Continuous Optimization

An evolutionary artificial immune system for multi-objective optimization

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Abstract

In this paper, an evolutionary artificial immune system for multi-objective optimization which combines the global search ability of evolutionary algorithms and immune learning of artificial immune systems is proposed. A new selection strategy is developed based upon the concept of clonal selection principle to maintain the balance between exploration and exploitation. In order to maintain a diverse repertoire of antibodies, an information-theoretic based density preservation mechanism is also presented. In addition, the performances of various multi-objective evolutionary algorithms as well as the effectiveness of the proposed features are examined based upon seven benchmark problems characterized by different difficulties in local optimality, non-uniformity, discontinuity, non-convexity, high-dimensionality and constraints. The comparative study shows the effectiveness of the proposed algorithm, which produces solution sets that are highly competitive in terms of convergence, diversity and distribution. Investigations also demonstrate the contribution and robustness of the proposed features.

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Keywords: Evolutionary algorithms; Artificial immune systems; Multi-objective optimization; Clonal selection principle

1. Introduction

Many real-world problems involve the simultaneous optimization of various competing specifications and constraints that are difficult, if not impossible, to solve without the aid of powerful optimization algorithms. In the recent years, many different population-based stochastic optimization methods such as evolutionary algorithms (EA), evolutionary strategies (ES) and particle swarm optimization (PSO) have been successful developed and applied to solve multi-objective (MO) problems. While it has been shown that these biologically inspired heuristics offers better performances over classical optimization approaches in complex MO problems, they are plagued by their own limitations such as premature convergence and poor exploitation abilities.

Artificial immune system (AIS) is a computational intelligence paradigm inspired by the biological immune system, which has found application in pattern recognition (Carter, 2000; Carvalho and...
Freitas, 1991), scheduling (Mori et al., 1998; Cui et al., 2001), control (Bersini, 1991; Kim and Lee, 2004), machine-learning (Hunt and Cooke, 1996; Timmis and Knight, 2001) and information systems security (Harmer et al., 2002; Dasgupta and Gonzalez, 2002). AIS has also been applied successfully to a variety of optimization problems and studies have shown that it possesses several attractive immune properties that allow EAs to avoid premature convergence (Fukuda et al., 1999) and improve local search (Bersini and Varela, 1991). However, the issue of MO optimization is rarely considered and the success of AIS in single objective (SO) problems may not extend well into MO problems where MO techniques are required to maintain a diverse and uniformly distributed solution set.

This paper considers the development of an evolutionary multi-objective immune algorithm (EMOIA) to exploit the complementary features of EA and AIS. The algorithm incorporates the features of clonal selection and immune memory to improve evolutionary search by identifying potential regions to explore while avoiding over emphasis in any region of the search space. The proposed clonal selection (CS) is different from many existing works in the sense that the selection and clonal rate of memory cells are based on the diversity in the evolving population. An entropy-based density assessment scheme (EDAS) is also proposed in this paper to distribute non-dominated solutions along the discovered Pareto-front uniformly for MO optimization. Unlike existing density assessment schemes, the assessment is based on the individuals’ contribution to the total information content of the archive, and can be applied in either the decision or objective domain space depending on the nature of the problem involved.

The remainder of this paper is organized as follows: Section 2 provides a brief introduction to MO optimization while Section 3 provides some background information on AIS for MO optimization. The computational framework of AIS for MO optimization, details of EMOIA implementation and the proposed features of CS and EDAS are described in Section 4. Extensive empirical studies are conducted in Section 5, including a comparative study of the proposed algorithm with well-known MO optimization algorithms on a number of benchmark problems, further investigation on the effects of the proposed EDAS and parameter sensitivity analysis. Conclusions are drawn in Section 6.

2. Background information

In general, many real-world applications involve complex optimization problems with various competing specifications and constraints. Without loss of generality, we consider a minimization problem with decision space, \(X\), a subset of real numbers. For the minimization problem, it tends to find a parameter set \(P\) for

\[
\min_{P \in X} F(P), \quad P \in \mathbb{R}^D,
\]

where \(P = \{p_1, p_2, \ldots, p_D\}\) is a vector with \(D\) decision variables and \(F = \{f_1, f_2, \ldots, f_M\}\) are \(M\) objectives to be minimized.

The solution to MO optimization problem exists in the form of an alternate tradeoff known as Pareto optimal set where each objective component of any non-dominated solution in the set can only be improved by degrading at least one of its other objective components. Pareto dominance can be used to assess the relative strength or fitness between any two candidate solutions in MO optimization and the concept has been widely adopted in the research of MO optimization since it was proposed by Pareto et al. (1896). Specifically, a vector \(F_a\) is said to dominate another vector \(F_b\), denoted as

\[
F_a \preceq F_b, \text{ iff } f_{a, i} \leq f_{b, i} \forall i
\]

\[
= \{1, 2, \ldots, M\} \text{ and } \exists j
\]

\[
\in \{1, 2, \ldots, M\} \text{ where } f_{a, j} < f_{b, j}.
\]

3. Artificial immune systems

AIS for optimization have been proposed and implemented in different ways. For instance, immune algorithms developed by Bersini and Varela (1991), Toma et al. (2000) are based on the immune network theory while other researchers such as Cui et al. (2001) and Coello Coello and Cortes (2005) developed AIS based on the concepts of clonal selection principle. Similar to the other stochastic optimization techniques, the AIS maintains and adapts a repertoire of candidate solutions to the problem at hand, which is analogous to immune system’s response to antigens (Ag). In this context, the candidate solutions are called antibodies (Ab), and are associated with an affinity measure that provides an indication of its performance.
3.1. Biological immune system

The biological immune system, consisting of the innate and adaptive immune systems, is an effective and efficient defence mechanism against infections. The innate immune system serves as the first line of defence, employing phagocytes to destroy infectious pathogens and remains relatively constant, independent of antigenic exposure. On the other hand, the adaptive immune system produces and adapts lymphocytes (T-cells and B-cells) in response to specific Ags, improving their effectiveness with every encounter.

The principle of clonal selection describes how the adaptive immune system reacts to Ags and improves its capability of recognizing and eliminating them. When exposed to an antigenic stimulus, T-cells and B-cells that best recognize the infectious pathogen will proliferate and differentiate into effector cells. T-effectors can either be lymphokine secretors which promote the production of Abs or Tk cells which eliminates antigens while B-cells are antibody secretors. While both types of lymphocytes are crucial in the initialization and control of the adaptive immune response, the adaptability of B-cells allow the immune system to improve itself with each encounter of a given Ag. In contrast to T-cell clonal expansion, the variable region of the B-cell also suffers from somatic mutation which plays an important role in the creation of a diverse repertoire of Abs.

Apart from plasma cells, B-cells also proliferate and differentiate into long-lived B-memory cells. While the plasma cells are active antibody secretors, the memory cells circulate around the body producing little or no antibodies. Upon exposure to recognized antigenic stimulus, the memory cells differentiate quickly into plasma cells capable of producing high affinity antibodies by preselecting the specific antigen. Therefore, the presence of both mutation and selection processes in the B-cell clonal expansion allows the lymphocytes to increase repertoire diversity and improve their ability to recognize specific Ags.

