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# Multiobjective Immune Algorithm with Nondominated Neighbor-based Selection

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## Abstract

Nondominated Neighbor Immune Algorithm (NNIA) is proposed for multiobjective optimization by using a novel nondominated neighbor-based selection technique, an immune inspired operator, two heuristic search operators, and elitism. The unique selection technique of NNIA only selects minority isolated nondominated individuals in the population. The selected individuals are then cloned proportionally to their crowding-distance values before heuristic search. By using the nondominated neighbor-based selection and proportional cloning, NNIA pays more attention to the less-crowded regions of the current trade-off front. We compare NNIA with NSGA-II, SPEA2, PESA-II, and MISA in solving five DTLZ problems, five ZDT problems and three low-dimensional problems. The statistical analysis based on three performance metrics including the Coverage of two sets, the Convergence metric, and the Spacing, show that the unique selection method is effective, and NNIA is an effective algorithm for solving multiobjective optimization problems. The empirical study on NNIA's scalability with respect to the number of objectives shows that the new algorithm scales well along the number of objectives.

## Keywords

Multiobjective optimization, evolutionary algorithm, artificial immune system, crowding-distance, Pareto-optimal solution.

## 1 Introduction

Many real-world problems have several objectives to be optimized at the same time. The simultaneous optimization of multiple objectives is different from single objective optimization in that there is no unique solution to multiobjective optimization problems (MOPs), but instead, we aim at finding all of the good trade-off solutions which must be considered equivalent in the absence of information concerning the relevance of each objective relative to the others. Evolutionary algorithms (EAs) have been recognized to be well suited to multiobjective optimization since early in their development because they deal simultaneously with a set of possible solutions. The ability to handle complex problems, involving features such as discontinuities, multimodality, disjoint

feasible spaces and noisy function evaluations, reinforces the potential effectiveness of EAs in multiobjective optimization (Fonseca and Fleming, 1995). The vector evaluated genetic algorithm (Schaffer, 1984) was probably the first multiobjective optimization EA (MOEA) to search for multiple Pareto-optimal solutions concurrently in a single run. Since the middle 1990s, the number of literatures about MOEAs increased greatly and many MOEAs were proposed one after another. The Niche Pareto Genetic Algorithm (Horn and Nafpliotis, 1993) and the Non-dominated Sorting Genetic Algorithm (Srinivas and Deb, 1993) were representative of them. These MOEAs were characterized by the use of selection mechanisms based on Pareto ranking and fitness sharing to maintain diversity (Coello Coello, 2003). In the past few years, some MOEAs using elitism strategy were presented such as the Strength Pareto Evolutionary Algorithm (SPEA) (Zitzler and Thiele, 1999), the Pareto Archived Evolution Strategy (PAES) (Knowles and Corne, 2000), the Pareto Envelope based Selection Algorithm (PESA) (Corne et al., 2000), the Multi-Objective Messy Genetic algorithm (MOMGA) (Van Veldhuizen and Lamont, 2000), the revised version of PESA with region-based selection (PESA-II) (Corne et al., 2001), the Micro Genetic Algorithm (microGA) (Coello Coello and Pulido, 2001), the improved version of NSGA (NSGA-II) with a more efficient nondominated sorting method, elitism and a crowded comparison operator without specifying any additional parameters for diversity maintaining (Deb et al., 2002a), and the improved version of SPEA (SPEA2) with a revised fitness assignment strategy, a nearest neighbor density estimation technique and an enhanced archive truncation method (Zitzler et al., 2002). These MOEAs can be considered to be different MOEAs in the sense that their different ways to do selection (or fitness assignment) and population maintenance in multiobjective spaces. Coello Coello maintains an evolutionary multiobjective optimization repository at ([www.lania.mx/~ccoello/EMOO](http://www.lania.mx/~ccoello/EMOO)) in which almost all of these algorithms can be found.

The human immune system (HIS) is a highly evolved, parallel and distributed adaptive system. The information processing abilities of HIS provide important aspects in the field of computation. This emerging field is referring to as the Artificial Immune Systems (AIS) (Tarakanov and Dasgupta, 2000). In recent years, AIS have received significant amount of interest from researchers and industrial sponsors. Applications of AIS include such areas as machine learning, fault diagnosis, computer security, and optimization (Nicosia et al., 2004; Jacob et al., 2005). Recently, Coello Coello proposed an artificial immune system algorithm MISA (Coello Coello and Cortes, 2002, 2005) based on the clonal selection principle (Burnet, 1959) to solve multiobjective optimization problems. We also proposed an immune algorithm IDCMA (Jiao et al., 2005) which is the groundwork of this paper. Both the two algorithms adopted binary representation. Freschi and Repetto (2005) proposed a vector Artificial Immune System (VAIS) based on the multimodal optimization algorithm opt-aiNet (de Castro and Timmis, 2002).

In this paper, we propose a novel multiobjective algorithm, called Nondominated Neighbor Immune Algorithm (NNIA). In NNIA, the fitness value of each nondominated individual is assigned as the average distance of two nondominated individuals on either side of this individual along each of the objectives, namely, the crowding-distance defined by (Deb et al., 2002a). According to the fitness values, only partial nondominated individuals with greater crowding-distance values are selected to do proportional cloning, recombination, and hypermutation. So in a single generation, NNIA pays more attention to the less-crowded regions (referred to Section 2.3) in the current trade-off front.

The remainder of this paper is organized as follows: Section 2 describes related background including multiobjective optimization, immune system inspired optimization algorithms, and three terms used in this paper. Section 3 describes the main loop of NNIA. The fitness assignment, population evolution, and computational complexity of NNIA are also analyzed in Section 3. In Section 4, five DTLZ problems (Deb et al., 2002b), five ZDT problems (Zitzler et al., 2000) and three low-dimensional problems are used to evaluate NNIA's effectiveness by comparing with NSGA-II, SPEA2, PESA-II and MISA, based on three performance metrics, the Coverage of two sets (Zitzler and Thiele, 1998), the Convergence metric (Deb and Jain, 2002), and the Spacing (Schott, 1995). The comparison of NNIA with and without recombination, and NNIA's scalability along the number of objectives will also be investigated. In Section 5, concluding remarks are presented.

## 2 Related Background

### 2.1 Multiobjective Optimization

Multiobjective Optimization (Deb, 2001; Coello Coello et al., 2002) seeks to optimize a vector of functions,

$$\mathbf{F}(\mathbf{x}) = (f_1(\mathbf{x}), f_2(\mathbf{x}), \dots, f_k(\mathbf{x}))^T \quad (1)$$

subject to  $\mathbf{x} = (x_1, x_2, \dots, x_m) \in \Omega$ . Where  $\mathbf{x}$  is called the decision vector, and  $\Omega$  is the feasible region in decision space.

Considering a maximization problem for each objective, it is said that a decision vector  $\mathbf{x}_A \in \Omega$  dominates another vector  $\mathbf{x}_B \in \Omega$  (written as  $\mathbf{x}_A \succ \mathbf{x}_B$ ) if and only if

$$\forall i = 1, 2, \dots, k \quad f_i(\mathbf{x}_A) \geq f_i(\mathbf{x}_B) \wedge \exists j = 1, 2, \dots, k \quad f_j(\mathbf{x}_A) > f_j(\mathbf{x}_B) \quad (2)$$

We say that a vector of decision variables  $\mathbf{x}^* \in \Omega$  is a Pareto-optimal solution or nondominated solution if there does not exist another  $\mathbf{x} \in \Omega$  such that  $\mathbf{x} \succ \mathbf{x}^*$ .

Then the Pareto-optimal set is defined as

$$\mathbf{P}^* \triangleq \{\mathbf{x}^* \in \Omega \mid \neg \exists \mathbf{x} \in \Omega, \mathbf{x} \succ \mathbf{x}^*\} \quad (3)$$

So the Pareto-optimal set is the set of all Pareto-optimal solutions. The corresponding image of the Pareto-optimal set under the objective function space

$$\mathbf{PF}^* \triangleq \{\mathbf{F}(\mathbf{x}^*) = (f_1(\mathbf{x}^*), f_2(\mathbf{x}^*), \dots, f_k(\mathbf{x}^*))^T \mid \mathbf{x}^* \in \mathbf{P}^*\} \quad (4)$$

is called the Pareto-optimal front. The aim of an MOEA is to find a set of Pareto-optimal solutions approximating the true Pareto-optimal front.

### 2.2 Immune System Inspired Optimization Algorithms

The immune system's ability to adapt its B-cells to new types of antigens is powered by processes known as clonal selection and affinity maturation by hypermutation (Garrett, 2005). The majority immune system inspired optimization algorithms are based on the applications of the clonal selection and hypermutation (Hart and Timmis, 2005). The first immune optimization algorithm may be (Fukuda et al., 1993) that included an abstraction of clonal selection to solve computational problems. But the clonal selection algorithm for optimization has been popularized mainly by de Castro and Von Zuben's CLONALG (de Castro and Von Zuben, 2002). CLONALG selects part fittest antibodies to clone proportionally to their antigenic affinities. The hypermutation operator

performs an affinity maturation process inversely proportional to the fitness values generating the matured clone population. After computing the antigenic affinity of the matured clone population, CLONALG creates randomly part new antibodies to replace the lowest fitness antibodies in current population and retain best antibodies to recycle. de Castro and Timmis (2002) proposed an artificial immune network called opt-aiNet for multimodal optimization. In opt-aiNet, antibodies are part of an immune network and the decision about the individual which will be cloned, suppressed or maintained depends on the interaction established by the immune network. Garrett (2004) has presented an attempt to remove all the parameters from the clonal selection algorithm. This method, which is called ACS for short, attempts to self-evolve various parameters during a single run. Cutello and Nicosia proposed an immune algorithm for optimization called opt-IA (Cutello et al., 2004, 2005b). Opt-IA uses three immune operators, cloning, hypermutation and aging. In hypermutation operator, the number of mutations is determined by mutation potential. The aging operator eliminates old individuals to avoid premature convergence. Opt-IA also uses a standard evolutionary operator,  $(\mu + \lambda)$ -selection operator. As far as multiobjective optimization is concerned, MISA (Coello Coello and Cortes, 2002, 2005) may be the first attempt to solve general multiobjective optimization problems using artificial immune systems. MISA encodes the decision variables of the problem to be solved by binary strings, clones the Pareto-optimal and feasible solutions, and applies two types of mutation to the clones and other individuals, respectively. More recently, Freschi and Repetto (2005) proposed a vector Artificial Immune System (VAIS) for solving multiobjective optimization problems based on the opt-aiNet. VAIS adopted the flowchart of opt-aiNet and the fitness assignment method in SPEA2 with some simplification that for nondominated individuals the fitness is the strength defined in SPEA2 and for dominated individuals the fitness is the number of individuals which dominate them. Cutello et al. (2005a) modified the (1+1)-PAES using two immune inspired operators cloning and hypermutation and applied the improved PAES to solving the protein structure prediction problem. In order to compare these algorithms clearly, we summarize their key techniques in Table 1.

In (Jiao et al., 2005), we have proposed an immune algorithm for multiobjective optimization named Immune Dominance Clonal Multiobjective Algorithm (IDCMA). IDCMA assigned the fitness values of current dominated individuals as the values of a custom distance measure, termed as Ab-Ab affinity, between the dominated individuals and one of the nondominated individuals found so far. According to the values of Ab-Ab affinity, all dominated individuals (antibodies) are divided into two kinds, subdominant antibodies and cryptic antibodies. And heuristic search only applies to the subdominant antibodies while the cryptic antibodies are redundant and have no function during search, but they can become subdominant (active) antibodies in the subsequent evolution. But recently, we found that the IDCMA which adopts binary string representation and the Ab-Ab affinity based selection on dominated individuals had difficulties in converging to the true Pareto-optimal front and obtaining the well-distributed solutions for some complicate problems, e.g. the DTLZ problems (Deb et al., 2002b). So we modified the IDCMA by using real-coded representation and a new selection technique and population maintenance strategy, the NNIA was proposed accordingly.

