N for the next generation. If $\mathbf{Ab}(t+1)$ is not full, dominated antibodies with a better Pareto fitness are selected and some genes of these antibodies are then randomly selected to be replaced by randomly generated genes. These restructured antibodies are finally added to the new population until the population is full in order to further enhance the population diversity. This process actually mimics the process of receptor editing in the biological immune system. However, if the number of non-dominated antibodies found exceeds the population limit, only N non-dominated antibodies with higher Ab-Ab affinity are selected.

Step 9B: The memory set $\mathbf{P}(t)$ is updated and used to store all the non-dominated solutions from the surviving populations for the replacement of the previous memory set $\mathbf{P}(t-1)$. These best solutions are non-dominated with regard to both the antibodies in the current generation and the antibodies that tried to enter the memory set in previous generations.

Step 10: The termination function returns True if an optimal Pareto front is found, i.e., no significant changes (change within an acceptable range, η) on performance metrics of the memory set over successive iterations, *term_max*. The optimization process will also terminate if the predetermined maximum number of iterations T_{max} is performed. If these conditions are not satisfied Steps 3 to 9 are repeated until one of the predetermined termination conditions is met.

4 NUMERICAL EXPERIMENTS

In this benchmarking study, a set of experiments based on several multi-objective numerical optimization problems was performed to benchmark the proposed algorithm with other well-known multi-objective optimization algorithms, that is, two immune algorithms – MISA (Coello Coello and Cortés, 2005) and NNIA (Gong et al., 2008) and two other evolutionary algorithms – NSGA-II (Deb et al., 2000) and SPEA2 (Zitzler et al., 2001). All these experiments were conducted using a computer with Xeon E5-2620 2 GHz CPU with 2 GB RAM and the Excel with VBA was used as an implementation platform.

4.1 Test Problems for Multi-objective Optimization

Several numerical functions with different characteristics and degrees of complexity reported in

the literature are selected to validate SCMIA. The test functions employed in this study are taken from three sources, including the traditional test problems used in early multi-objective optimization studies, namely SCH proposed by Schaffer (Schaffer, 1984) and FON proposed by Fonseca & Fleming (Fonseca and Fleming, 1995), as well as the ZDT test suite proposed by Zitzler et al. (Zitzler et al., 2000). In this study, ZDT5 is not selected for the benchmarking study largely because it is formulated based on binary coding, which is different from our study with the focus on real coding.

4.2 Performance Metrics

Three performance metrics are adopted to examine the quality of solution set in terms of the optimality and diversity in order to provide a quantitative comparison of the results, including 1) Error Ratio (ER) (Van Veldhuizen, 1999), 2) Spacing (S) (Schott, 1995), and 3) Inverted Generational Distance (IGD) (D. A. Van Veldhuizen and G. B. Lamont, 1998).

4.3 Experimental Setup

To conduct the experiments, the true Pareto front for each test problem is required. The true Pareto fronts of the test problems are generated by enumeration. However, since infinite number of solutions to be generated along the true Pareto fronts is impossible, a large number of random solutions, that is, 10,000 solutions are generated for representing the true Pareto fronts. In this research, the decision variables of all algorithms are real coded despite some of them originally are binary coded. Since the experimental results may be sensitive to runtime parameters of SCMIA, the runtime parameters are manually tuned based on preliminary sensitivity analysis. Three parameters, namely active population size, maximum clone size and mutation factor, are chosen for the sensitivity analysis. Based on the results of the sensitivity analysis, the parameters of **SCMIA** were set as follows: Initial population size, N = 100; Size of active population, N_A = 40; Size of the memory population, N_m = 100; Maximum number of clone for each cell, max_clone = 20; Exponential distribution coefficient, ρ = 0.05. To allow a fair comparison among the algorithms compared, the parameters of the benchmarking algorithms were set with same values and the values suggested by the researchers in their original papers as follows: **MISA**: Initial population size, N = 100; Size of clone population, N_c = 600; Size of the memory population, N_m = 100; Number of grid subdivisions, $subd\_size$ = 25; Initial mutation rate, ω = 0.6 (it decreases linearly over time until reaching the rate of $1/m$, where m is the number of decision variables.). **NNIA**: Size of dominant population, N_p = 100; Size of active population, N_A = 20; Size of clone population, N_c = 100; Crossover probability, p_c = 0.9; Mutation probability, p_m = $1/m$; Distribution indexes for crossover and mutation operators, n_c and n_m = 20. **NSGA-II**: Initial population size, N = 100; Crossover probability, p_c = 0.9; Mutation probability, p_m = $1/m$; Distribution indexes for crossover and mutation operators, n_c and n_m = 20. **SPEA2**: Initial population size, N = 100; Archive size, N_m = 100; Crossover probability, p_c = 0.9; Mutation probability, p_m = $1/m$; Distribution indexes for crossover and mutation operators, n_c and n_m = 20.