3.2. Artificial immune systems for MO optimization

Due to the intrinsic similarities between the computational frameworks of EA and AIS, immune-inspired mechanisms can be easily incorporated into the evolutionary optimization process and most exiting works, even in the context of MO optimization, represent some form of hybridization of AIS-EA. In particular, immune-inspired selection schemes are often employed in evolutionary techniques to overcome the problem of premature convergence. Despite the potential advantages of immune properties, the development of immune algorithms for MO problems is rarely considered until recently. This section provides a brief overview of the existing MO immune algorithms, highlighting the mechanisms that improve the effectiveness of MO optimization.

Yoo and Hajela (1999) presented a hybrid AIS-EA for a MO structural design problem, which applies an extension of the immune-based fitness sharing scheme (Hajela and Lee, 1996) to handle the constraints and multiple objectives. In this scheme, a random sample of Abs is selected without replacement at every step, matched against a specified Ag, and a reward based on hamming distance is added to the fitness of the winning Ab.

Cui et al. (2001) also implemented a hybrid algorithm with an aggregated fitness function involving the optimization objectives and affinity. Population diversity is maintained by an entropy-based affinity measure similar to the method of niching with a similarity constant that plays a role analogous to the sharing parameter. The approach is validated in a comparative study against MOGA (Fonseca and Fleming, 1993) on a flow shop scheduling problem.

The major drawback of the aforementioned techniques is associated with the weighted fitness function used to guide the optimization process; it is sensitive to the weight settings as well as the shape of the Pareto front. Furthermore, there is a lack of an explicit diversity preservation mechanism to maintain a diverse and uniformly distributed Pareto front.

In order to improve the balance between exploration and exploitation, Luh et al. (2003) presented a relatively complex realization of the biological immune system with a variety of variation operators such as somatic recombination, somatic mutation, gene conversion, etc. The multi-objective immune algorithm (MOIA) can be considered as a two stage optimization process, (1) the clonal proliferation process where non-dominated solutions are subjected to hypermutation and (2) an antibody diversification process where antibodies selected on basis of avidity values undergo a variety of variation operations.

Coello Coello and Cortes (2005) presented a multi-objective immune system algorithm (MISA),
which extends the clonal selection principle to identify appropriate candidate solutions for clonal expansion. Selection is performed on the basis of Pareto dominance relationship and feasibility while the cloning rate depends on the degree of similarity between the selected antibodies to promote sampling of the less crowded region. A secondary population is also employed to store the non-dominated solutions found and an adaptive grid mechanism is incorporated to ensure the uniform distribution of the stored solutions.

Freschi and Repetto (2005) proposed a vector artificial immune system (VAIS) that is based on the artificial immune network (De Castro and Timmis, 2002) for MO optimization. The VAIS is different from the algorithms described thus far because of the absence of any explicit diversity preservation mechanism. Instead, a suppression operator is used to suppress similar solutions to prevent over representation of these solutions in the memory. In addition, VAIS implements a ranking scheme which is modified from the strength Pareto approach adopted in strength Pareto evolutionary algorithm 2 (SPEA2) (Zitzler et al., 2001) such that diversity information is not considered at all. Two methods are applied to handle infeasible solutions. The first method simply discards infeasible solutions and it is applied when new solutions are generated. The second method is applied whenever a solution becomes infeasible after mutation and it involves an iterative process of reducing mutation strength with a bisection rule until the mutated clone becomes feasible.

Jiao et al. (2005) proposed an immune dominance clonal multi-objective algorithm (IDCMA) which maintains three different populations of solutions. The first population denoted as the immune dominance Abs population is used to store the set of non-dominated solutions with the best immune differential degree. In every generation, IDCMA generates a new population of Abs and a set of these Abs are selected based on their affinity to undergo cloning and recombination. The set of recombined Abs form the second population which is denoted as the generic Abs population. The rest of the Abs will constitute the third population known as the immune energy Abs population.

4. Evolutionary artificial immune system

This section describes the proposed evolutionary multi-objective immune algorithm, which incorporates the immune features of pattern recognition and immune learning through the mechanism of clonal selection and immune memory for MO problems. In particular, archive diversity is maintained by the proposed entropy-based density assessment technique while evolving population diversity is maintained by a new clonal selection scheme. Archive diversity ensures that a representative set of non-dominated solutions is stored while evolving population diversity is crucial to the discovery of a diverse, well-distributed and near-optimal solution set.

4.1. Computational framework

The algorithmic representation for the biological immune system is summarized in Table 1. Similar to Fukuda et al. (1999) and Cui et al. (2001), the antigenic stimulus and the antibodies are defined as the MO problem to be solved and the potential solutions to the problem respectively. Intuitively, the affinity of the antibodies is associated with how well it solves the problem which is defined in terms of Pareto dominance. Immune memory is implemented in the form of a fixed-sized archive and memory cells are represented by non-dominated antibodies. In order to promote antibody diversity and to facilitate the exchange of good information among antibodies, antibodies are subjected to genetic operators such as crossover and mutation after the processes of clonal selection and expansion.

4.2. Algorithmic flow of EMOIA

In order to design an algorithm that is capable of exploiting the complementary features of EA and

<table>
<thead>
<tr>
<th>Immune system</th>
<th>EMOIA</th>
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<tbody>
<tr>
<td>Antigen</td>
<td>MO problem</td>
</tr>
<tr>
<td>Antibody</td>
<td>Candidate solution</td>
</tr>
<tr>
<td>Immune memory</td>
<td>Archive</td>
</tr>
<tr>
<td>Memory cell</td>
<td>Archived solution or non-dominated antibody</td>
</tr>
<tr>
<td>Clonal selection</td>
<td>Selection of antibodies contributing to quality of solution set</td>
</tr>
<tr>
<td>Affinity calculation</td>
<td>Identification of antibodies</td>
</tr>
<tr>
<td>Antibody production</td>
<td>Evolution</td>
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</table>
AIS, a few features such as archive, entropy-based density assessment scheme (EDAS), clonal selection and genetic operators are incorporated in the EMOIA. The flowchart of EMOIA is shown in Fig. 1. The evolutionary process starts with the random initialization of the initial population of Abs. After which, all Abs are evaluated based on the respective objective functions and non-dominated Abs are updated into the archive as memory cells. The archive is updated at each cycle, e.g., if the candidate solution is not dominated by any members in the archive, it will be added to the archive. Likewise, any memory cells dominated by this solution will be removed from the archive. When the predetermined archive size, \( archivebd \), is reached, a recurrent truncation process (Khor et al., 2005) based on the EDAS is used to remove the most ineffective archive member. The EDAS will be described in the Section 4.4. The rationale of eliminating memory cells based on EDAS is to maintain a set of uniformly distributed memory cells in the archive.