Table 1: Main optimization algorithms inspired by immune system

Algorithm	Fitness Assignment	Key Components	Applications
CLONALG	The objective function to be optimized	Elitist selection, Cloning, mutation, death	Single objective optimization problems (SOPs)
Opt-aiNet	The objective function to be optimized and the Euclidean distance between two individuals	Elitist selection, Cloning, mutation, network suppression, death	SOPs
ACS	The objective function to be optimized	Elitist selection, Cloning, mutation, death	SOPs
opt-IA	The objective function to be optimized	$(\mu + \lambda)$ -selection, Cloning, Hypermutation, Hypermacromutation, Aging	SOPs
MISA	The objective functions and the Pareto dominance relationships, the Euclidean distance between two individuals	Elitist selection according to fitness and diversity, Cloning, uniform mutation and non-uniform mutation, archive update	MOPs
VAIS	For Pareto-optimal individuals the fitness is the strength defined in SPEA2 and for dominated individuals the fitness is the number of individuals which dominate them	Cloning, mutation, clonal selection, suppression, death, archive update	MOPs
I-PAES	The Pareto dominance relationships	Cloning, mutation, clonal selection, (1+1)-selection, archive update	MOPs

### 2.3 Summary of Related Terms

In this paper, we follow the nomenclature of immunology and define the terms as follows.

#### 2.3.1 Antibody and Antibody Population

For the MOP

$$\begin{cases} \max \mathbf{F}(\mathbf{x}) = (f_1(\mathbf{x}), f_2(\mathbf{x}), \dots, f_k(\mathbf{x}))^T \\ \text{subject to } \mathbf{x} \in \Omega \end{cases} \quad (5)$$

where  $\mathbf{x} = (x_1, x_2, \dots, x_m)$ ,  $\Omega$  is the feasible region, and  $k \geq 2$ , an antibody  $\mathbf{b} = (b_1, b_2, \dots, b_l)$  is the coding of variable  $\mathbf{x}$ , denoted by  $\mathbf{b} = e(\mathbf{x})$ , and  $\mathbf{x}$  is called the decoding of antibody  $\mathbf{b}$ , expressed as  $\mathbf{x} = e^{-1}(\mathbf{b})$ . In this study, we adopt real-valued presentation, i.e.  $\mathbf{b} = e(\mathbf{x}) = \mathbf{x}$ , so  $l = m$ , and  $\mathbf{b} \in \Omega$ . An antibody population

$$\mathbf{B} = \{\mathbf{b}_1, \mathbf{b}_2, \dots, \mathbf{b}_n\}, \mathbf{b}_i \in \Omega, 1 \leq i \leq n \quad (6)$$

is an  $n$ -dimensional group of antibody  $\mathbf{b}$ , where the positive integer  $n$  is the size of antibody population  $\mathbf{B}$ .

#### 2.3.2 Dominant Antibody

For the MOP in equation (5), the antibody  $\mathbf{b}_i$  is a dominant antibody in the antibody population  $\mathbf{B} = \{\mathbf{b}_1, \mathbf{b}_2, \dots, \mathbf{b}_n\}$ , if and only if there is no antibody  $\mathbf{b}_j \in \mathbf{B}$  that satisfies the equation (7)

$$\forall p = 1, 2, \dots, k \quad f_p(e^{-1}(\mathbf{b}_j)) \geq f_p(e^{-1}(\mathbf{b}_i)) \wedge$$

$$\exists q = 1, 2, \dots, k \quad f_q(e^{-1}(\mathbf{b}_j)) > f_q(e^{-1}(\mathbf{b}_i)) \quad (7)$$

So the dominant antibodies are the nondominated individuals in population  $\mathbf{B}$ . In this paper, we denote the set of dominant antibodies as  $\mathbf{D}$ , and denote dominant antibodies as  $\mathbf{d}$  with different suffixes.

In order to explain the concepts of antibody, antibody population and dominant antibody, we give a simple example as follows. For the MOP in equation (5), if a vector  $\mathbf{x}_1 = (0.5, 0.2, 4, 5)$  belongs to the feasible region  $\Omega$ , then  $\mathbf{x}_1$  is a candidate solution of the MOP, the corresponding antibody is denoted by  $\mathbf{b}_1 = (0.5, 0.2, 4, 5)$ . If  $\mathbf{b}_1 = (0.5, 0.2, 4, 5)$ ,  $\mathbf{b}_2 = (0.7, 0.6, 4, 7)$ , and  $\mathbf{b}_3 = (0.2, 0.6, 6, 1)$  are three antibodies, then the set  $\mathbf{B} = \{\mathbf{b}_1, \mathbf{b}_2, \mathbf{b}_3\}$  is an antibody population with size 3. In the antibody population  $\mathbf{B} = \{\mathbf{b}_1, \mathbf{b}_2, \mathbf{b}_3\}$ , if both  $\mathbf{b}_2$  and  $\mathbf{b}_3$  do not dominate  $\mathbf{b}_1$ , then  $\mathbf{b}_1$  is a dominant antibody in the antibody population  $\mathbf{B}$ .

### 2.3.3 Crowding-distance

In our multiobjective algorithm, the dominant antibodies in  $\mathbf{D}$  are ranked according to how much they contribute to the diversity of objective function values. This can be measured by the crowding-distance (Deb et al., 2002a). For the MOP in equation (5), the crowding-distance of a dominant antibody  $\mathbf{d} \in \mathbf{D}$  is given by

$$\zeta(\mathbf{d}, \mathbf{D}) \triangleq \sum_{i=1}^k \frac{\zeta_i(\mathbf{d}, \mathbf{D})}{f_i^{\max} - f_i^{\min}} \quad (8)$$

where  $f_i^{\max}$  and  $f_i^{\min}$  are the maximum and minimum value of the  $i$ -th objective and

$$\zeta_i(\mathbf{d}, \mathbf{D}) = \begin{cases} \infty, & \text{if } f_i(\mathbf{d}) = \min\{f_i(\mathbf{d}') | \mathbf{d}' \in \mathbf{D}\} \text{ or } f_i(\mathbf{d}) = \max\{f_i(\mathbf{d}') | \mathbf{d}' \in \mathbf{D}\} \\ \min\{f_i(\mathbf{d}') - f_i(\mathbf{d}'') | \mathbf{d}', \mathbf{d}'' \in \mathbf{D} : f_i(\mathbf{d}'') < f_i(\mathbf{d}) < f_i(\mathbf{d}')\}, & \text{otherwise} \end{cases} \quad (9)$$

Based on the crowding-distance  $\zeta(\mathbf{d}, \mathbf{D})$ , we can estimate the density of dominant antibodies surrounding  $\mathbf{d}$  in the population  $\mathbf{D}$ . If  $\zeta(\mathbf{d}, \mathbf{D}) > \zeta(\mathbf{d}', \mathbf{D})$ ,  $\mathbf{d}, \mathbf{d}' \in \mathbf{D}$ , then  $\mathbf{d}$  is a less-crowded individual, and  $\mathbf{d}$  lies in a less-crowded region of the trade-off front, in contrast to  $\mathbf{d}'$ .

## 3 Description of the Algorithm

In this section, we describe a novel multiobjective optimization algorithm, termed as Nondominated Neighbor Immune Algorithm (NNIA). NNIA stores nondominated individuals found so far in an external population, called Dominant Population. Only partial less-crowded nondominated individuals, called active antibodies are selected to do proportional cloning, recombination, and static hypermutation (Cutello et al., 2004). Furthermore, the population storing clones is called Clone Population. Dominant Population, Active Population, and Clone Population at time  $t$  are represented by time-dependent variable matrices  $\mathbf{D}_t$ ,  $\mathbf{A}_t$  and  $\mathbf{C}_t$ , respectively. The main loop of NNIA is as follows.

### Algorithm1: Nondominated Neighbor Immune Algorithm

**Input:**  $G_{max}$  (maximum number of generations)  
 $n_D$  (maximum size of Dominant Population)  
 $n_A$  (maximum size of Active Population)

$n_C$  (size of Clone Population)

**Output:**  $\mathbf{D}_{Gmax+1}$  (final approximate Pareto-optimal set)

- Step1: Initialization:** Generate an initial antibody population  $\mathbf{B}_0$  with the size  $n_D$ . Create the initial  $\mathbf{D}_0 = \phi$ ,  $\mathbf{A}_0 = \phi$ , and  $\mathbf{C}_0 = \phi$ . Set  $t = 0$ .
- Step2: Update Dominant Population:** Identify dominant antibodies in  $\mathbf{B}_t$ ; Copy all the dominant antibodies to form the temporary dominant population (denoted by  $\mathbf{DT}_{t+1}$ ); If the size of  $\mathbf{DT}_{t+1}$  is not greater than  $n_D$ , let  $\mathbf{D}_{t+1} = \mathbf{DT}_{t+1}$ . Otherwise, calculate the crowding-distance values of all individuals in  $\mathbf{DT}_{t+1}$ , sort them in descending order of crowding-distance, choose the first  $n_D$  individuals to form  $\mathbf{D}_{t+1}$ .
- Step3: Termination:** If  $t \geq Gmax$  is satisfied, export  $\mathbf{D}_{t+1}$  as the output of the algorithm, Stop; Otherwise,  $t = t + 1$ .
- Step4: Nondominated Neighbor – based Selection:** If the size of  $\mathbf{D}_t$  is not greater than  $n_A$ , let  $\mathbf{A}_t = \mathbf{D}_t$ . Otherwise, calculate the crowding-distance values of all individuals in  $\mathbf{D}_t$ , sort them in descending order of crowding-distance, choose the first  $n_A$  individuals to form  $\mathbf{A}_t$ .
- Step5: Proportional Cloning:** Get the clone population  $\mathbf{C}_t$  by applying the proportional cloning to  $\mathbf{A}_t$ .
- Step6: Recombination and Hypermutation:** Perform recombination and hypermutation on  $\mathbf{C}_t$  and set  $\mathbf{C}'_t$  to the resulting population.
- Step7:** Get the antibody population  $\mathbf{B}_t$  by combining the  $\mathbf{C}'_t$  and  $\mathbf{D}_t$ ; go to Step2.

When the number of dominant antibodies is greater than the maximum limitation and the size of dominant population is greater than the maximum size of active population, both the reduction of dominant population and the selection of active antibodies use the crowding-distance based truncation selection. The proportional cloning, recombination and hypermutation operators are described as follows.

### 3.1 Proportional Cloning

In immunology, Cloning means asexual propagation so that a group of identical cells can be descended from a single common ancestor, such as a bacterial colony whose members arise from a single original cell as the result of mitosis. Following the works summarized in Section 2.2, in this study, the proportional cloning  $\mathbf{T}^C$  on the active population  $\mathbf{A} = \{\mathbf{a}_1, \mathbf{a}_2, \dots, \mathbf{a}_{|\mathbf{A}|}\}$  is defined as

$$\begin{aligned} \mathbf{T}^C(\mathbf{a}_1 + \mathbf{a}_2 + \dots + \mathbf{a}_{|\mathbf{A}|}) &= \mathbf{T}^C(\mathbf{a}_1) + \mathbf{T}^C(\mathbf{a}_2) + \dots + \mathbf{T}^C(\mathbf{a}_{|\mathbf{A}|}) \\ &= \{\mathbf{a}_1^1 + \mathbf{a}_1^2 + \dots + \mathbf{a}_1^{q_1}\} + \{\mathbf{a}_2^1 + \mathbf{a}_2^2 + \dots + \mathbf{a}_2^{q_2}\} + \\ &\quad \dots + \{\mathbf{a}_{|\mathbf{A}|}^1 + \mathbf{a}_{|\mathbf{A}|}^2 + \dots + \mathbf{a}_{|\mathbf{A}|}^{q_{|\mathbf{A}|}}\} \end{aligned} \quad (10)$$

where  $\mathbf{T}^C(\mathbf{a}_i) = \{\mathbf{a}_i^1 + \mathbf{a}_i^2 + \dots + \mathbf{a}_i^{q_i}\}$ ,  $\mathbf{a}_i^j = \mathbf{a}_i$ ,  $i = 1, 2, \dots, |\mathbf{A}|$ ,  $j = 1, 2, \dots, q_i$ .  $q_i$  is a self-adaptive parameter. The representation + is not the arithmetical operator, but only separates the antibodies here.  $q_i = 1$  denotes that there is no cloning on antibody  $\mathbf{a}_i$ .

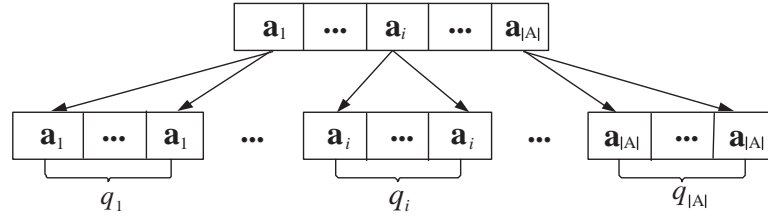


Figure 1: Illustration of the proportional cloning.

