Lecture Notes in Computer Science, vol. 7665, pp. 92–99, 2012.

In: Huang, T. et al. (eds) *19th Int Conf on Neural Information Processing - ICONIP'2012*, **Doha, Qatar, Nov 12-15, 2012.**

A Human-Simulated Immune Evolutionary Computation Approach

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Abstract

Premature convergence to local optimal solutions is one of the main difficulties when using evolutionary algorithms in real-world optimization problems. To prevent premature convergence and degeneration phenomenon, this paper proposes a new optimization computation approach, human-simulated immune evolutionary algorithm (HSIEA). Considering that the premature convergence problem is due to the lack of diversity in the population, the HSIEA employs the clonal selection principle of artificial immune system theory to preserve the diversity of solutions for the search process. Mathematical descriptions and procedures of the HSIEA are given, and four new evolutionary operators are formulated which are clone, variation, recombination, and selection. Two benchmark optimization functions are investigated to demonstrate the effectiveness of the proposed HSIEA.

Key words: Human-simulated intelligence, Artificial immune systems, Evolutionary algorithm, Clonal selection, Evolutionary operators

1. Introduction

Evolutionary algorithms (EAs) are one of the important approaches in stochastic search techniques with the essential characteristics of parallelism, adaptiveness and randomicity. However, there are still challenging difficulties when applying EAs to large-scale and complex real-world optimization problems. One of such difficulties is premature convergence, which occurs when the population reaches a suboptimal state on which most of the operations are no longer functional to produce improved offspring [1,2].

Much effort has been made to improve the performance of EAs. Cen [3] and Yang *et al.* [4] have proposed a hybrid scheme, in which simulated annealing is employed to help an adaptive genetic algorithm escape from local optima and thus prevent premature convergence.

Accepted version on 23 Aug 2012

Meanwhile, the tabu search algorithm was introduced to increase convergence speed. Herrera *et al.* [1] presented gradual distributed real-coded genetic algorithms that apply a different crossover operator to each subpopulation to deal with the premature problem. Using the concept of information theory, Yeh and Jang [5] and Bhattacharya [6] developed information-guided evolutionary operators to avoid premature convergence. Other developments in this area include references [7] and [8].

Among the developments of various EAs, the Mind Evolutionary Algorithm (MEA) [9,10] was proposed through introducing human-simulated machine learning. It simulates the process of human thinking and learning in certain social environments [11]. In spite of these advances, some shortcomings are also exposed in the applications of the MEA. Because MEA's operators amend the individuals of the population randomly, the degeneration phenomenon becomes inevitable. In particular, when solving a complex real-world problem, the problem's characteristics, which can help resolve the degeneration and improve the convergence speed, are ignored by the MEA.

Artificial immune system technologies are new developments following artificial neural networks and EAs. There have been many successful artificial immune system applications, especially in the optimization area [12,13]. The clonal selection principle is a basic and important model in an artificial immune system. Xie *et al.* [14] incorporated this model into the MEA to deal with the premature convergence problem. However, detailed understanding of the clone selection principle with applications in complex real-world optimization problems are yet to be developed. This motivates the research of this work.

This paper proposes a new optimization computation approach: human-simulated immune evolutionary algorithm (HSIEA). Similar to the MEA, the HSIEA simulates the evolution process of human society and makes use of the co-evolution and information-guided mechanism. However, the HSIEA is fundamentally different from the MEA in algorithm architecture and operators. It will be shown that the HSIEA solves the premature and degeneration problems and outperforms the MEA in computational efficiency.

The paper is organized as follows. Section 2 formalizes the fundamentals of the HSIEA. The flowchart of the HSIEA is developed in section 3. Then, two benchmark functions are investigated to ascertain the good performance of the HSIEA in section 4. Finally, section 5 concludes the paper.

2. Fundamentals of the HSIEA

Investigations into the human intelligence development have revealed that two important and universal modes exist: similar-taxis and dissimilation. The similar-taxis refers to human being's capability of adopting existing technique validated by others to handle various problems; while the dissimilation describes human being's prowess in developing innovative approach from existing ones to deal with unknown fields of the world. These two different modes interact to each other to drive the progress of human intelligence development. During this progress, society division and cooperation are also developed with the understanding that no one will survive and succeed without such an collaborative society environment and the aims of every person's study are definite at the same time. From this understanding, a human-simulated evolutionary computation model can be developed with its mechanism being illustrated in Fig. 1.

As a multi-group-based evolutionary algorithm, the HSIEA applies the **similar-taxis searching scheme** to achieve the local optimal competition. Two types of similar-taxis searching processes have been embedded into the HSIEA: individual similar-taxis and group similar-taxis.

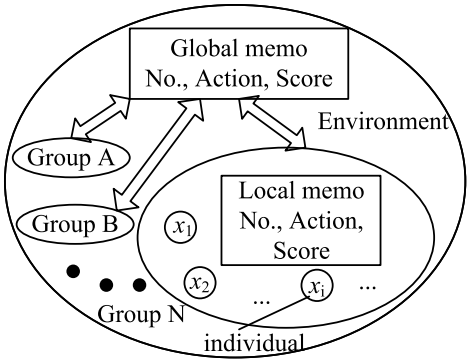

Figure 1. *The Mechanism of the human-simulated evolutionary algorithm.*

In individual similar-taxis searching, an individual becomes the winner in a group through local competition, and the winner's information is recorded in the local memos. This process is executed repeatedly, producing a local optimal solution for each group.