After the archiving process, appropriate Abs are selected into the mating pool which has the same size as the evolving population. The selection process is actually a two stage process. The first stage involves the cloning of memory cells from the archive by means of the proposed clonal selection scheme which will be described in Section 4.5. These cloned memory cells will form only part of the mating pool solution. As illustrated in Fig. 1, binary tournament selection will be conducted to fill up the archive with Abs from the evolving population and archive in the second stage. This binary tournament selection is performed on the basis of constrained-dominance scheme which will be described in Section 4.3 and the EDAS will be used in the event when both Abs are incomparable.

In contrast to conventional AIS paradigm where mutation is the main source of Abs variation, Abs will be subjected to both crossover and mutation in the EMOIA. In particular, the Abs in the mating pool is subjected to naïve uniform crossover (Deb, 2001) and uniform mutation. For each Abs undergoing the mutation operation, each decision variable is perturbed by a uniformly distributed number on the interval \( \frac{-\text{uppbdmut}}{C0} \), \( \frac{\text{lowbdmut}}{C0} \). In order to promote exploration in the initial stages and exploitation in the later stages, the mutation strength \( S \) is adapted as

\[
S = (\text{uppbdmut} - \text{lowbdmut}) \cdot \frac{\text{Genbd} - \text{gen}}{\text{Genbd}} + \text{lowbdmut},
\]

where \( Genbd \) is the maximum number of generations to be carried out and \( gen \) is the current generation of the evolutionary process. In this paper, \( \text{uppbdmut} \) and \( \text{lowbdmut} \) are set as 0.4 and 0.2, respectively. The optimization process is repeated until the maximum number of evaluations is met.

4.3. Constrained dominance scheme

In order to evolve solutions that satisfy the various constraints, a constrained Pareto dominance scheme is applied in this paper. In particular, an Abs \( F_a \) dominates an Abs \( F_b \) if,

1. \( F_a \) is feasible and \( F_b \) is infeasible.
2. Both solutions are infeasible and \( F_a \) has fewer constraint violations than \( F_b \).
3. Both solutions are infeasible, have the same number of constraint violations and \( F_a \) dominates \( F_b \) in terms of the objective values.
4. Both solutions are feasible and \( F_a \) dominates \( F_b \) in terms of the objective values.
4.4. Entropy-based density assessment

In this paper, an entropy-based density assessment scheme is proposed to maintain a uniformly distributed set of non-dominated solutions. Unlike existing density assessment schemes such as niche sharing (Goldberg, 1989), crowding (Deb et al., 2002) and clustering (Zitzler and Thiele, 1999) where assessment of each individual solution is only dependent on its’ immediate neighbours, the proposed scheme is based on the individuals’ contribution to the total information content of the archive. In addition, EDAS is different from the approach presented by Cui et al. (2001) in two aspects: (1) density assessment is performed in the objective space instead of the genotype space and (2) it does not require the specification of any additional parameters such as the similarity constant. In particular, the width of the kernel used to estimate the distribution is adapted based on the size of the objective space along the optimization process.

This method is motivated by the immune system ability to maintain a regulated repertoire of lymphocytes that is representative of the actual antigenic environment. Similarly, it is necessary to maximize the information conveyed by the memory cells about the problem at hand. Since information theory provides us with a mathematical formalization of the intuitive notion of information, the concept of entropy or information gain is applied here to quantify the information contributed by each memory cell to the archive.

In order to compute the entropy of each memory cell, consider the archive \( Y \) as a statistical population containing \(| Y |\) non-dominated Abs or memory cells in an \( m \)-dimensional feature space which can be modeled as

\[
\bar{Y} = \{ \vec{y}_i | i = 0, 1, 2, \ldots, |Y| \},
\]

where \( \vec{y}_i \in \mathbb{R}^m \) \( \forall i = 1, 2, \ldots, |Y| \), \( \vec{y}_i \in [lowbd_j, uppbd_j] \) is a memory cell with a probability,

\[
p_{\vec{y}_i} = P(\vec{y}_i \in \bar{Y}).
\]

Entropy is defined in terms of probability density and the entropy of \( \vec{y}_i \) is given by the logarithmic function

\[
I(\vec{y}_i) = -\log(p_{\vec{y}_i}).
\]

The entropy of any particular memory cell can be interpreted as the information that can be gained by the archive when it is part of it.

Since entropy is defined in terms of probability density, density estimation is required to construct an estimate of an unobservable underlying probability density function based on observed Abs. In this paper, the Parzen window density estimation which is a non-parametric method of estimating the probability density function is applied to estimate the probability density. The Parzen window can be defined as

\[
\hat{p}(\vec{y}) = \frac{1}{|Y|} \sum_{\vec{y}_i} K(\vec{y} - \vec{y}_i),
\]

where \( K \) is the kernel function. In this paper, the multi-variate Gaussian kernel is used and it can be described by

\[
K(\vec{y}) = \frac{1}{(2\pi)^{\frac{m}{2}}|\Sigma|^\frac{1}{2}} \exp \left( -\frac{1}{2} \vec{y}^T \Sigma^{-1} \vec{y} \right),
\]

where \( \Sigma \) is the covariance matrix, \( T \) is the transpose operator, \( M \) is the number of objectives and the kernel width is defined by \( \sigma = \sqrt{\Sigma} \), \( \sigma \in \mathbb{R}^M \). It is known that the Parzen window is sensitive to the kernel width setting. Therefore, \( \sigma \) is adapted along the optimization process,

\[
\sigma_j = \frac{uppbd_j - lowbd_j}{archivebd},
\]

where \( uppbd_j \) and \( lowbd_j \) denotes the maximum and minimum values along the \( j \)th dimension of the feature space found in the archive respectively. Consequently, Eq. (6) can be rewritten as

\[
I(\vec{y}_i) = \hat{p}(\vec{y}_i)|\Sigma|^\frac{1}{2} \log \left( \hat{p}(\vec{y}_i)|\Sigma|^\frac{1}{2} \right).
\]

Eq. (10) can be easily extended for the calculation of the entropy of Abs in the evolving population. Intuitively, an antibody with a higher \( I \) will have a better contribution to the overall information content of the archive. Note that \( I \) is maximized when the memory cells are uniformly distributed along the Pareto front. As mentioned before, recurrent truncation will be performed to remove the most ineffective memory cell when the predetermined archive size is reached. In particular, the memory cell with the least \( I \) is removed to accommodate a new memory cell with better information contribution to the archive. This will allow the archive to maintain a set of uniformly distributed memory cells in the archive.
4.5. Clonal selection

In AIS, the selection of non-dominated solutions or memory cells from the archive for the cloning process (Luh and Chueh, 2004; Coello Coello and Cortes, 2005) can result in fast convergence speed due to high selection pressure. However, the selection of memory cells based on its density in the archive can also result in rapid loss of evolving population diversity, particularly if there are isolated points on the Pareto front. This motivates the development of a clonal selection (CS) scheme which is dependent on the diversity in the evolving population instead. In contrast to existing works, the selection and cloning rate of memory cells are based on the degree of their representation (\(dr\)) in the evolving population. The rationale is that the evolving population provides a better indication of the less explored regions of the search space.