In this study, the individual with greater crowding-distance value is reproduced more times, viz. the individual with greater crowding-distance value has a larger  $q_i$ . Because the crowding-distance values of boundary solutions are positive infinity, before computing the value of  $q_i$  for each active antibody, we set the crowding-distance values of the boundary individuals (in objective space) be equal to the double values of the maximum value of active antibodies except the boundary individuals. Then the values of  $q_i$  are calculated as

$$q_i = \left\lceil n_c \times \frac{\zeta(\mathbf{a}_i, \mathbf{A})}{\sum_{j=1}^{|\mathbf{A}|} \zeta(\mathbf{a}_j, \mathbf{A})} \right\rceil, \quad (11)$$

where  $\zeta(\mathbf{a}_j, \mathbf{A})$  denotes the crowding-distance value of the active antibodies  $\mathbf{a}_j$ ,  $n_c$  is an expectant value of the size of the clone population. For example, suppose that there are five antibodies in an active population for solving a bi-objective optimization problem and the corresponding values of objective functions are (1.0, 0), (0.9, 0.2), (0.6, 0.4), (0.2, 0.7), and (0, 1.0). Therefore, the crowding-distance values of the five individuals are 2.4, 0.8, 1.2, 1.2, and 2.4, respectively. If  $n_c = 40$ , then  $q_1 = \lceil 40 \times \frac{2.4}{2.4+0.8+1.2+2.4} \rceil = 12$  and  $q_2 = 4, q_3 = 6, q_4 = 6, q_5 = 12$ . Note that, we use the ceil function here, therefore the clone population size  $\sum_{j=1}^{|\mathbf{A}|} q_i$  is sometimes greater than the expectant value  $n_c$ . However, the subsequent update of Dominant Population and nondominated neighbor-based selection make sure the size of Dominant Population and Active Population not greater than  $n_D$  and  $n_A$ , respectively.

Figure 1 illustrates the procedure of the proportional cloning. All the antibodies in sub-population  $\{\mathbf{a}_i^1, \mathbf{a}_i^2, \dots, \mathbf{a}_i^{q_i}\}$  are the result of the cloning on antibody  $\mathbf{a}_i$ , and have the same property as  $\mathbf{a}_i$ . In fact, cloning on antibody  $\mathbf{a}_i$  is to make multiple identical copies of  $\mathbf{a}_i$ . The aim is that the greater the crowding-distance value of an individual, the more times the individual will be reproduced. So there exist more chances to do search in less-crowded regions of the trade-off front.

### 3.2 Recombination and Hypermutation

If  $\mathbf{C} = (\mathbf{c}_1, \mathbf{c}_2, \mathbf{c}_3, \dots, \mathbf{c}_{|\mathbf{C}|})$  is the resulting population from applying the proportional cloning to  $\mathbf{A} = (\mathbf{a}_1, \mathbf{a}_2, \mathbf{a}_3, \dots, \mathbf{a}_{|\mathbf{A}|})$ , then the recombination  $\mathbf{T}^R$  on the clone population  $\mathbf{C}$  is defined as

$$\begin{aligned} & \mathbf{T}^R(\mathbf{c}_1 + \mathbf{c}_2 + \dots + \mathbf{c}_{|\mathbf{C}|}) \\ &= \mathbf{T}^R(\mathbf{c}_1) + \mathbf{T}^R(\mathbf{c}_2) + \dots + \mathbf{T}^R(\mathbf{c}_{|\mathbf{C}|}) \\ &= \text{crossover}(\mathbf{c}_1, \mathbf{A}) + \text{crossover}(\mathbf{c}_2, \mathbf{A}) + \dots + \text{crossover}(\mathbf{c}_{|\mathbf{C}|}, \mathbf{A}) \end{aligned} \quad (12)$$



where  $crossover(c_i, \mathbf{A}), i = 1, 2, \dots, |\mathbf{C}|$ , denotes selecting equiprobably one individual from the two offspring generated by a general crossover operator on clone  $c_i$  and an active antibody selected randomly from  $\mathbf{A}$ .

In this study, we use static hypermutation operator (Cutello et al., 2004) on the clone population after recombination. Cutello et al. (2004) designed three hypermutation methods, namely, static hypermutation (the number of mutations is independent from the fitness values), proportional hypermutation (the number of mutations is proportional to the fitness value), and inversely proportional hypermutation (the number of mutations is inversely proportional to the fitness value). We chose the static hypermutation in our algorithm due to the following reasons:

(1) The hypermutation operator is implemented on the clone population after recombination. If we chose the proportional hypermutation or the inversely proportional hypermutation, we have to calculate the fitness values for all the individuals of the clone population. However, in other phases of NNIA, the dominated individuals are not assigned fitness. Therefore we have to define a fitness assignment strategy to dominated individuals only for the hypermutation operator unless we use a mutation operator independent from the fitness values.

(2) In order to reduce complexity, the number of fitness evaluations is as low as possible. Suppose we define a fitness assignment strategy suitable for the proportional hypermutation or the inversely proportional hypermutation, we have to calculate the fitness values of all recombined clones before mutation.

(3) The experimental study in (Cutello et al., 2004) showed that the inversely proportional hypermutation did only slightly better than static and proportional hypermutation in solving the Trap function problems. But if the combination of multiple operators was not considered, the static hypermutation achieved the best results among the three hypermutation operators in solving the protein structure prediction problems.

Depending on the above reasons, we adopt the static hypermutation operator. If  $\mathbf{R} = (\mathbf{r}_1, \mathbf{r}_2, \mathbf{r}_3, \dots, \mathbf{r}_{|\mathbf{R}|})$  is the clone population after recombination, then the static hypermutation operator  $\mathbf{T}^H$  on the population  $\mathbf{R}$  is defined as

$$\begin{aligned} \mathbf{T}^H(\mathbf{r}_1 + \mathbf{r}_2 + \dots + \mathbf{r}_{|\mathbf{R}|}) &= \mathbf{T}^H(\mathbf{r}_1) + \mathbf{T}^H(\mathbf{r}_2) + \dots + \mathbf{T}^H(\mathbf{r}_{|\mathbf{R}|}) \\ &= mutate(\mathbf{r}_1) + mutate(\mathbf{r}_2) + \dots + mutate(\mathbf{r}_{|\mathbf{R}|}) \end{aligned} \quad (13)$$

where  $mutate(\mathbf{r}_i), i = 1, 2, \dots, |\mathbf{R}|$ , denotes changing each element of the variable vector  $\mathbf{r}_i$  by a general mutation operator with probability  $p_m$ , so each individual in the clone population  $\mathbf{R}$  at each time step will undergo about  $m \times p_m$  mutations, where  $m$  is the dimension of variable vector.

### 3.3 Fitness Assignment and Population Evolution

It can be seen that NNIA uses some well-known techniques such as storing the nondominated individuals previously found externally and reducing the number of nondominated individuals stored without destroying the characteristics of the trade-off front. Furthermore, NNIA adopts a novel selection technique. In NNIA, the dominant population is set as an external population for elitism. The fitness values of the individuals in the dominant population are assigned as the values of the crowding-distance, which serves as an estimate of the perimeter of the cuboid formed by the nearest neighbors as the vertices in objective space. The selection is therefore biased towards individuals with a high isolation value. Only partial nondominated individuals (much less than nondominated individuals found so far) with high crowding-distance values are

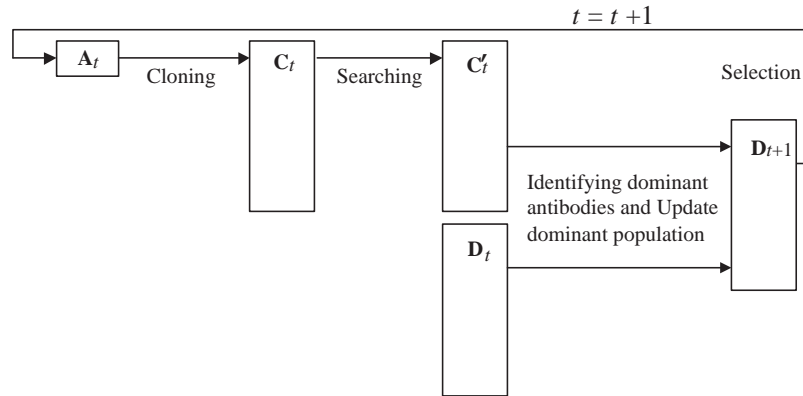


Figure 2: Population Evolution of NNIA.

selected. And Cloning, recombination, and mutation only apply to the selected individuals (active antibodies). So in a single generation, only less-crowded individuals perform heuristic search in order to obtain more solutions in the less-crowded regions of the trade-off fronts. In contrast to NSGA-II, the nondominated neighbor-based selection and the proportional cloning makes the less-crowded individuals have more chances to do recombination and mutation. The population evolution in a single generation at time  $t$  is shown in Figure 2.

### 3.4 Computational Complexity

Analyzing NNIA's computational complexity is revealing. In this section, we only consider population size in computational complexity. Assuming that the maximum size of dominant population is  $n_D$ , the maximum size of active population is  $n_A$ , the clone population size is  $n_C$ , then the time complexity of one generation for the algorithm can be calculated as follows:

The time complexity for identifying nondominated individuals in the population is  $O((n_D + n_C)^2)$ ; the worst time complexity for updating the dominant population is  $O((n_D + n_C) \log(n_D + n_C))$ ; the worst time complexity for nondominated neighbor-based selection is  $O(n_D \log(n_D))$ ; the time complexity for cloning is  $O(n_C)$ ; and the time complexity for recombination and mutation is  $O(n_C)$ . So the worst total time complexity is

$$O((n_D + n_C)^2) + O((n_D + n_C) \log(n_D + n_C)) + O(n_D \log(n_D)) + 2O(n_C). \quad (14)$$

According to the operational rules of the symbol  $O$ , the worst time complexity of one generation for NNIA can be simplified as

$$O((n_D + n_C)^2). \quad (15)$$

So the cost of identifying the nondominated individuals in the population dominates the computational complexity of NNIA. We will do some empirical study on NNIA's run-time complexity in Section 4.4.

## 4 Evaluation of NNIA'S Effectiveness

In this section, we compare PESA-II (Corne et al., 2001), NSGA-II (Deb et al., 2002a), SPEA2 (Zitzler et al., 2002), and MISA (Coello Coello and Cortes, 2005) with NNIA in solving thirteen well-known multiobjective function optimization problems including three low-dimensional bi-objective problems, five ZDT problems (Zitzler et al., 2000) and five DTLZ problems (Deb et al., 2002b). The NNIA toolbox for Matlab 7.0 designed by the authors for solving the thirteen problems and twenty other problems is available at the first author's homepage (<http://see.xidian.edu.cn/iip/mggong/Projects/NNIA.htm>). All the simulations run at a personal computer with P-IV 3.2G CPU and 2G RAM.

### 4.1 Experimental Setup

First, we describe the thirteen test problems used in this study. The first three low-dimensional bi-objective problems, named SCH, DEB and KUR, were defined by Schaffer (1984), Deb (1999) and Kursawe (1991), respectively. The next five ZDT problems were developed by Zitzler et al. (2000). The last five DTLZ problems were developed by Deb et al. (2002b). These MOPs have been cited in a number of significant past studies in this area. The first three MOPs are either simple or not scalable, where the number of decision variables is no more than 3. The five ZDT problems have 30 or 10 decision variables. All the above eight problems have two objectives. The five DTLZ problems can be scaled to any number of decision variables and objectives. Their Pareto-optimal fronts illustrated by a set of 200 uniform points on them are shown in Figure 3. Hereinto, the Pareto-optimal fronts of the five ZDT problems and the five DTLZ problems have been mathematically defined in (Zitzler et al., 2000; Deb et al., 2002b). The three low-dimensional problems, SCH, DEB and KUR do not have mathematical defined Pareto-optimal fronts. However, their approximate Pareto-optimal fronts have been illustrated in some literature (Deb, 1999; Van Veldhuizen, 1999; Deb, 2001). Here we derive their approximate Pareto-optimal fronts deterministically as follows,

**Algorithm2: The deterministic algorithm of approximating Pareto-optimal fronts**

*Step1: Generating finite discrete points uniformly distributed in the decision space.*

*Step2: Calculate the objective function values of all the points.*

*Step3: Select all the nondominated individuals from these points as the approximate Pareto-optimal set, and the corresponding image under the objective space constitute the approximate Pareto-optimal front; Stop.*

In order to approximate the Pareto-optimal fronts with sufficient resolution, here we set the number of discrete points at  $10^6$ . The running time for getting the approximate Pareto-optimal fronts of SCH, DEB and KUR is about 18 hours by using a personal computer with P-IV 3.2G CPU and 2G RAM.