4.4 Experimental Results and Analysis

For test problems, the same parameters and hardware configurations are used with 100 generations over 15 trials being performed. The results of comparing the proposed algorithm with the benchmarking algorithms are shown in the following tables.

Table 2: Spacing (S).

	SCMIA	MISA	NNIA	NSGA-II	SPEA2
	Mean (Standard Deviation)				
FON	1.28E-02 (1.47E-03)	1.60E-02 (4.23E-03)	1.80E-02 (1.44E-03)	1.49E-02 (3.53E-03)	1.84E-02 (1.07E-02)
SCH	9.95E-02 (1.42E-01)	2.23E-02 (2.07E-02)	1.15E-01 (2.29E-02)	1.02E-01 (2.57E-02)	2.31E-01 (7.42E-02)
ZDT 1	1.41E-02 (4.16E-03)	8.99E-02 (6.48E-02)	1.76E-02 (1.52E-03)	2.46E-02 (4.61E-03)	1.18E-01 (9.79E-02)
ZDT 2	1.12E-02 (1.94E-03)	2.24E-02 (2.48E-02)	2.03E-02 (2.58E-03)	2.44E-02 (5.02E-03)	1.42E-01 (9.82E-02)
ZDT 3	2.40E-02 (7.42E-03)	1.24E-01 (7.10E-02)	3.02E-02 (5.80E-03)	2.64E-02 (5.78E-03)	1.26E-01 (8.21E-02)
ZDT 4	2.74E-02 (2.19E-02)	0.27 (0.32)	1.73E-02 (1.25E-03)	2.59E-01 (4.30E-01)	3.05E-01 (1.28E-01)
ZDT 6	3.22E-02 (3.51E-02)	3.41E-02 (5.00E-03)	1.39E-02 (1.64E-03)	2.26E-02 (1.86E-02)	8.28E-02 (2.57E-02)

Table 3: Error Ratio (ER).

	SCMIA	MISA	NNIA	NSGA-II	SPEA2
	Mean (Standard Deviation)				
FON	2.08E-01 (1.17E-01)	0.00 (0.00)	8.87E-02 (3.02E-02)	8.00E-03 (7.75E-03)	4.28E-01 (2.33E-01)
SCH	7.33E-03 (1.28E-02)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	3.73E-02 (4.37E-02)
ZDT 1	8.00E-03 (6.76E-03)	1.00 (0.00)	1.33E-03 (3.52E-03)	2.00E-03 (5.61E-03)	1.00 (0.00)
ZDT 2	7.33E-03 (4.58E-03)	1.00 (0.00)	0.00 (0.00)	2.00E-02 (4.34E-02)	1.00 (0.00)
ZDT 3	1.43E-02 (7.64E-03)	1.00 (0.00)	0.00 (0.00)	7.33E-03 (1.16E-02)	1.00 (0.00)
ZDT 4	2.53E-02 (1.81E-02)	1.00 (0.00)	0.00 (0.00)	2.59E-01 (4.30E-01)	1.00 (0.00)
ZDT 6	0.00 (0.00)	1.00 (0.00)	0.00 (0.00)	1.00 (0.00)	1.00 (0.00)

Table 4: Inverted Generational Distance (IGD).

	SCMIA	**MISA**	**NNIA**	**NSGA-II**	**SPEA2**
	Mean (Standard Deviation)				
FON	1.28E-03 (4.59E-04)	1.15E-04 (1.54E-05)	7.18E-04 (1.10E-04)	3.37E-04 (5.17E-05)	7.52E-03 (1.36E-02)
SCH	1.39E-03 (4.32E-03)	5.59E-05 (8.09E-06)	5.49E-05 (1.55E-05)	5.54E-05 (1.08E-05)	3.70E-03 (6.26E-03)
ZDT 1	5.43E-04 (3.90E-04)	3.65E-02 (5.44E-03)	2.06E-04 (9.30E-05)	4.14E-04 (2.37E-04)	6.47E-02 (1.65E-02)
ZDT 2	4.03E-04 (2.90E-04)	6.19E-02 (1.63E-02)	4.17E-05 (3.59E-05)	9.37E-04 (7.99E-04)	9.19E-02 (1.40E-02)
ZDT 3	4.81E-04 (1.62E-04)	3.86E-02 (7.73E-03)	1.14E-04 (5.80E-05)	2.95E-04 (1.25E-04)	5.50E-02 (1.70E-02)
ZDT 4	7.45E-03 (4.37E-03)	3.45 (1.08)	7.45E-05 (5.40E-05)	1.14E-03 (1.41E-03)	4.41E-01 (1.42E-01)
ZDT 6	1.09E-02 (5.20E-03)	4.05E-01 (1.13E-02)	4.43E-05 (1.24E-05)	1.17E-01 (2.60E-02)	3.68E-01 (7.66E-02)