CS scheme is a two stage process involving the calculation of \(dr\) for each memory cell and then the cloning rate assignment based on the computed \(dr\) for the memory cells. There are two steps involved in the calculation of \(dr\) for each memory cell, \(\bar{y}_i\). The first step determines the Abs in the evolving population that are representative of the memory cells. Since we are only interested guiding the search towards better and less explored regions in the search space, only a subset of the evolving population denoted as \(P^*\) where \(x_k \in P^*\) is only dominated by memory cells is considered in the calculation of \(dr\). An Abs, \(x_k \in P^*\) is representative of a particular memory cell \(\bar{y}_i\) along the \(j\)th dimension if,

\[
x_{k,j} \in R_{ij} \text{ iff } ||y_{i,j} - x_{k,j}|| \leq \hat{\lambda}_{ij},
\]

where \(\hat{\lambda}_{ij}\) is the range of similarity and \(R_{ij}\) denotes the set of Abs that are representative of \(\bar{y}_i\) along the \(j\)th dimension. For simplicity, \(\hat{\lambda}_{ij}\) is adapted along the optimization process as \(0.15 \cdot (upp_{bd_j} - low_{bd_j})\) where \(upp_{bd_j}\) and \(low_{bd_j}\) denotes the maximum and minimum values along the \(j\)th dimension of the objective space found in the archive respectively.

After the representatives of the memory cells are determined, the second step computes the \(dr\) of each memory cell \(\bar{y}_i\) in \(P^*\). \(dr\) is calculated by the following:

\[
dr(\bar{y}_i) = \sum_{j=1}^{n} \min_{x_k \in P} ||y_{i,j} - x_{k,j}|| \cdot E(y_{i,j}, x_{k,j}),
\]

\[
E(y_{i,j}, x_{k,j}) = \begin{cases} 
1 & \text{if } x_{k,j} \in R_{ij}, \\
0 & \text{otherwise,}
\end{cases}
\]

where \(||-||\) implies the 2-norm. A higher value of \(dr\) implies that a lesser degree of similarity between the memory cell and its representatives and, hence denotes a lower level of representation in the evolving population. Intuitively, memory cells with higher \(dr\) should play a more active role in the subsequent adaptation process and assigned higher cloning rates.

The cloning rate assignment requires the ranking of the memory cells in terms of \(dr\) and the overall cloning procedure is outlined in the following pseudocode. The rationale of cloning higher number of memory cells with a lesser degree of representation is to promote exploration and exploitation of the less populated regions. The actual distribution of the clonal rates across the different ranks shown in the pseudocode is empirically derived from exhaustive experimentation and the effects of different cloning rate settings will be studied empirically in the next section. As mentioned in Section 4.2, memory cells selected and cloned by CS will only form part of the mating pool. The rest of the mating pool Abs will be selected through tournament selection.

**Determine degree of representation**

Calculate \(dr_{ij}\) for all \(\bar{y}_i\)

Calculate rank for all \(\bar{y}_i\) based on \(dr_{ij}\)

**Perform cloning**

IF \(|Y| < 0.1 \cdot \text{archivebd}\)

Clone \(s_1 = 4\) copies of all \(\bar{y}_i\)

ELSEIF \(|Y| < 0.2 \cdot \text{archivebd}\)

Clone \(s_{21} = 3\) copies of the first 10 ranks of \(\bar{y}_i\)

Clone \(s_{22} = 2\) copies of the rest of \(\bar{y}_i\)

ELSE

Clone \(s_{31} = 2\) copies of the first 10 ranks of \(\bar{y}_i\)

Clone \(s_{32} = 2\) copies of the next 10 ranks of \(\bar{y}_i\)

Clone \(s_{33} = 1\) copy of the rest of \(\bar{y}_i\) up to rank \(0.5 \cdot \text{archivebd}\)

END

5. Simulation studies

In this section, extensive empirical studies are conducted to analyze the performance of the proposed EMOIA upon six benchmark problems. The different benchmark problems and performance metrics for MO optimization employed are described in Sections 5.1 and 5.2, respectively. Comparative studies
are conducted in Section 5.3 while the effects of the EDAS are examined in Section 5.4. This section concludes with a parameter sensitivity analysis in Section 5.5.

5.1. Benchmark problems

In the context of multi-objective optimization, these test functions must present sufficient difficulty to impede MO optimizer’s search for Pareto optimal solutions. Deb (1999) has identified several characteristics that may challenge algorithm’s ability to converge and maintain population diversity. Multi-modality is one of the characteristics that hinder convergence in MO optimization. Multi-modality essentially refers to the presence of multiple local Pareto fronts. Convexity, discontinuity and non-uniformity of the Pareto front may prevent population-based heuristics from finding a diverse set of solution. Seven benchmark problems; ZDT1, ZDT4, ZDT6, FON, KUR, DTLZ3 and CTP7 are employed in this paper. CTP7 is a constrained test problem. In order to challenge the algorithmic capability in handling high-dimensional objective space, DTLZ3 is setup as a five-objective problem. Many researchers, such as Knowles and Corne (2000), Corne et al. (2000), Deb et al. (2002), Tan et al. (2001), Zitzler et al. (2000, 2001), have used these problems in the validations of their algorithms. Therefore these problems should serve as a good basis for the assessment of algorithmic performance.