More details of the test problems can be found in (Deb, 2001; Zitzler et al., 2000; Deb et al., 2002b). It is necessary to note that the performance of an MOEA in tackling multiobjective constrained optimization problems may be largely dependent on

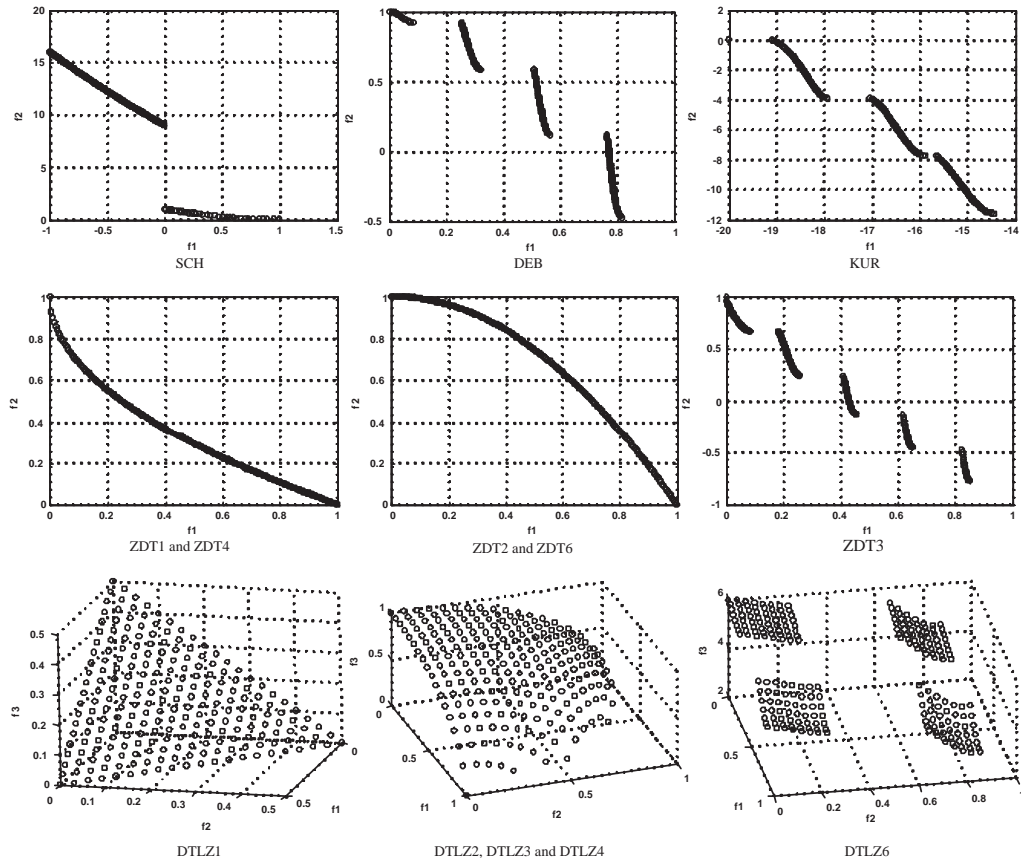


Figure 3: The Pareto-optimal fronts of the thirteen test problems illustrated by a set of 200 uniform points on them.

the constraint-handling technique used (Van Veldhuizen, 1999), so, we did not include side-constrained problems in this study. For the DTLZ problems, in Section 4.2, we set the values of  $k$  and  $|\mathbf{x}_k|$  be the values suggested by Deb et al. (2001, 2002b), i.e.,  $k = 3$  and  $|\mathbf{x}_k| = 5$  for DTLZ1,  $k = 3$  and  $|\mathbf{x}_k| = 10$  for DTLZ2, DTLZ3 and DTLZ4,  $k = 3$  and  $|\mathbf{x}_k| = 20$  for DTLZ6. In Section 4.4, we will study the scalability of NNIA along the number of objectives based on two of the five DTLZ problems with  $k$  increasing from 2 to 9.

Zitzler et al. (2003) suggested that for a  $k$ -objective optimization problem, at least  $k$  performances are needed to compare two or more solutions and an infinite number of metrics to compare two or more sets of solutions. Deb and Jain (2002) suggested a running performance metric for measuring the convergence to the reference set at each generation of an MOEA run. As the reference (Khare et al., 2003), in Section 4.2, we apply this metric only to the final Pareto-optimal set obtained by an MOEA to evaluate its performance. Zitzler et al. (2003) and Knowles et al. (2006) have suggested that the power of unary quality indicators was restricted. So we choose a binary quality metric, the Coverage of two sets (Zitzler and Thiele, 1998). We also adopt the Spacing

metric (Schott, 1995) to measure the diversity in the population. The three metrics are summarized as follows.

**Coverage of Two Sets:** Let  $\mathbf{A}, \mathbf{B}$  be two approximate Pareto-optimal sets. The function  $I_C$  maps the ordered pair  $(\mathbf{A}, \mathbf{B})$  to the interval  $[0, 1]$ :

$$I_C(\mathbf{A}, \mathbf{B}) \triangleq \frac{|\{\mathbf{b} \in \mathbf{B}; \exists \mathbf{a} \in \mathbf{A} : \mathbf{a} \succeq \mathbf{b}\}|}{|\mathbf{B}|} \quad (16)$$

where  $\succeq$  means dominate or equal (also called weakly dominate). The value  $I_C(\mathbf{A}, \mathbf{B}) = 1$  means that all decision vectors in  $\mathbf{B}$  are weakly dominated by  $\mathbf{A}$ .  $I_C(\mathbf{A}, \mathbf{B}) = 0$  implies no decision vector in  $\mathbf{B}$  is weakly dominated by  $\mathbf{A}$ . Note that always both directions have to be considered because  $I_C(\mathbf{A}, \mathbf{B})$  is not necessarily equal to  $1 - I_C(\mathbf{B}, \mathbf{A})$ .

**Convergence Metric:** Let  $\mathbf{P}^* = (\mathbf{p}_1, \mathbf{p}_2, \mathbf{p}_3, \dots, \mathbf{p}_{|\mathbf{P}^*|})$  be the reference or target set of points on the true Pareto-optimal front and  $\mathbf{A} = (\mathbf{a}_1, \mathbf{a}_2, \mathbf{a}_3, \dots, \mathbf{a}_{|\mathbf{A}|})$  be the final approximate Pareto-optimal set obtained by an MOEA. Then for each point  $\mathbf{a}_i$  in  $\mathbf{A}$ , the smallest normalized Euclidean distance to  $\mathbf{P}^*$  will be:

$$d_i = \min_{j=1}^{|\mathbf{P}^*|} \sqrt{\sum_{m=1}^k \left( \frac{f_m(\mathbf{a}_i) - f_m(\mathbf{p}_j)}{f_m^{\max} - f_m^{\min}} \right)^2} \quad (17)$$

Here,  $f_m^{\max}$  and  $f_m^{\min}$  are the maximum and minimum values of the  $m$ -th objective function in  $\mathbf{P}^*$ . The convergence metric is the average value of the normalized distance for all points in  $\mathbf{A}$ .

$$C(\mathbf{A}) \triangleq \frac{\sum_{i=1}^{|\mathbf{A}|} d_i}{|\mathbf{A}|} \quad (18)$$

The convergence metric represents the distance between the set of approximate Pareto-optimal solutions and the true Pareto-optimal fronts. Hence lower values of the convergence metric represent good convergence ability. Similar metrics were proposed by Schott (1995), Rudolph (1998), Zitzler et al. (2000) and Van Veldhuizen and Lamont (2000) et al.

**Spacing:** Let  $\mathbf{A}$  be the final approximate Pareto-optimal set obtained by an MOEA. The function  $S$

$$S \triangleq \sqrt{\frac{1}{|\mathbf{A}| - 1} \sum_{i=1}^{|\mathbf{A}|} (\bar{d} - d_i)^2} \quad (19)$$

where

$$d_i = \min_j \left\{ \sum_{m=1}^k |f_m(\mathbf{a}_i) - f_m(\mathbf{a}_j)| \right\} \quad \mathbf{a}_i, \mathbf{a}_j \in \mathbf{A} \quad i, j = 1, 2, \dots, |\mathbf{A}|, \quad (20)$$

$\bar{d}$  is the average value of all  $d_i$ , and  $k$  is the number of objective functions. A value of zero for this metric indicates all the nondominated solutions found are equidistantly spaced in objective space.

#### 4.2 Comparison of NNIA with PESA-II, SPEA2, NSGA-II and MISA

In order to solve MOPs, many MOEAs have been proposed as mentioned in Section 1. Following Coello Coello's recent review of evolutionary multiobjective optimization field (Coello Coello, 2005, 2006), NSGA-II, SPEA2, PESA-II, and some others can be considered as representative of the state-of-the-art in multiobjective optimization. In this section, NNIA was compared with PESA-II, NSGA-II, SPEA2 and MISA. NSGA-II was proposed by Deb et al. (2002a) as an improvement of NSGA by using a more efficient nondominated sorting method, elitism and a crowded comparison operator without specifying any additional parameters for diversity maintaining. SPEA2 was proposed by Zitzler et al. (2002) as a revised version of SPEA by incorporating a revised fitness assignment strategy, a nearest neighbor density estimation technique and an enhanced archive truncation method. The revised fitness assignment strategy takes for each individual into account the number of individuals it dominates and it is dominated by. PESA-II was proposed by Corne et al. (2001) as a revised version of PESA by introducing a new selection technique, region-based selection. In region-based selection technique, selective fitness is assigned to the hyperboxes (Corne et al., 2001) in objective space instead of the Pareto-optimal individuals. Its update of auxiliary population (external population) also used the hyperboxes division. MISA (Coello Coello and Cortes, 2002, 2005) may be the first attempt to solve general multiobjective optimization problems using artificial immune systems. MISA encodes the decision variables of the problem to be solved by binary strings, clones the nondominated and feasible solutions, and applies two types of mutation to the clones and other individuals, respectively. MISA updates its external population by using the grid based techniques used in PAES (Knowles and Corne, 2000).

Table 2: Tuned parameter values

Parameter	PESA-II	SPEA2	NSGA-II	NNIA
Crossover probability $p_c$	0.8	0.8	0.8	1
Distribution index for SBX	15	15	15	15
Mutation probability $p_m$	$1/n$	$1/n$	$1/n$	$1/n$
Distribution index for polynomial mutation	20	20	20	20

We use the simulated binary crossover (SBX) operator and polynomial mutation (Deb and Beyer, 2001) for NNIA, PESA-II, NSGA-II and SPEA2. The SBX and polynomial mutation has been adopted in many MOEA papers (Zitzler et al., 2002; Deb et al., 2002a; Deb and Jain, 2002; Khare et al., 2003; Igel et al., 2007). Before the actual experimentation, some tuning of the parameters involved was required. Finding the values of parameters for which an MOEA works best is a difficult MOP in itself. We tuned the parameter values on DTLZ2 and DTLZ3 as (Khare et al., 2003) when obtained the best value of the Convergence metric described in Section 4.1. The tuned parameter values are listed in Table 2 where  $n$  is the number of variables. Because MISA is a binary-coded algorithm, the mutation is bit-flip with the probability described in (Coello Coello and Cortes, 2005). For SPEA2, we use a population of size 100 and an external population of size 100. For NSGA-II, the population size is 100. For PESA-II, the internal population size is 100, the archive size is 100, and the number of hyper-grid cells per dimension is 10. For NNIA, the maximum size of dominant population  $n_D = 100$ , the maximum size of active population  $n_A = 20$ , and the size of clone population  $n_C = 100$ . For MISA, the population size is 100, the size of the external population is 100, the total