Firstly, we compare the results of the mean and standard deviation of the three metrics, namely, ER, S and IGD over 15 trials obtained by the proposed algorithm - SCMIA with that of the other immune algorithms, namely, MISA and NNIA. From the above tables, we found that SCMIA generally is able to provide a similar result as other immune algorithms do, which is close to the true Pareto front PF_{true} and in some cases SCMIA can even outperform them. As for the traditional test problems (FON and SCH), MISA, NNIA and NSGA-II can generate slightly better results in the proximity aspect by achieving better performances in terms of ER and IGD. For the ZDT test suite, SCMIA and NNIA can generate much better results, which completely outperform the results generated by MISA in terms of the proximity and diversity with much lower values in the three metrics in all of the five ZDT test problems. By comparing SCMIA with NNIA, SCMIA performs better in diversity aspect with smaller S values in three (ZDT 1, 2 and 3) of the five ZDT test problems while NNIA performs better in proximity aspect with lower ER in four (ZDT 1, 2, 3 and 4) of the five ZDT test problems and the standard deviation of zero in ER indicates NNIA can consistently achieve the best performance in all trials. With regard to the convergence rate, MISA is the worst one among these three algorithms, which is revealed through the much higher ER and IGD in all of the five ZDT test problems. The standard deviation of zero in ER indicates MISA consistently cannot converge to the true Pareto front within 100 generations in all trials. In conclusion, it is shown that although NNIA is the best one in the proximity aspect, SCMIA is able to achieve better results in the diversity aspect among these three immune algorithms.

Secondly, we compare the results obtained by SCMIA with that of the other evolutionary algorithms, namely, NSGA-II and SPEA2. For the traditional test problems, NSGA-II can generate the best results in the proximity aspect because it achieves the best performance in terms of ER and IGD for the two traditional test problems, whereas SCMIA and SPEA2 obtain the similar results in the proximity aspect. With respect to the diversity, SCMIA achieves the best performance in terms of S for the traditional test problems. For the ZDT test suite, SCMIA can generate the best results in terms of the diversity with much lower values in S in almost all of the five ZDT test problems except ZDT6. In terms of the proximity, SCMIA can also outperform NSGA-II and SPEA2 in three (ZDT 2, 4 and 6) of the five ZDT test problems because SCMIA has lower values in ER and IGD. With respect to the convergence rate, SPEA2 is the worst

one among these three algorithms, which is revealed through the very high ER in all of the five ZDT test problems. The standard deviation of zero in ER indicates SPEA2 consistently cannot converge to the true Pareto front within 100 generations in all trials. In conclusion, it is shown that SCMIA outperforms the other evolutionary algorithms for most of the benchmark test problems especially in the diversity aspect.

Several important points can be concluded based on the results. Firstly, the proposed SCMIA provides comparable results regarding the other four algorithms against which it is compared. Although it does not always provide the best performance in terms of the three metrics adopted, it is able to generate reasonably good approximations of the true Pareto front of each test problem under investigation, including those with a convex, a nonconvex or a disconnected Pareto front. Also, it is generally shown to outperform MISA and SPEA2 with the quality of solution being similar to NNIA and NSGA-II in approximating the true Pareto front in terms of the proximity, diversity and convergence in almost all test problems. Finally, SCMIA clearly performs better than other benchmarking algorithms in the diversity aspect. This is largely attributed to the operators employed in the algorithm, including selection, cloning, hypermutation, crossover, and suppression. The selection operator, cloning operator and hypermutation operator incorporate the crowding-distance as a measure to select antibodies for undergoing the subsequent evolutionary processes, generate a number of copies to explore the solution space especially the less-crowded regions, and bring variation to the clone population respectively, in order to produce better offspring and increasing population diversity. The diversity is further enhanced through the crossover operation while the quick convergence can be ensured by preventing from being trapped into local optima because some good genes from the active parent can be passed to the offspring while bad genes would have a chance to be replaced with better genes through hypermutation. The suppression operator helps reduce antibody redundancy, hence significantly minimizes the number of unnecessary searches and increases the population diversity.

5 CONCLUSION AND FUTURE WORK

This research develops a hybrid immune algorithm - SCMIA for solving multi-objective optimization problems. The results show that SCMIA is able to generate a well-distributed set of solutions while it represents good approximation to the true Pareto-optimal set for most of the benchmark problems. Such satisfactory results are largely attributed to the characteristics of the algorithm, namely, distributed nature, self-organization, specificity, memory and learning capabilities from AIS as well as the complementary effect from crossover operation of GA to the hypermutation operation in AIS due to their different style of solution space traversal.

Future research could extend this approach to solve real world complex business problems with real world dynamics and to solve large scale problems with a large number of parameters, operators and equipment involved in order to establish the practical value of the algorithm in multi-objective optimization context.

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