Table 2
Benchmark Problems

<table>
<thead>
<tr>
<th>Benchmark problem</th>
<th>Definition</th>
</tr>
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</table>
| 1 ZDT1            | $f_1(x_1) = x_1$  
                  | $g(x_2, \ldots, x_m) = 1 + 9 \cdot \sum_{i=2}^{m} x_i / (m-1)$  
                  | $h(f_i, g) = 1 - \sqrt{f_1 / g}$  
                  | where $m=30$ and $x_i \in [0, 1]$ |
| 2 ZDT4            | $f_1(x_1) = x_1$  
                  | $g(x_2, \ldots, x_m) = 1 + 10 \cdot \sum_{i=2}^{m} x_i^2 - 10 \cos(4 \pi x_i)$  
                  | $h(f_i, g) = 1 - \sqrt{f_1 / g}$  
                  | where $m=10$ and $x_i \in [0, 1]$ and $x_2, \ldots, x_m \in [-5, 5]$ |
| 3 ZDT6            | $f_1(x_1) = 1 - \exp(-4 x_1 \sin^4(\pi x_1))$  
                  | $g(x_2, \ldots, x_m) = 1 + 9 \cdot \left[\sum_{i=2}^{m} (x_i - 1)^2 / (m-1)\right]^{0.25}$  
                  | $h(f_i, g) = 1 - (f_i/g)^2$  
                  | where $m=10$ and $x_i \in [0, 1]$ |
| 4 FON             | Minimize $f_1, f_2$  
                  | $f_1(x_1, \ldots, x_8) = 1 - \exp[-\sum_{i=1}^{8} (x_i - 1/\sqrt{8})^2]$  
                  | $f_2(x_1, \ldots, x_8) = 1 - \exp[-\sum_{i=1}^{8} (x_i - 1/\sqrt{8})^2]$  
                  | where $-2 \leq x_i \leq 2, \forall i = 1, 2, \ldots, 8$ |
| 5 KUR             | Minimize $f_1, f_2$  
                  | $f_1(x) = \sum_{i=1}^{2} \left[-10 \exp(-0.2 \sqrt{x_i^2 + x_i + 1})\right]$  
                  | $f_2(x) = \sum_{i=1}^{3} \left[|x_i|^{0.8} + 5 \sin(x_i)\right]$  
                  | where $-5 \leq x_i \leq 5, \forall i = 1, 2, 3$ |
| 6 DTLZ3           | $f_1(x) = (1 + g(x_M)) \cos(x_1 / \pi / 2) \cdots \cos(x_{M-1} / \pi / 2)$  
                  | $f_2(x) = (1 + g(x_M)) \cos(x_1 / \pi / 2) \cdots \sin(x_{M-1} / \pi / 2)$  
                  | $f_M(x) = (1 + g(x_M)) \sin(x_1 / \pi / 2)$  
                  | $g(x_M) = 100(1 + \sum_{k=x_M}^{x_M} (x_i - 0.5)^2 - \cos(20\pi(x_i - 0.5)))$  
                  | $x_M = \{x_M, \ldots, x_{M+9}\}$  
                  | where $x_i \in [0, 1], \forall i = 1, 2, \ldots, M + 9$ |
| 7 CTP7            | $f_1(x_1) = x_1$  
                  | $g(x_2, \ldots, x_m) = 1 + 9 \cdot \sum_{i=2}^{m} x_i / (m-1)^{0.5}$  
                  | $f_2(x_2, \ldots, x_m) = g \cdot (1 - \frac{c}{g})$  
                  | subject to  
                  | $C(f_1, f_2) \equiv \cos(\theta)[f_2 - e] - \sin(\theta)f_1 \geq a \sin[b \sin(\theta)(f_2 - e) + \cos(\theta)f_1]^4]^{0.5}$  
                  | where $m=10, x_i \in [0, 1], \theta = -0.05 \pi, a = 40, b = 5, c = 1, d = 6, e = 0$ |
test suite for a fair comparison of different multi-objective algorithms (see Table 2).

5.2. Performance metrics

In comparative studies, the choice of performance metrics is very important. The optimization goal of MO algorithms is (1) to minimize distance between the generated and true Pareto front, (2) to obtain a good distribution and (3) to obtain a good spread. Hence, the performance metric should take all these objectives into account. In this work, three different quantitative performance interpretation of MO optimization are applied to validate the effectiveness of the proposed measures, together with the selected algorithms. These metrics are taken from references such as Deb (2001), Veldhui zen and Lamont (1999), Zitzler et al. (2000), and are chosen since they have been widely used for performance comparisons in MO optimization.

Generational distance (GD) is a measure of the distance between the true and generated Pareto front. This metric of individual distance representing the distance is given by

\[ GD = \left( \frac{1}{n} \sum_{i=1}^{n} d_i^2 \right)^{1/2}, \]  

(14)

Table 3

Indices of the different algorithms

<table>
<thead>
<tr>
<th>Index</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
</tr>
</thead>
<tbody>
<tr>
<td>Algorithm</td>
<td>EMOIA</td>
<td>IMOEIA</td>
<td>NSGAII</td>
<td>SPEA2</td>
<td>PAES</td>
</tr>
</tbody>
</table>

Table 4

Parameter setting for different algorithms

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>Populations</td>
<td>Population size 100 in EMOIA, IMOEIA, NSGAII, and SPEA2; Population size 1 in PAES</td>
</tr>
<tr>
<td>archivebd</td>
<td>100</td>
</tr>
<tr>
<td>Coding</td>
<td>Real number coding for EMOIA; Binary coding for IMOEIA, NSGAII, SPEA2 and PAES</td>
</tr>
<tr>
<td>Chromosome length</td>
<td>15 Bits for each variable</td>
</tr>
<tr>
<td>Selection</td>
<td>Binary tournament selection</td>
</tr>
<tr>
<td>Crossover method</td>
<td>Naïve crossover for EMOIA; Uniform crossover for IMOEIA, NSGAII, SPEA2 and PAES</td>
</tr>
<tr>
<td>Crossover rate</td>
<td>0.8</td>
</tr>
<tr>
<td>Mutation method</td>
<td>Bit-flip mutation in IMOEIA, NSGAII, SPEA2 and PAES; Adaptive for EMOIA</td>
</tr>
<tr>
<td>Mutation rate</td>
<td>0.1 for EMOIA; 1/chromosome_length for ZDT1, ZDT4, ZDT6, DTLZ3 and CTP7 in IMOEIA, NSGAII, SPEA2 and PAES; 1/bit_number for FON and KUR in IMOEIA, NSGAII, SPEA2 and PAES</td>
</tr>
<tr>
<td>Hyper-grid size</td>
<td>2^3 per dimension for DTLZ3; 2^5 per dimension for others</td>
</tr>
<tr>
<td>Evaluations</td>
<td>30,000 for FON; 10,000 for KUR and ZDT6; 28,000 for DTLZ3; 50,000 for ZDT1 and ZDT4; 40,000 for CTP7</td>
</tr>
</tbody>
</table>

Fig. 2. The evolved Pareto front from (a) EMOIA, (b) IMOEIA, (c) NSGAII, (d) SPEA2 and (e) PAES for ZDT1.
where \( n \) is the number of members in \( \text{PF}_{\text{known}} \), \( d_i \) is the Euclidean distance (in objective space) between the member \( i \) of \( \text{PF}_{\text{known}} \) and its nearest member of \( \text{PF}_{\text{true}} \). A smaller value of GD implies better convergence.

The metric of spacing (\( S \)) (Scott, 1995) measures how “evenly” members in \( \text{PF}_{\text{known}} \) are distributed. It is defined as

\[
S = \left[ \frac{1}{n} \sum_{i=1}^{n} (d_i - \bar{d})^2 \right]^{1/2},
\]

where \( n \) is the number of members in \( \text{PF}_{\text{known}} \), \( d_i \) is the Euclidean distance (in objective space) between the member \( i \) of \( \text{PF}_{\text{known}} \) and its nearest member of \( \text{PF}_{\text{true}} \). A smaller value of \( S \) implies a more uniform distribution of solutions in \( \text{PF}_{\text{known}} \).