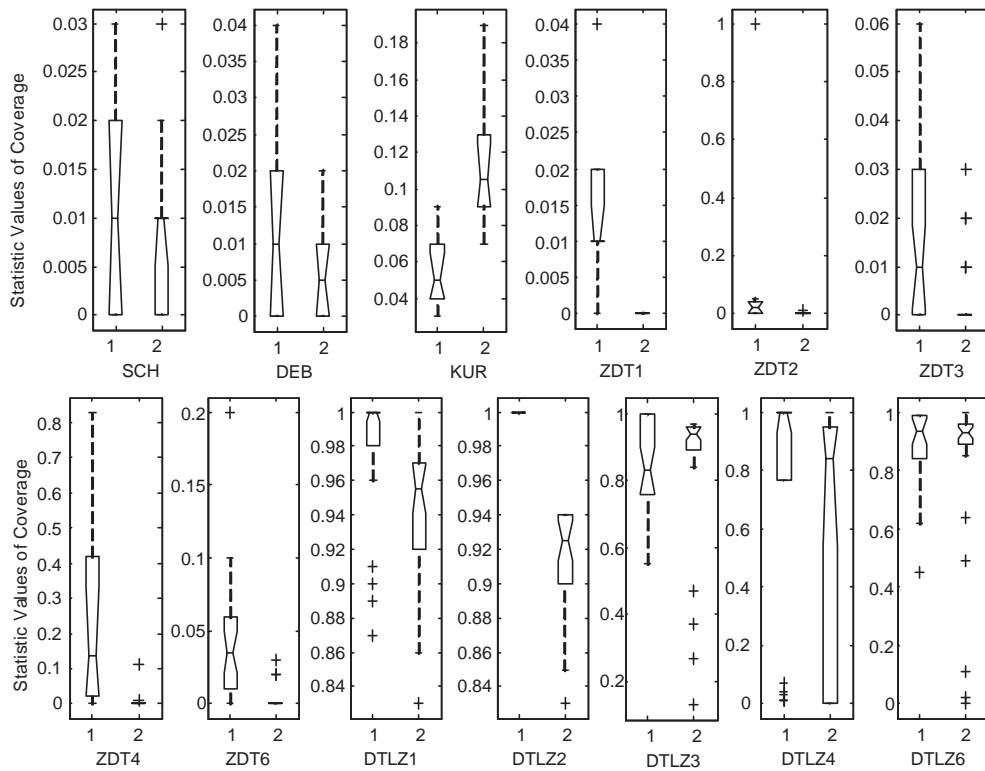


Figure 4: Statistical Values of the Coverage of the two sets obtained by NNIA and PESA-II in solving the thirteen problems. Here, box plots are used to illustrate the distribution of these samples. In a notched box plot the notches represent a robust estimate of the uncertainty about the medians for box-to-box comparison. Symbol '+' denote for outliers. The thirteen plots denote the results of the thirteen problems respectively. In each plot, the left box represents the distribution of  $I_C(\mathbf{I}, \mathbf{P})$  and the right box represents the distribution of  $I_C(\mathbf{P}, \mathbf{I})$ .

number of clones is 600, the number of grid subdivisions is 25, these four values are suggested by Coello Coello and Cortes (2005), and the coding length for each decision variable is 30. It is difficult to formulate the optimal and evidential stop criterion for an MOEA (Coello Coello, 2005). Researchers usually stop the algorithm when it reaches a given number of iterations or function evaluations. In this section the number of function evaluations is kept at 50 000 (not including the function evaluations during initialization) for all the five algorithms.

In the following experiments, we performed 30 independent runs on each test problem. Figures 4 to 7 show the box plots (McGill et al., 1978) of NNIA against PESA-II, NSGA-II, SPEA2 and MISA based on the Coverage of two sets. In the following,  $\mathbf{I}$  denotes the solution set obtained by NNIA,  $\mathbf{P}$  denotes the solution set obtained by PESA-II,  $\mathbf{S}$  denotes the solution set obtained by SPEA2,  $\mathbf{N}$  denotes the solution set obtained by NSGA-II, and  $\mathbf{M}$  denotes the solution set obtained by MISA.

The comparison between NNIA and PESA-II in the Coverage of two sets shows

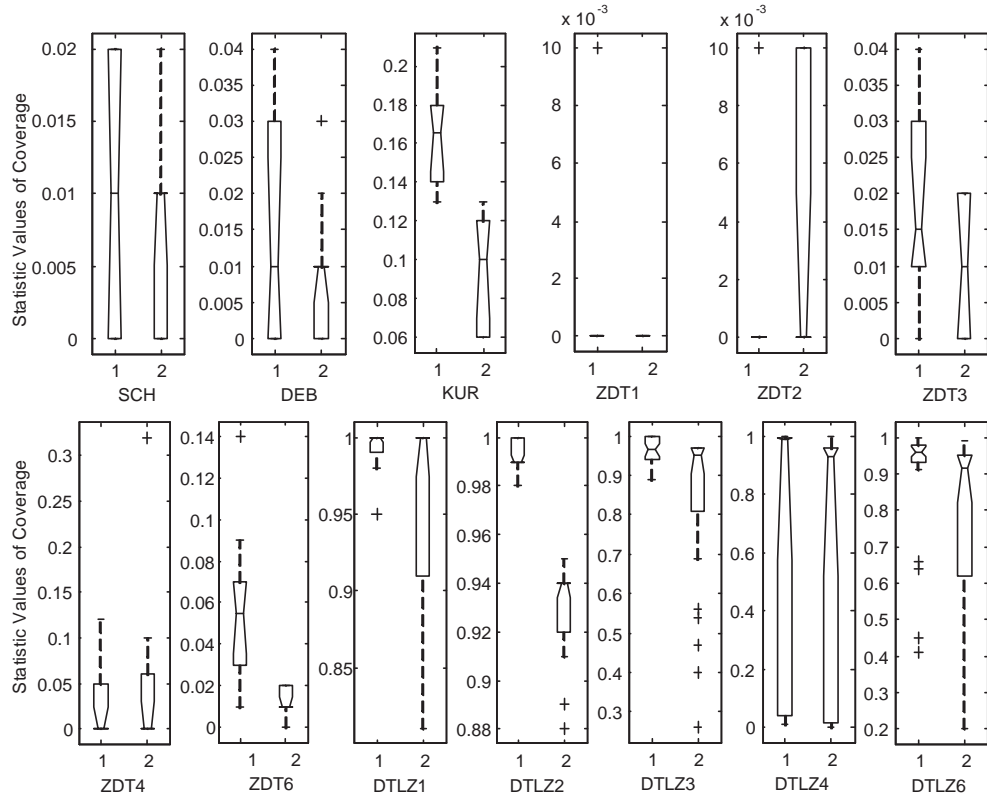


Figure 5: Box plots of the Coverage of the two sets obtained by NNIA and NSGA-II in solving the thirteen problems. The thirteen plots denote the results of the thirteen problems respectively. In each plot, the left box represents the distribution of  $I_C(\mathbf{I}, \mathbf{N})$  and the right box represents the distribution of  $I_C(\mathbf{N}, \mathbf{I})$ .

that most of the values of  $I_C(\mathbf{I}, \mathbf{P})$  and  $I_C(\mathbf{P}, \mathbf{I})$  for the five DTLZ problems are greater than 0.5, therefore, the majority of the solutions obtained by PESA-II are weakly dominated by the solutions obtained by NNIA (Especially for DTLZ2, all the PESA-II's solutions are weakly dominated by NNIA's ones over 30 independent runs), while the majority of the solutions obtained by NNIA are also weakly dominated by the solutions obtained by PESA-II. The box plots of the other eight problems show that only minority solutions are weakly dominated by each other. As the analysis in (Zitzler et al., 2003),  $0 < I_C(\mathbf{A}, \mathbf{B}) < 1$  and  $0 < I_C(\mathbf{B}, \mathbf{A}) < 1$  shows neither  $\mathbf{A}$  weakly dominates  $\mathbf{B}$  nor  $\mathbf{B}$  weakly dominates  $\mathbf{A}$ , i.e.  $\mathbf{A}$  and  $\mathbf{B}$  are incomparable. But if only the values of Coverage be considered, the box plots of  $I_C(\mathbf{I}, \mathbf{P})$  are higher than the corresponding box plots of  $I_C(\mathbf{P}, \mathbf{I})$  in SCH, DEB, the five ZDT problems and the five DTLZ problems, while the box plot of  $I_C(\mathbf{P}, \mathbf{I})$  is higher than the corresponding box plot of  $I_C(\mathbf{I}, \mathbf{P})$  only in KUR.  $I_C(\mathbf{I}, \mathbf{P})$  denotes the ratio of the number of solutions obtained by PESA-II which are weakly dominated by the solutions obtained by NNIA to the total number of the solutions obtained by PESA-II in a single run. So in a sense (but neither  $\triangleright$ -compatible nor  $\triangleright$ -complete), NNIA did better than PESA-II in SCH, DEB, the five ZDT problems



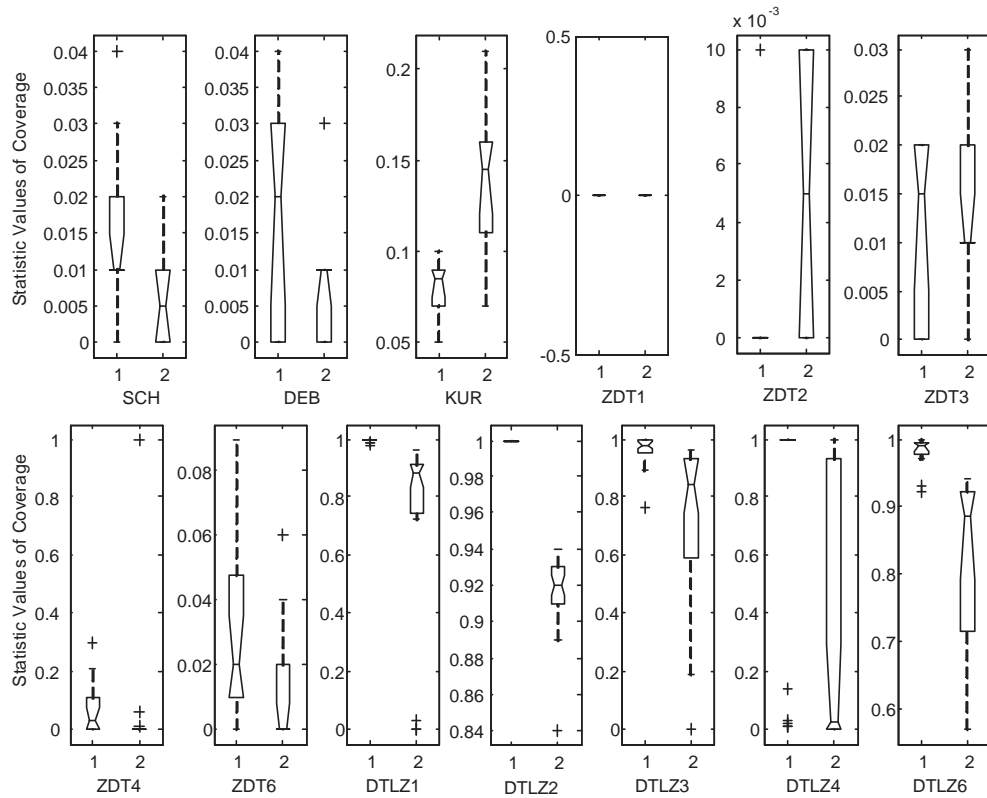


Figure 6: Box plots of the Coverage of the two sets obtained by NNIA and SPEA2 in solving the thirteen problems. The thirteen plots denote the results of the thirteen problems respectively. In each plot, the left box represents the distribution of  $I_C(\mathbf{I}, \mathbf{S})$  and the right box represents the distribution of  $I_C(\mathbf{S}, \mathbf{I})$ .

and the five DTLZ problems while PESA-II did better than NNIA in KUR as far as the Coverage is concerned.

The comparison between NNIA and NSGA-II and the comparison between NNIA and SPEA2 in terms of the Coverage are similar to the comparison between NNIA and PESA-II. But NNIA did better than NSGA-II in SCH, DEB, KUR, ZDT1, ZDT3, ZDT6 and the five DTLZ problems while NSGA-II did better than NNIA in ZDT2, ZDT4. Meanwhile, NNIA did better than SPEA2 in SCH, DEB, ZDT4, ZDT6 and the five DTLZ problems while SPEA2 did better than NNIA in KUR, ZDT2, and ZDT3 as far as the Coverage is concerned.