Zitzler et al. (2000) defined the metric of maximum spread (MS) measuring how well the true Pareto front is covered by the discovered Pareto front through the hyper-boxes formed by the extreme function values observed in the true Pareto front and generated Pareto front. In order to normalize the metric, this metric is modified as

\[
MS = \frac{1}{M} \sum_{m=1}^{M} \left( \frac{\max_{n=1}^{n} f_m^n - \min_{n=1}^{n} f_m^n}{F_{\text{max}}^m - F_{\text{min}}^m} \right)^2,
\]

where \( n \) is the number of members in the discovered Pareto front, \( f_m^n \) is the \( m \)th objective of member \( i \), \( F_{\text{max}}^m \), \( F_{\text{min}}^m \) are the maximum and minimum of the \( m \)th objective in the true Pareto front. A larger value of MS implies a better spread of solutions.

Fig. 3. Performance metric of (a) GD, (b) S, and (c) MS for ZDT1.

Fig. 4. The evolved Pareto front from (a) EMOIA, (b) IMOEA, (c) NSGAII, (d) SPEA2 and (e) PAES for ZDT4.
5.3. Comparative study

In order to examine the effectiveness of the proposed algorithm, a comparative study with IMOEA (Tan et al., 2001), SPEA2 (Zitzler et al., 2001), NSGAII (Deb et al., 2002) and PAES (Knowles and Corne, 2000) is carried out based upon the seven benchmark problems listed in Table 2. All algorithms are implemented with the constrained-dominance scheme described in Section 4.3. The indices of the five algorithms are listed in Table 3. The simulations are implemented in C++ on an Intel Pentium 4 2.8 GHz computer. Thirty independent runs are performed for each of the test

Fig. 5. Performance metric of (a) GD, (b) S, and (c) MS for ZDT4.

Fig. 6. The evolved Pareto front from (a) EMOIA, (b) IMOEA, (c) NSGAII, (d) SPEA2 and (e) PAES for ZDT6.

Fig. 7. Performance metric of (a) GD, (b) S, and (c) MS for ZDT6.
functions in order to obtain the statistical information, such as consistency and robustness of the algorithms. The various parameter settings for each algorithm are listed in Table 4.

(1) ZDT1: ZDT1 has a convex Pareto front with a large number of variables to be optimized. The evolved tradeoffs from the different algorithms with the best mean value of GD is showed in Fig. 2a–e while the distribution of the different performance metrics is represented by box plots in Fig. 3a–c. From the plots of the evolved tradeoffs in Fig. 2a–e, it can be observed that all algorithms are able of finding solutions near the global Pareto front. While IMOEA, SPEA2 and NSGAII are capable of competitive results in the aspects of S, the algorithms demonstrate varying degree of success with respect to the metrics of GD and MS. On the other hand, EMOIA is able to evolve a diverse and well-distributed near-optimal Pareto front for ZDT1 constantly within 50,000 evaluations as evident from Fig. 3a–c.

(2) ZDT4: ZDT4 challenges the algorithm’s ability to deal with the problem of multi-modality. The evolved tradeoffs from the different algorithms with the best mean value of GD is showed in Fig. 4a–e while the distribution of the different performance metrics is represented by box plots in Fig. 5a–c. It can be observed from Figs. 4b–e and 5a that IMOEA, NSGAII, SPEA2 and PAES are unable to find any solutions near the global Pareto front resulting in the relatively large GD for ZDT4 at the end of 50,000 evaluations. Furthermore, Fig. 4c shows these algorithms are unable to evolve a diverse set of solutions consistently. On the other hand, EMOIA is able to escape the local optima of ZDT4 consistently due to its feature of clonal selection, as reflected by its low value of GD. While EMOIA has a relatively high variance for S, it is
able to evolve a diverse solution set within 50,000 evaluations.

(3) ZDT6: ZDT6 has a biased search space and non-uniformly distributed solutions along the global tradeoffs, which makes it difficult for algorithms to evolve a well-distributed Pareto front. The evolved tradeoffs from the different algorithms with the best mean value of GD is showed in Fig. 6a–e while the distribution of the different performance metrics is represented by box plots in Fig. 7a–c. From Fig. 7a, it can be seen that IMOEA, NSGAII and SPEA2 is unable to find the global Pareto front

![Fig. 10. The evolved Pareto front from (a) EMOIA, (b) IMOEA, (c) NSGAII, (d) SPEA2 and (e) PAES for KUR.](image)

![Fig. 11. Performance metric of (a) GD, (b) S, and (c) MS for KUR.](image)

![Fig. 12. Performance metric of (a) GD, (b) S, and (c) MS for DTLZ3.](image)
for ZDT6 consistently within 10,000 evaluations. Although the performance of PAES on GD are better than the above mentioned three algorithms, PAES is unable to evolve a well-distributed solution set as shown in Fig. 7b. On the other hand, it is evident from Figs. 6a and 7a–c that EMOIA is able to evolve a near-optimal, diverse and well-distributed near-optimal Pareto front consistently for ZDT6 within 10,000 evaluations.

(4) FON: FON challenges the algorithm’s ability to find and maintain the entire tradeoffs curve uniformly. The evolved tradeoffs from the different algorithms with the best mean value of GD is showed in Fig. 8a–e while the distribution of the different performance metrics is represented by box plots in Fig. 9a–c. It can be observed from Figs. 8 and 9 that IMOEA, NSGAII, SPEA2 and PAES are only capable of finding some parts of the optimal Pareto front. On the other hand, the proposed EMOIA found no problems converging and maintaining a diverse solution set uniformly as reflected by the metric of MS in Fig. 9c. Furthermore, EMOIA offers the best performance in terms of solution distribution and optimality as evident from Fig. 9a and b probably due to its features of clonal selection and entropy-based diversity preservation scheme. While IMOEA, NSGAII and SPEA2 demonstrate similar performance with respect to the three performance metrics, PAES demonstrates the worst overall performance. This is probably because PAES is a non-population based approach.

(5) KUR: KUR is characterized by an optimal Pareto front that is non-convex and disconnected, i.e., it contains three distinct disconnected regions on the final tradeoffs. The decision variables correspond to the global tradeoffs for KUR are difficult to be discovered, since they are also disconnected in the decision variable space. The evolved tradeoff

![Graphs](image-url)  
**Fig. 13.** The evolved Pareto front from (a) EMOIA, (b) IMOEA, (c) NSGAII, (d) SPEA2 and (e) PAES for CTP7.

![Graphs](image-url)  
**Fig. 14.** Performance metric of (a) GD, (b) S, and (c) MS for CTP7.
with the best mean value of GD is showed in Fig. 10a–e while the distribution of the different performance metrics is represented by box plots in Fig. 11a–c. From the plots of the evolved tradeoffs in Figs. 10a–e and 11a, it can be observed that all algorithms have no problems overcoming the barrier of discontinuities. However, it can be observed from Fig. 11b and c that EMOIA is capable of evolving a more diverse and better distributed solution set as compared to IMOEA, NSGAII, SPEA2 and PAES.