The comparison between NNIA and MISA shows that for the five ZDT problems and the five DTLZ problems, the majority of the solutions obtained by MISA are weakly dominated by the solutions obtained by NNIA. But the majority of the solutions obtained by NNIA are weakly dominated by the solutions obtained by MISA only in DTLZ1, DTLZ2, and DTLZ3. We estimate that NNIA did better than MISA in all the problems as far as the Coverage is concerned because the box plots of  $I_C(\mathbf{I}, \mathbf{M})$  are higher than the corresponding box plots of  $I_C(\mathbf{M}, \mathbf{I})$  for all the test problems. The main

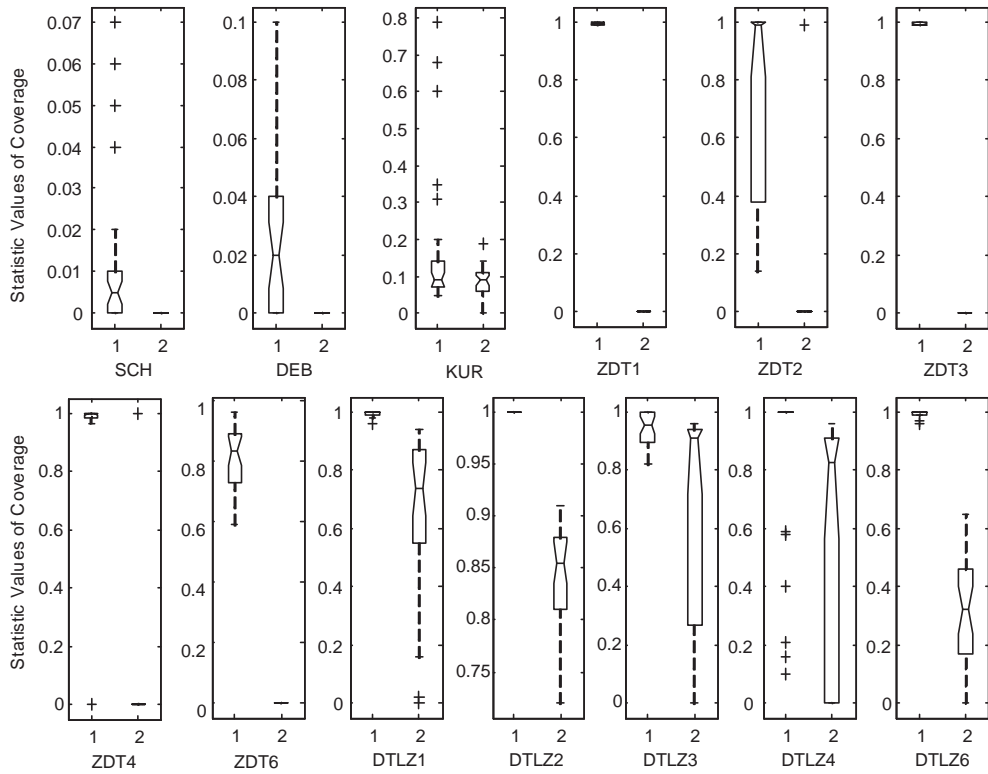


Figure 7: Box plots of the Coverage of the two sets obtained by NNIA and MISA in solving the thirteen problems. The thirteen plots denote the results of the thirteen problems respectively. In each plot, the left box represents the distribution of  $I_C(I, M)$  and the right box represents the distribution of  $I_C(M, I)$ .

limitation of MISA may be its binary representation. Since the test problems that we are dealing with have continuous spaces, real encoding should be preferred to avoid problems related to Hamming cliffs and to achieve arbitrary precision in the optimal solution (Khare et al., 2003). We think it is not appropriate to compare the performance of a binary-coded algorithm with respect to a real-coded algorithm, but MISA's special operators (two types of mutation in Step 8 and Step 9 of MISA) were designed for antibodies represented by binary strings. However, in a sense, MISA has the ability to approximate these real-coded algorithms by using the binary representation with enough coding length.

Figure 8 and Figure 9 illustrate the box plots based on the Convergence metric over 30 independent runs for the thirteen problems. In this section, for calculating the values of the Convergence metric, we use the set of 200 uniform points on the Pareto-optimal front as shown in Figure 3.

Figure 8 and Figure 9 show that, for the three low-dimensional problems, all the five algorithm can obtain the values less than  $10^{-2}$  in almost all the 30 independent runs. For the five ZDT problems, DTLZ2, DTLZ4 and DTLZ6, the differences between the corresponding values obtained by NNIA, PESA-II, NSGA-II and SPEA2 are small.

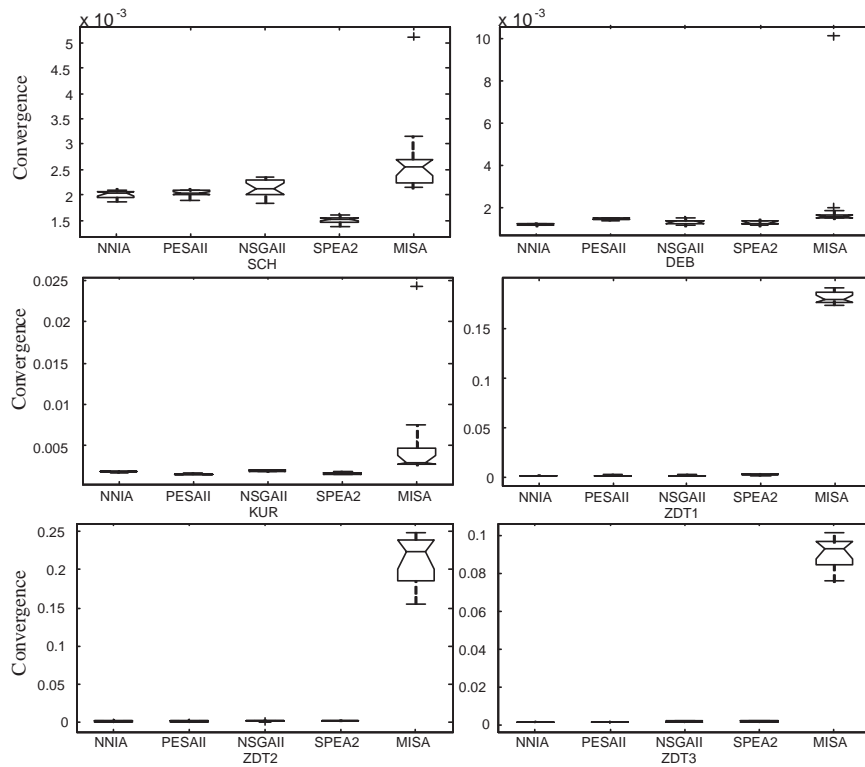


Figure 8: Box plots of the Convergence metric obtained by NNIA, PESA-II, NSGA-II, SPEA2, and MISA in solving the SCH, DEB, KUR, ZDT1, ZDT2, and ZDT3.

Hereinto, NNIA did a little better than others in ZDT1, ZDT4, ZDT6, and DTLZ2. PESA-II did a little better than others in ZDT3 and DTLZ6. NNIA and PESA-II obtained similar values in ZDT2. NNIA, NSGA-II and SPEA2 obtained similar values in DTLZ4. For DTLZ1 and DTLZ3, NNIA did much better than the other four algorithms even though DTLZ1 and DTLZ3 have  $(11^{|\mathbf{x}_k|-1})$  and  $(3^{|\mathbf{x}_k|-1})$  local Pareto-optimal fronts, respectively. Deb et al. (2001) and Khare et al. (2003) claimed that for DTLZ3, both NSGA-II and SPEA2 could not quite converge on to the true Pareto-optimal fronts in 500 generations (50 000 function evaluations). We have found that PESA-II also did badly in solving DTLZ3, but NNIA did very well. Overall, as far as the Convergence metric is concerned, NNIA did best in DEB, ZDT1, ZDT4, ZDT6, DTLZ1, DTLZ2 and DTLZ3 (seven out of the thirteen problems).

Figure 10 and Figure 11 illustrate the box plots based on the Spacing metric over 30 independent runs for the thirteen problems.

Figure 10 and Figure 11 show that SPEA2 did best in nine problems in terms of the diversity metric Spacing. SPEA2 used an expensive archive truncation procedure whose worst run-time complexity is  $O(N^3)$ , where  $N$  is the number of non-dominated individuals. PESA-II and MISA reduced their nondominated individuals using a hyper-grid based scheme, whose grid size was a crucial factor (Khare et al., 2003). NNIA reduced nondominated solutions using the crowded comparison proce-

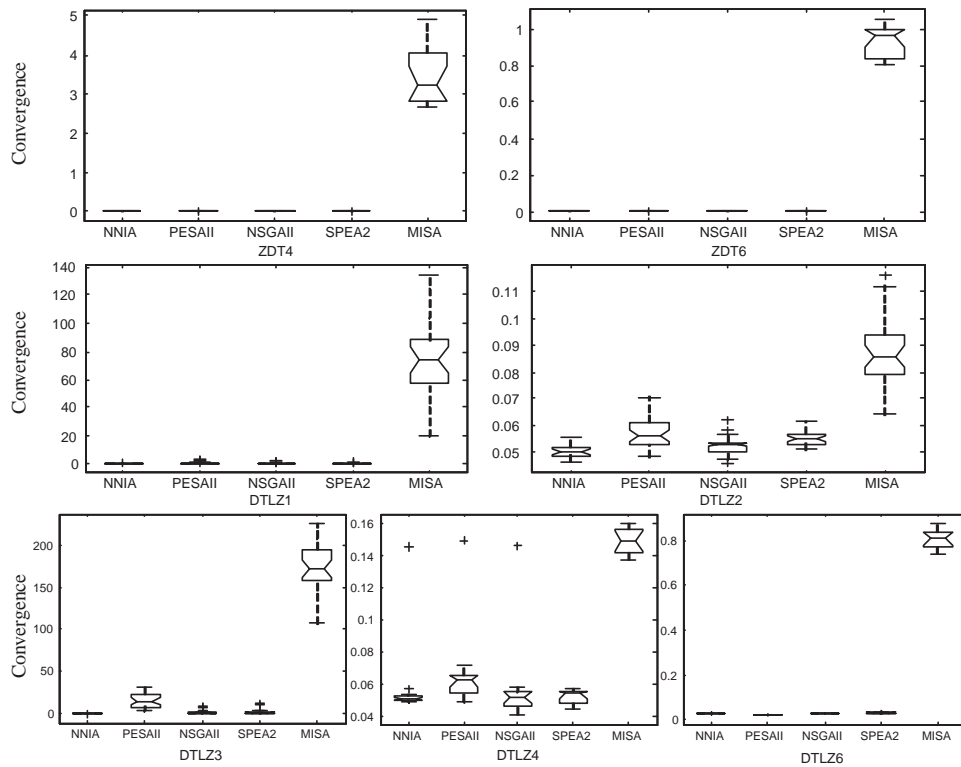


Figure 9: Box plots of the Convergence metric obtained by NNIA, PESA-II, NSGA-II, SPEA2, and MISA in solving the ZDT4, ZDT6, and DTLZ problems.

ture (Deb et al., 2002a), whose worst run-time complexity is only  $O(N \log(N))$ . Except SPEA2, the box plots of Spacing obtained by NNIA are lower than those obtained by NSGA-II, PESA-II and MISA in DEB, ZDT1, ZDT3, ZDT4, ZDT6, DTLZ1, DTLZ3 and DTLZ4 (eight out of the thirteen problems), while PESA-II did best (except SPEA2) in ZDT2, DTLZ2 and DTLZ6, NSGA-II did best (except SPEA2) in KUR, and MISA did best (except SPEA2) in SCH. For DTLZ1 and DTLZ3, NNIA did best in all the five algorithms because the other four algorithms could not quite converge on to the true Pareto-optimal fronts. Overall, SPEA2 is the best algorithm in diversity maintenance, but the differences between the values of Spacing obtained by NNIA, PESA-II and NSGA-II are unobvious.

Overall considering the experimental results, we can conclude that

(1) For the three low-dimensional problems, all the five algorithms were capable to approximate the true Pareto-optimal fronts.

(2) For DTLZ2, DTLZ4, DTLZ6 and the five ZDT problems, NNIA did best in four out of the eight problems in terms of the Convergence metric. SPEA2 did best in seven out of the eight problems in terms of diversity maintenance. Except SPEA2, NNIA did best in six out of the eight problems in terms of diversity maintenance.

(3) For DTLZ1 and DTLZ3 problems, NSGA-II, SPEA2, PESA-II and MISA could not quite converge on to the true Pareto-optimal fronts in 50 000 function evaluations,

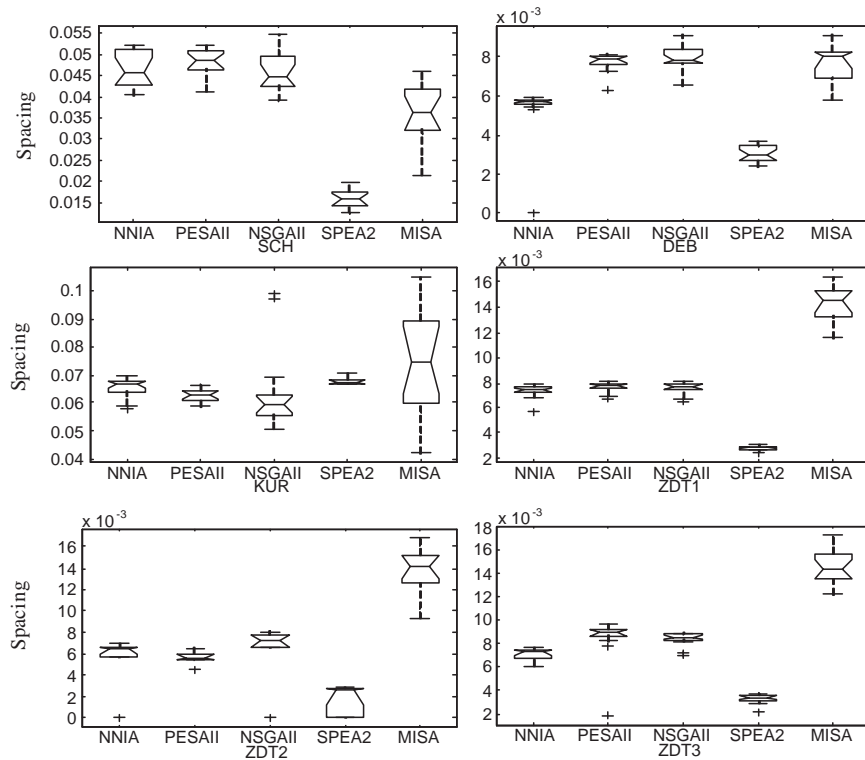


Figure 10: Box plots of the Spacing metric obtained by NNIA, PESA-II, NSGA-II, SPEA2, and MISA in solving the SCH, DEB, KUR, ZDT1, ZDT2, and ZDT3.

but NNIA were capable to approximate the true Pareto-optimal fronts.

In the experiments, NNIA and NSGA-II adopt the same heuristic search operators (simulated binary crossover and polynomial mutation) and archive maintenance method. NNIA is different from NSGA-II only in its individual selection and cloning before heuristic search. Therefore, the better performance of NNIA in contrast to NSGA-II is resulted from the unique nondominated neighbor-based selection method cooperating with the proportional cloning, which makes the less-crowded individuals have more chances to do heuristic search. NNIA is different from PESA-II, SPEA2 and MISA both in its way to do selection and archive maintenance. NNIA also outperformed PESA-II, SPEA2 and MISA in convergence for the majority of the test problems. Depending on these empirical comparisons, we conclude that the nondominated neighbor-based selection technique is effective, and NNIA is an effective algorithm for solving MOPs.

### 4.3 Comparison of NNIA with and without Recombination

Most of the existing immune inspired optimization algorithms, especially some pure clonal selection algorithms, did not use recombination. However, we think that recombination should not be forbidden in AIS community. Some immunologists have claimed that recombination is a mode of receptor editing used by the B cell antibodies

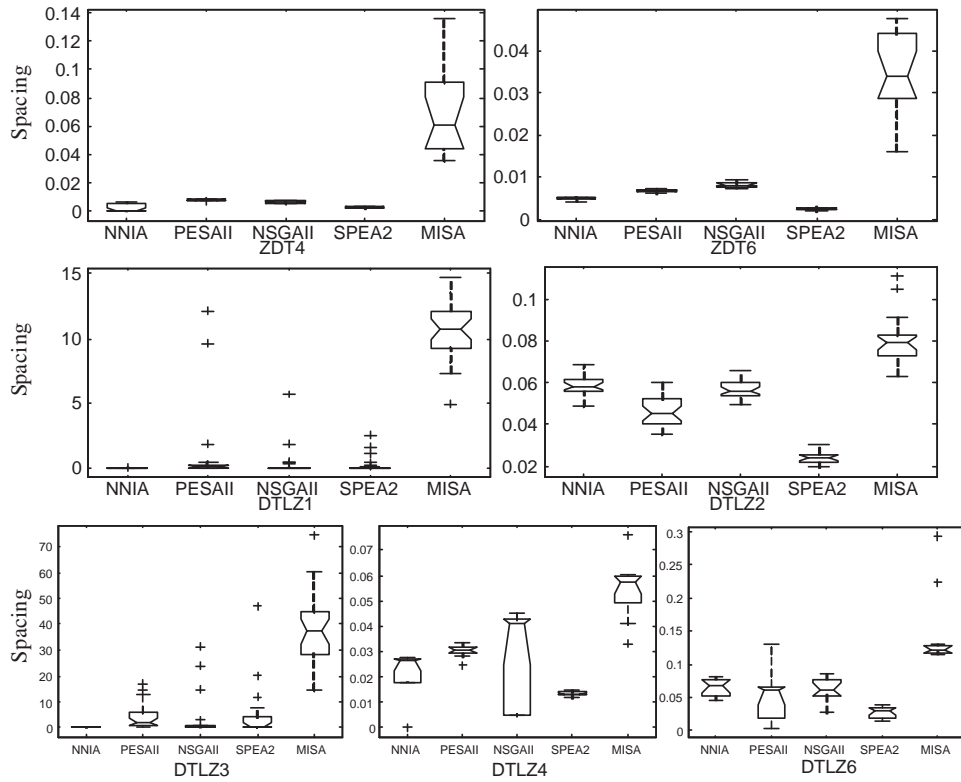


Figure 11: Box plots of the Spacing metric obtained by NNIA, PESA-II, NSGA-II, SPEA2, and MISA in solving the ZDT4, ZDT6, and DTLZ problems.

to improve their affinity (George and Gray, 1999). de Castro and Von Zuben (2002) also claimed that genetic recombination and mutation are the two central processes involved in the production of antibodies, even though they did not use recombination in their pure clonal selection algorithm CLONALG according to the clonal selection theory (Burnet, 1959).

In Section 4.2, the simulated binary crossover (SBX) was introduced as the recombination operator. SBX has been adopted in many MOEA papers (Zitzler et al., 2002; Deb et al., 2002a; Deb and Jain, 2002; Khare et al., 2003; Igel et al., 2007). In order to identify the improvement produced by SBX, we performed the proposed algorithm with SBX (denoted by NNIA) and without SBX (denoted by NNIA-X) 30 independent runs on each test problem, respectively. The parameter settings are the same as Section 4.2. Figure 12 illustrates the box plots based on the Coverage of the two sets obtained by NNIA and NNIA-X. Here,  $I$  denotes the solution set obtained by NNIA, and  $I^{-X}$  denotes the solution set obtained by NNIA-X.

The comparison between NNIA and NNIA-X in Coverage shows that

For ZDT1, ZDT2, ZDT3, ZDT4, DTLZ1, DTLZ2, DTLZ3 and DTLZ4, the box plots of  $I_C(I, I^{-X})$  are obviously higher than the corresponding box plots of  $I_C(I^{-X}, I)$ . Therefore, NNIA did much better than NNIA-X in solving these eight problems as far as the Coverage is concerned.

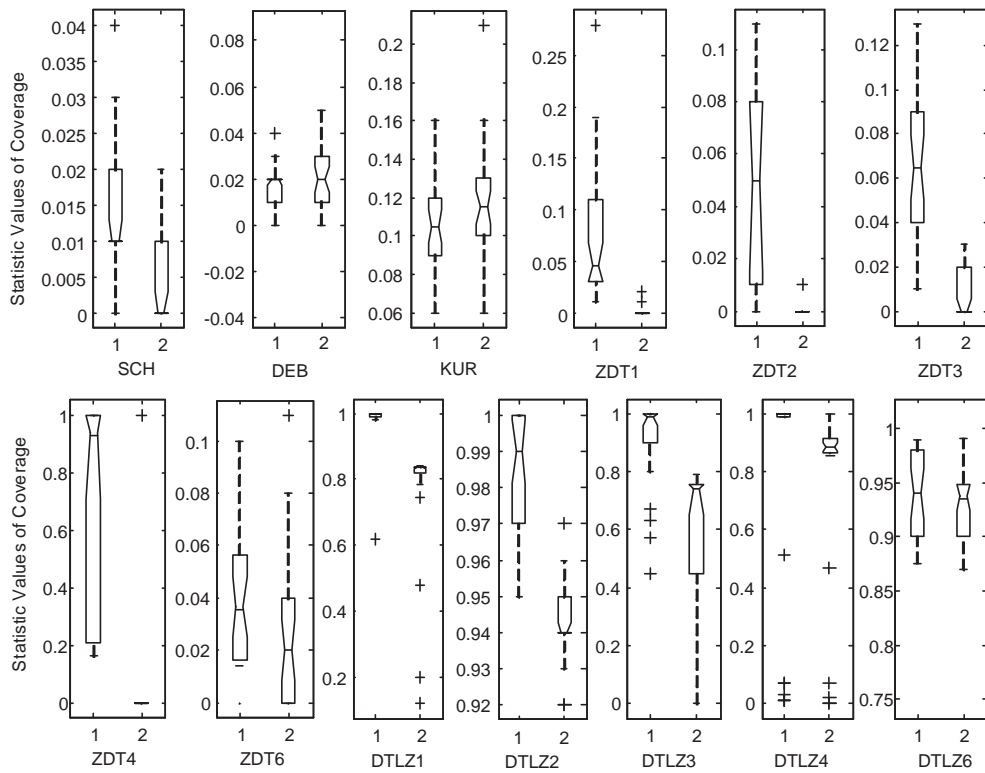


Figure 12: Box plots of the Coverage of the two sets obtained by NNIA with and without SBX, in solving the thirteen problems. The thirteen plots denote the results of the thirteen problems respectively. In each plot, the left box represents the distribution of  $I_C(\mathbf{I}, \mathbf{I}^{-\mathbf{X}})$  and the right box represents the distribution of  $I_C(\mathbf{I}^{-\mathbf{X}}, \mathbf{I})$ .

For SCH, ZDT6 and DTLZ6, the box plots of  $I_C(\mathbf{I}, \mathbf{I}^{-\mathbf{X}})$  are slightly higher than the corresponding box plots of  $I_C(\mathbf{I}^{-\mathbf{X}}, \mathbf{I})$ . Therefore, NNIA did a little better than NNIA-X in solving these three problems.

For DEB and KUR, the box plots of  $I_C(\mathbf{I}^{-\mathbf{X}}, \mathbf{I})$  are slightly higher than the corresponding box plots of  $I_C(\mathbf{I}, \mathbf{I}^{-\mathbf{X}})$ . Therefore, NNIA-X did a little better than NNIA in solving these two problems.

Overall, NNIA did better than NNIA-X in solving eleven out of the thirteen problems. NNIA-X only did a little better than NNIA in solving the two low-dimensional problems DEB and KUR.

Based on the above empirical results, we did not abandon the recombination in our algorithm because our aim was to construct a useful algorithm for multiobjective optimization rather than a pure clonal selection algorithm. Furthermore, the recombination of genes involved in the production of antibodies differs somewhat from the recombination of parental genes in sexual reproduction used in genetic algorithms. In the former, the recombination on a clone is performed as a crossover between the clone and a randomly selected active antibody. It realized replacing at random some gene segments of the clone by the corresponding ones of the selected active antibody. The

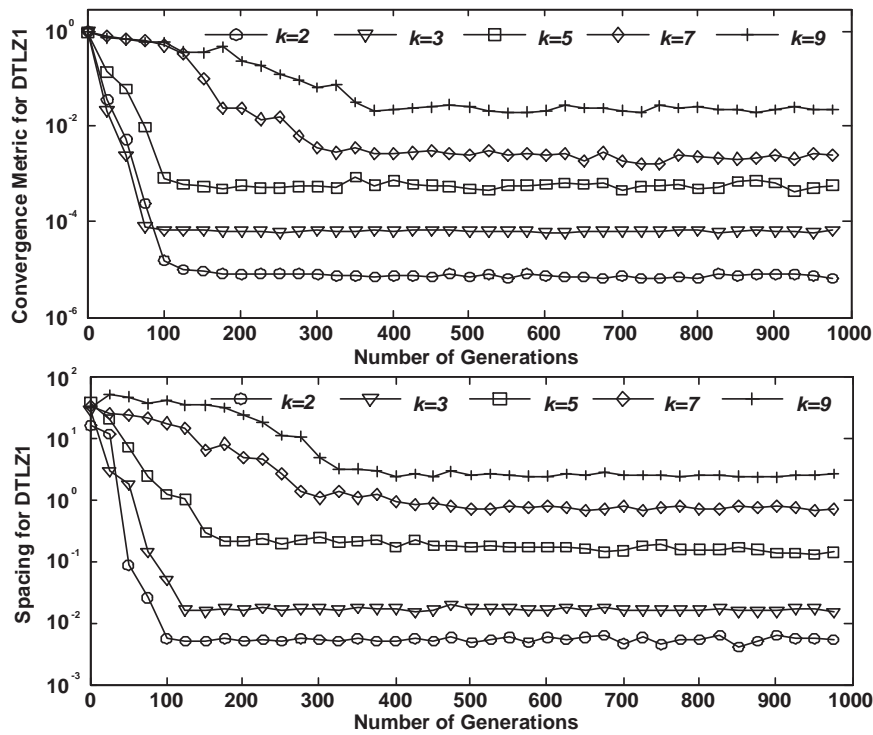


Figure 13: Mean values of the normalized Convergence metric (the upper plot) and the Spacing (the nether plot) versus number of generations over 30 independent runs when NNIA solves DTLZ1 with various numbers of objectives. A logarithmic (base 10) scale is used for the Y-axis.

latter involves the crossover of two parents to generate offspring. However, the similarity between them is also obviously, because the similarity between biological evolution and the production of antibodies is even more striking as claimed in (de Castro and Von Zuben, 2002).