(6) DTLZ3: DTLZ3 is used to evaluate the performance of MOEAs in producing adequate pressure for driving the evolution of individuals towards the large Pareto front in the high-dimensional objective domain. Similar to ZDT4, it also challenges the algorithm’s ability to deal with multi-modality. The distribution of the different performance metrics is represented by box plots in Fig. 12a–c. From Fig. 12a, it is clear that only EMOIA and PAES are capable of handling high-dimensional objective space. In particular, NSGAII, SPEA2 and IMOEA still have solutions that are far away from the optimal Pareto front as evident by the high values of GD. Fig. 12c shows that EMOIA is capable of evolving a more diverse Pareto front as compared to IMOEA, PAES and SPEA2. It seems that EMOIA performs poorly on the metric of $S$. However, further investigation shows that it is due to the presence of non-dominated solutions that are located at the extreme edges of the evolved Pareto front. These solutions usually have a small improvement in one objective that is gained at the expense of significant degradation of others.

(7) CTP7: The constraint makes parts of CTP7 infeasible, resulting in a discontinuous Pareto front. This problem challenges the MOEA ability to maintain adequate diversity in order to discover all regions of the Pareto front. The evolved tradeoffs for an arbitrary run from the different algorithms with the best mean value of GD is showed in Fig. 13a–e while the distribution of the different performance metrics is represented by box plots in Fig. 14a–c. From Figs. 13 and 14a, it is observed that all algorithms except PAES are capable of finding a near optimal Pareto front. However, the algorithms have different degree of success in maintaining diversity and finding all the discontinuous regions of the Pareto front. For instance, IMOEAA is unable to locate any solutions in the extreme region along $f_2$ for all 30 runs resulting in poor MS values.

5.4. Effects of entropy-based density assessment

In this section, the effectiveness of the proposed EDAS is examined through a comparative study against the technique of niche sharing (NS). Thirty independent simulation runs are performed for the test problems of ZDT1 and FON. The niche radius is a key parameter that affects algorithmic performance. In practice, the niche radius is difficult to estimate because there is no priori knowledge about the shape of the Pareto front for many problems. Fonseca and Fleming (1993) gave some bounding guidelines of appropriate niche radius when the number of individuals in the population and the minimum/maximum values in each objective dimension are given. The niche radius adopted in this section is based on extensive experimental studies and is set as $\frac{1}{\text{archivebd}}$.

The performances of EDAS and NS in terms of GD, S and MS are summarized in Tables 5–7.

<table>
<thead>
<tr>
<th>Problem</th>
<th>Method</th>
<th>GD</th>
<th>EDAS</th>
</tr>
</thead>
<tbody>
<tr>
<td>ZDT1</td>
<td>Mean</td>
<td>0.001903</td>
<td>0.002307</td>
</tr>
<tr>
<td></td>
<td>Std</td>
<td>0.002340</td>
<td>0.000436</td>
</tr>
<tr>
<td>FON</td>
<td>Mean</td>
<td>0.005931</td>
<td>0.005053</td>
</tr>
<tr>
<td></td>
<td>Std</td>
<td>0.000562</td>
<td>0.000351</td>
</tr>
</tbody>
</table>

Table 5: GD performance by different density assessment schemes for ZDT1 and FON

<table>
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<tr>
<th>Problem</th>
<th>Method</th>
<th>S</th>
<th>EDAS</th>
</tr>
</thead>
<tbody>
<tr>
<td>ZDT1</td>
<td>Mean</td>
<td>0.335688</td>
<td>0.216951</td>
</tr>
<tr>
<td></td>
<td>Std</td>
<td>0.152815</td>
<td>0.033864</td>
</tr>
<tr>
<td>FON</td>
<td>Mean</td>
<td>0.200729</td>
<td>0.206287</td>
</tr>
<tr>
<td></td>
<td>Std</td>
<td>0.021675</td>
<td>0.031867</td>
</tr>
</tbody>
</table>

Table 6: S performance by different density assessment schemes for ZDT1 and FON

<table>
<thead>
<tr>
<th>Problem</th>
<th>Method</th>
<th>MS</th>
<th>EDAS</th>
</tr>
</thead>
<tbody>
<tr>
<td>ZDT1</td>
<td>Mean</td>
<td>0.995417</td>
<td>1.000000</td>
</tr>
<tr>
<td></td>
<td>Std</td>
<td>0.007563</td>
<td>0.000000</td>
</tr>
<tr>
<td>FON</td>
<td>Mean</td>
<td>0.924121</td>
<td>0.955796</td>
</tr>
<tr>
<td></td>
<td>Std</td>
<td>0.018966</td>
<td>0.013011</td>
</tr>
</tbody>
</table>

Table 7: MS performance by different density assessment schemes for ZDT1 and FON
respectively. In addition, the Kolmogorov–Smirnov (KS) test is applied to assess the statistical difference of the simulation results. An asterisk (*) is appended to the metric value when there is no statistical significance. It can be observed that the solution sets evolved by EDAS and NS are better in the aspect of GD for FON and ZDT1, respectively. Nonetheless, EDAS provides greater consistency as indicated by the low values of standard deviation. EDAS only allows the algorithm to achieve competitive performance in the metric of S while attaining better performance in the aspects of MS, demonstrating the merits of the diversity assessment scheme. Even though NS has a slight edge in S for FON, the KS test revealed that the results are not statistically different.

5.5. Parameter sensitivity analysis

(1) Effects of $\sigma_j$ on EDAS: The maintenance of a well-distributed and diverse Pareto front depends on appropriate settings of the kernel width $\sigma_j$ for the estimation of the information gain for each memory cell in EDAS. Although $\sigma_j$ is adaptive based on the evolved tradeoffs, it is also important to examine how it affects the performance of EMOIA. Simulations are conducted for $\sigma_j = \{1, 2, 3, 4, 5\} \frac{\text{upperbd}_j - \text{lowerbd}_j}{\text{archivedbd}}$ and 30 independent simulation runs are performed for the test problems of ZDT1 and FON. The median, first and third quartile performances of EMOIA with the various settings with respect to the different metrics are plotted in Figs. 15 and 16.

![Fig. 15. EMOIA performances in the aspects of (a) GD, (b) S, and (c) MS for ZDT1 at various settings of $\sigma_j$.](image1)

![Fig. 16. EMOIA performances in the aspects of (a) GD, (b) S, and (c) MS for FON at various settings of $\sigma_j$.](image2)

![Fig. 17. EMOIA performances in the aspects of (a) GD, (b) S, and (c) MS for ZDT1 at various settings of $\lambda_{i,j}$.](image3)
In general, it can be observed that the convergence and distribution of the evolved solution set improves with decreasing $\sigma_j$ and EMOIA performs best at the original setting of $\sigma_j = \frac{(uppbd_j - lowbd_j)}{archivebd}$. This is expected since the entropy of the archive is maximized only if all memory cells have a unique contribution to the overall information content at this particular setting, i.e. uniformly distributed along the Pareto front. At larger settings of $\sigma_j$, the probability density is over-smoothed and the contribution of Abs cannot be determined properly. This results in the degradation of EMOIA ability to distribute solutions uniformly. On the other hand, EMOIA remains robust in the aspects of diversity as evident from Figs. 15c and 16c. In fact, MS actually improved with increasing $\sigma_j$ in the case of FON.