#### 4.4 Scalability of NNIA along the Number of Objectives

In this section, we will study the NNIA’s scalability in the Convergence metric, the Spacing, and running time with respect to the number of objectives. Among the thirteen test problems, only the five DTLZ problems are scalable to have any number of objectives. As suggested by Deb et al. (2002b), DTLZ1 can be used to investigate an MOEA’s ability to scale up its performance in a large number of objectives, and DTLZ3 can be used to investigate an MOEA’s ability to converge to the true Pareto-optimal front. Here, DTLZ1 and DTLZ3 with 2 to 9 objectives are used for the empirical study. In order to investigate the change of these metrics along the number of generations, we set the number of generations as a considerable large value 1000. Some references have implied that MOEAs with small population size have difficulties in converging to the Pareto-optimal front with well-distributed solutions for complicated problems, especially for the MOPs with more than 3 objectives (Khare et al., 2003; Tan et al., 2001;



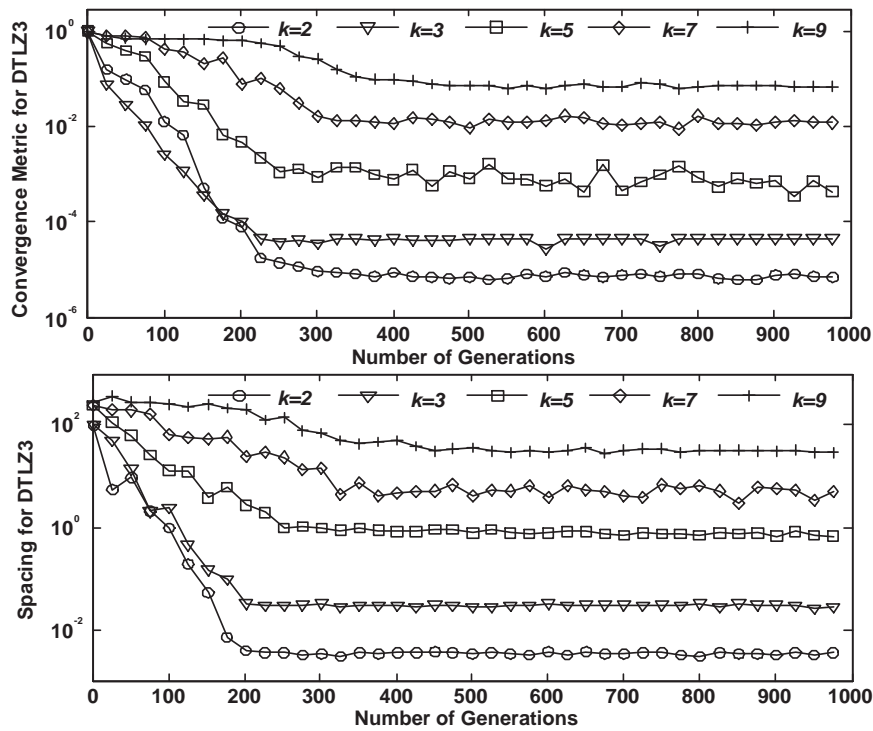


Figure 14: Mean values of the normalized Convergence metric (the upper plot) and the Spacing (the nether plot) versus number of generations over 30 independent runs when NNIA solves DTLZ3 with various numbers of objectives. A logarithmic (base 10) scale is used for the Y-axis.

Deb, 2001). In order to bate the influence of population size, here we double the values of population size, namely, the maximum size of dominant population  $n_D = 200$ , the maximum size of active population  $n_A = 50$ , and the size of clone population  $n_C = 200$ . Other parameters are the same as Section 4.2. The number of points on true Pareto-optimal front for calculating the values of the convergence metric is 200 when  $k=2$  and 3, 500 when  $k=5$ , and 1000 when  $k=7$  and 9. Figure 13 and Figure 14 show the mean values of the normalized Convergence metric (Deb and Jain, 2002) and Spacing over 30 independent runs in 1 to 1000 generations when NNIA solves DTLZ1 and DTLZ3 with 2, 3, 5, 7 and 9 objectives, respectively.

For DTLZ1, when  $k=2, 3, 5$ , NNIA obtains the approximate minimum values of the Convergence metric and Spacing in no more than 150 generations. When  $k=7$  and 9, NNIA needs to iterate about 350 generations to obtain the approximate minimum values of the Convergence metric and the Spacing. For DTLZ3, when  $k=2, 3, 5$  and 7, NNIA obtains the approximate minimum values of convergence metric and Spacing in no more than 300 generations. When  $k=9$ , NNIA does not get acceptable values of convergence metric and Spacing with the population size used here because DTLZ3 introduce more difficulties to an MOEA in converging to Pareto-optimal front and in finding a diverse set of solutions (Khare et al., 2003).

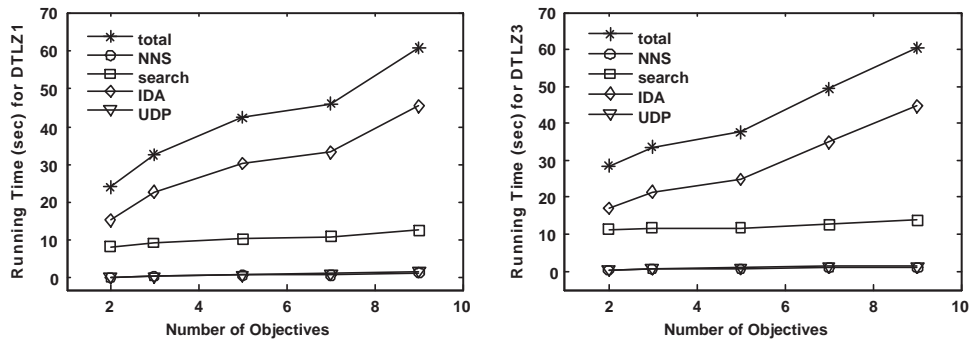


Figure 15: Mean values of each operator’s running time and the total running time versus number of objectives when NNIA solves DTLZ1 and DTLZ3 with various numbers of objectives.

Figure 15 shows the running time of NNIA in solving DTLZ1 and DTLZ3 using the parameters mentioned above. All the values of time are recorded using Matlab 7.0 program running at a personal computer with P-IV 3.2G CPU and 2G RAM. The running time of the operators including nondominated neighbor-based selection (NNS), cloning, recombination and mutation (search), update dominant population (UDP) and identifying dominant antibodies (IDA), are given too. It can be seen that, the cost of identifying the nondominated individuals in the population dominates the run-time complexity of NNIA. It is obvious that the complexity of NNIA along the number of objectives is approximately linear when the number of generations is the same.

## 5 Concluding Remarks

We have proposed a novel multiobjective algorithm based on a nondominated neighbor-based selection technique, an immune inspired operator, two heuristic search operators, and elitism. In NNIA, the fitness value of nondominated individuals is assigned as the crowding-distance. The selection technique only performs on nondominated individuals and selects minority isolated individuals to clone proportionally to crowding-distance values, recombine and mutate. Some immunologists claimed that repertoire diversity of antibody underlies the immune response however the majority of antibodies do not play any active role during the immune response (Pannetier et al., 1995; Cziko, 1995; Baranzini et al., 1999; Parkin and Cohen, 2001). NNIA simulated this mechanism by selecting only the minority of nondominated individuals with greater crowding-distance values as active antibodies, and performing the proportional cloning, recombination, and hypermutation only on these active antibodies. It realized the enhanced local search around the active antibodies which are the less-crowded individuals in objective space.

NSGA-II, SPEA2, PESA-II and some other MOEAs can be considered as different MOEAs because they adopt different ways to do selection and population maintenance. In contrast to NSGA-II, the nondominated neighbor-based selection and proportional cloning make the less-crowded individuals have more chances to do recombination and mutation. So in a single generation, NNIA pays more attention to the less-crowded regions of the current trade-off front. The essential difference between NNIA and MISA

is in their different selection methods and population maintenance strategies as well as individual representation methods. MISA adopts binary representation, clones all the nondominated individuals (and feasible individuals for constraint problems), and applies two types of mutation to the clones and other 'not so good' individuals, respectively. MISA updates its external population by using the grid based techniques used in PAES which need a crucial parameter, the number of grid cells. The difference between NNIA and VAIS also lies in their selection and population maintenance strategies. VAIS adopts the flowchart of opt-aiNet and the fitness assignment method in SPEA2 with some simplification. VAIS maintains its external population (memory population) using the suppression mechanism like opt-aiNet based on the Euclidean distance in objective space and a threshold for suppression. We can also find some similar points between NNIA and PESA-II, PAES, SPEA2, e.g. storing the nondominated individuals previously found externally and reducing the number of nondominated individuals stored without destroying the characteristics of the trade-off front, because our algorithm is constructed inspired from them.

Most of the immune system inspired optimization algorithms essentially evolve solutions to problems via repeated application of a cloning, mutation and selection cycle to a population of candidate solutions and remaining good solutions in the population. Just as Hart and Timmis (2005) said, anyone familiar with the EA literature will recognize all of these features as equally applicable to an EA. It may be due to the striking similarity between the functioning of immune system and the adaptive biological evolution. In particular, the central processes involved in the production of antibodies, genetic recombination and mutation, are the same ones responsible for the biological evolution of species (de Castro and Von Zuben, 2002).

The main contribution of this study to MO field may be its unique selection technique. The selection technique only selects minority isolated nondominated individuals based on their crowding-distance values. The selected individuals are then cloned proportionally to their crowding-distance values before heuristic search. By using the nondominated neighbor-based selection and proportional cloning, the new algorithm realizes the enhanced local search in the less-crowded regions of the current trade-off front. Depending on the enhanced local search, NNIA can solve MOPs with a simple procedure. The experimental study on NNIA, SPEA2, NSGA-II, PESA-II and MSIA in solving three low-dimensional problems, five ZDT problems and five DTLZ problems has shown that NNIA was able to quite converge to the true Pareto-optimal fronts in solving most of the test problems. More important, for the complicated problems DTLZ1 and DTLZ3, NNIA did much better than the other four algorithms. Depending on these empirical comparisons, we concluded that the nondominated neighbor-based selection method is effective, and NNIA is an effective algorithm for solving multiobjective optimization problems.

An issue should be addressed in the future research is the population size self-adaptive dynamic strategy. Some references have implied that MOEAs with small population size have difficulties in converging to the true Pareto-optimal front and obtaining the well-distributed solutions for some complicated problems (Deb, 2001; Tan et al., 2001; Khare et al., 2003). The dependence between the problem complexity and the population size of NNIA should be solved correctly. However, to estimate the correct population size for a given problem can not be done a priori as the complexity of the problem generally can not be inferred ahead of time. The population size self-adaptive dynamic strategy using the rate of nondominated individuals or the relation between dominated and nondominated individuals may be an interesting direction of

the future research.

The formulation of an efficient stopping criterion for MOEAs has been claimed as one of the fundamental topics that must be properly addressed in MOEA area (Rudenko and Schoenauer, 2004; Coello Coello, 2005). However, it is difficult to formulate the optimal and evidential stop criterion as judging the advance of the optimization can become as complex as the MOP itself. Furthermore, single-objective EAs can stop when the fitness does not improve during a given number of generations, but such stopping criterion does not easily extend to the multiobjective framework. Therefore, researchers usually stop the algorithm when the algorithm reaches a given number of iterations or function evaluations as used in this study. A more appropriate stopping criterion should be addressed in the future research.

Applying an effective constraint-handling technique to the proposed algorithm for solving constrained MOPs is also our future work.

Most of the existing artificial immune system algorithms for multiobjective optimization are inspired from the clonal selection principle. Some immunological theories are not well explored in the field of multiobjective optimization, such as Negative Selection (Zhou and Dasgupta, 2007) and Danger Theory (Aickelin and Cayzer, 2002). An investigation of their potential for multiobjective optimization may be another direction of the future research.

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