(2) Effects of $\lambda_{ij}$ and cloning rates on CS: In order to investigate the robustness of CS to parameter sensitivity, a number of simulations are performed with different settings of $\lambda_{ij} = \{0.11, 0.13, 0.17, 0.19\} \cdot (uppbd_j - lowbd_j)$ as well as the various numbers of clones under different conditions in the cloning procedure. The various cloning rates determine the degree at which elitist memory cells and dominated solutions are cloned for the next generation and it is interesting to analyze it affects the optimization process. In addition, multiple comparison tests are performed based on the one-way analysis of variance to determine the presence of any statistical significance in results between different settings.

Thirty independent simulation runs with different settings of $\lambda_{ij}$ are performed for the test problems of ZDT1 and FON and the median, first and third quartile performances are shown in Figs. 17 and 18, respectively. From the results, it is observed that the CS is capable of performing consistently and effectively within a large range of $\lambda_{ij}$ settings for ZDT1 and FON. This fact is also validated by the multiple comparison test, which demonstrates that there is no significant statistical difference in all aspects of GD, S and MS.

The performances of EMOIA with different cloning numbers for ZDT1 and FON are shown in Figs. 19 and 20, respectively. For each experimental set up, a particular clone number is varied while maintaining the original setting for the other parameters. Figs. 19a and 20a show that EMOIA performance remains consistent in all aspects of convergence and diversity for both problems when the number of memory cells is small, a fact that is validated by the multiple comparison tests. More significantly, it implies that high evolutionary pressure at the initial stages do not lead to premature convergence for EMOIA. When the size of the archive increases to 20% of $archivebd$, the cloning rates, $s_{21}$ and $s_{22}$, have a more significant impact on the convergence of EMOIA for FON. In particular, EMOIA attained significantly better performance in the metric of GD at $s_{21} = 3$ and $s_{22} = 2$, while algorithmic performance remains invariant for other settings. Nonetheless, it can also be easily noted that EMOIA still outperforms the other test algorithms by comparing Fig. 20b and c with Fig. 9 at these settings. When the size of the archive increases beyond 20% of $archivebd$, only the distribution of EMOIA is affected by the cloning rates of $s_{31}$ and $s_{32}$. In the case of FON, these two cloning rates have an impact on convergence and diversity while distribution of solutions remains invariant. For both problems, the multiple comparison tests showed that $s_{31}$ has a greater influence on EMOIA performance. Remember that increasing $s_{31}$ and $s_{32}$ will allow a greater number of memory cells to be cloned into the evolving population. Since the memory cells cloned are based on their degree of representation in the evolving population, this allows EMOIA to improve solution set diversity as evident from Fig. 20d for FON. However, the
Fig. 19. Performance relative to the original settings in the aspects of GD, S, and MS for ZDT1 at (a) $s_1 = \{2, 4, 6, 8, 10\}$, (b) $s_{21} = \{1, 2, 3, 4, 5\}$, (c) $s_{22} = \{1, 2, 3, 4, 5\}$, (d) $s_{31} = \{1, 2, 3, 4, 5\}$, and (e) $s_{32} = \{1, 2, 3, 4, 5\}$. 
Fig. 20. Performance relative to the original settings in the aspects of GD, S, and MS for FON at (a) $s_1 = \{2, 4, 6, 8, 10\}$, (b) $s_{21} = \{1, 2, 3, 4, 5\}$, (c) $s_{22} = \{1, 2, 3, 4, 5\}$, (d) $s_{31} = \{1, 2, 3, 4, 5\}$, and (e) $s_{32} = \{1, 2, 3, 4, 5\}$. 
tradeoffs between convergence and diversity can be observed by comparing the trend of GD and MS over the various settings in Fig. 20d. It is also worth noting that the performance of EMOIA for ZDT1 in the metric of MS remains invariant to the various cloning rates.

(3) Effects of lowbd\textsubscript{mut, i} and uppbd\textsubscript{mut, i} on mutation: In order to examine the robustness of EMOIA to various settings of sensitivity of the lowbd\textsubscript{mut, i} and uppbd\textsubscript{mut, i}, a number of simulations are performed with different settings of lowbd\textsubscript{mut, i} = \{0.05, 0.1, 0.15, 0.2, 0.25\} and uppbd\textsubscript{mut, i} = \{0.25, 0.3, 0.35, 0.4, 0.45\} for ZDT1 and FON. Algorithmic performances for ZDT1 and FON with the various settings of lowbd\textsubscript{mut, i} are shown in Figs. 21 and 22, respectively. Likewise, simulation results for ZDT1 and FON with the various settings of uppbd\textsubscript{mut, i} are shown in Figs. 23 and 24.

By comparing Figs. 21 and 22, it can be observed that the performance of EMOIA is relatively more robust in ZDT1 as compared to FON. A lower lowbd\textsubscript{mut, i} typically implies more exploitation allowing the EMOIA to achieve better convergence as well as diversity as in the case of FON. On the contrary, EMOIA performs better in the aspect of convergence as indicated by the metric of GD when lowbd\textsubscript{mut, i} is increased. From Figs. 23 and 24, it can be observed that the performance of EMOIA remains competitive over different settings of uppbd\textsubscript{mut, i} for both ZDT1 and FON. As before, a multiple comparison test is performed and it demonstrates that there is no significant statistical differ-

Fig. 21. EMOIA performances in the aspects of (a) GD, (b) S, and (c) MS for ZDT1 at various settings of lowbd\textsubscript{mut, i}.

Fig. 22. EMOIA performances in the aspects of (a) GD, (b) S, and (c) MS for FON at various settings of lowbd\textsubscript{mut, i}.

Fig. 23. EMOIA performances in the aspects of (a) GD, (b) S, and (c) MS for ZDT1 at various settings of uppbd\textsubscript{mut, i}.
ence between the various settings for $uppbd_{mut,i}$ in all aspects of GD, S and MS.

6. Conclusions

A new evolutionary multi-objective immune algorithm has been designed to exploit the complementary features of evolutionary algorithms and artificial immune systems. In particular, two new features in the form of an entropy-based density assessment and a clonal selection scheme have been proposed. In contrast to existing works, the proposed clonal selection scheme is based on the diversity in the evolving population. The proposed entropy-based density assessment is based on the individuals’ contribution to the total information content of the archive, and can be applied in either the decision or objective space depending on the nature of the problem involved. In addition, the effectiveness of the proposed algorithm is validated upon seven benchmark problems characterized by different difficulties in local optimality, non-uniformity, discontinuity, non-convexity, high-dimensionality and constraints. The comparative study shows the effectiveness of the proposed algorithm, which produces solution sets that are highly competitive in terms of convergence, diversity and distribution. The parameter sensitivity analysis conducted reveals further insights to the EMOIA performance and validates the robustness of algorithmic performance to parametric variations.

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References


Fig. 24. EMOIA performances in the aspects of (a) GD, (b) S, and (c) MS for FON at various settings of $uppbd_{mut,i}$.