In group similar-taxis searching, all groups exchange information for replenishing knowledge that cannot be achieved by any group itself. Also, the global memos will determine the parameter spaces and the number of iterations for every group in the next iteration. Group similar-taxis will be executed when individual similar-taxis meets the terminal condition.

Dissimilation searching is a searching process in which the global solution is selected from the local optimal solutions produced in the similar-taxis searching. Along with the operation of the similar-taxis, some individuals produce several temporary groups in course of searching the whole solution space. If the scores of any temporary group are higher than those of any mature superior group, the temporary group would replace the superior group and become a new superior group. Thus, dissimilation searching is a global competition process.

Mathematically, the HSIEA is formulated as

$$\begin{aligned} HSIEA = \{&\Phi, X, M, N, K, f(X), D(X_i, X_j), \\ &O((T_C, P_C), (T_V, P_V), (T_R, P_R), (T_S, P_S)), E\}, \end{aligned} \tag{1}$$

where Φ is the antigen, i.e., the optimized function for the numerical optimization problem; X represents the solution space of the optimized function and mathematically is the whole of the antibodies set $\{Ab_i(t)\}$, $Ab_i(t)$ indicates the t^{th} time individual; $M \in I$ is the number of initial antibodies (candidates of solutions); $N \in I$ is the number of groups with the highest affinity between the antigen and antibody; K is the number of antibodies in each groups; $f(X)$ denotes the affinity between the antigen and antibody; $D(X_i, X_j)$ is the affinity between antibodies X_i and X_j; O is the operators of the HSIEA; and E is the terminal criterion; respectively. The four operators of the HSIEA are denoted by (T_C, P_C) for clone operator, (T_V, P_V) for variation operator, (T_R, P_R) for recombination operator, and (T_S, P_S) for selection operator, respectively.

Definition 1 ***Antigen-antibody affinity*** *denoted by $f(X)$ is defined as a calculating result after an antibody is substituted into the antigen Φ. It describes the matching degree of the optimal solution to the object function.*

Definition 2 ***Antibody-antibody affinity*** *$D(X_i, X_j)$ is a norm between two affinities*

when antibodies X_i and X_j are substituted into the antigen Φ:

$$D(X_i, X_j) = \|f(X_i) - f(X_j)\|, \tag{2}$$

where, $\|\cdot\|$ represents any norm.

Four evolutionary operators of the HSIEA, i.e., the clone operator, variation operator, recombination operator, and selection operator, are respectively described in the following four definitions. The symbol T_α indicates the correspondingly mapping of respective operators, the subscript α denotes the operators, t is the time of iteration, Ab means antibody, P_α is a probability.

Definition 3 ***The clone operator*** (T_C, P_C) *is defined as:*

$$T_C(X) = [T_C(Ab_i(t)]\,,\ i = P_C \times K, \tag{3}$$

$$P_C = \frac{1}{\sigma\sqrt{2\pi}} e^{\frac{-(x-\mu(X))^2}{2\sigma^2}} \tag{4}$$

where K is the size of an antibody group, μ is the expectation of X, and σ is the standard deviation selected from Equation (5):

$$\sigma_i = \begin{cases} 0.1, & \text{if } \Delta_{Ab_i} \geq 0.1; \\ \eta\Delta_{Ab_i}, & \text{if } \Delta_{Ab_i} < 0.1, \end{cases} \tag{5}$$

where, Δ_{Ab_i} is the Euclidean distance in the i^{th} dimension between the new winner and the best winner from older generation; $0 < \eta < 1$ is a constant. Then, the generation after the clone operation is called $Ab_i^{'}(t) = T_C(Ab_i(t))$.

Definition 4 ***The variation operator*** (T_V, P_V) *is defined as:*

$$T_V[X] = [T_V(Ab_i^{'}(t))],\ i = P_V \times K, \tag{6}$$

$$P_V = \begin{cases} P_V^{D_H}(1 - P_V)^{(1-D_H)}, & \text{if } Ab_i^{'}(t) \in Ab_i(t); \\ 0, & \text{if } Ab_i^{'}(t) \notin Ab_i(t), \end{cases} \tag{7}$$

where $D_H = d(Ab_i^{'}(t), Ab_i^{*}(t))$ represents the Hamming Distance of two antibodies. The clone variation operation with probability P_V is carried out on the antibodies generated by the clone operation. The generation of the population after the variation operation is expressed by $Ab_i^{*}(t) = T_V(Ab_i^{'}(t))$.

In order to reserve the information of the original population, the variation operator is only applied to the new antibodies generated by the clone operation.

Definition 5 ***The recombination operator*** (T_R, P_R) *is described as:*

$$T_R(X) = [T_R(Ab_i^{*}(t))],\ i = P_R \times K, \tag{8}$$

$$P_R = \begin{cases} > 0, \textit{ if same numbers 0, 1 in } Ab_i^*(t) \textit{ and } Ab_i^{\#}(t); \\ = 0, \textit{ else}, \end{cases} \tag{9}$$

where $Ab_i^{\#}(t) = T_R(Ab_i^*(t)) \cup T_V(Ab_i^{'}(t))$ *represents the generation after the recombination operation.*

Definition 6 ***The selection operator*** (T_S, P_S) *is described as:*

$$T_S(X) = [Ab_i^{\#}(t) \mid \max f(X) \textit{ or } \mid \min f(X)] \tag{10}$$

$$P_S = \begin{cases} 1, & \textit{if } f(Ab_i^{\#}(t)) > f(Ab_i(t+1)); \\ \exp(\Delta f/a), & \textit{if } \Delta f \geq 0 \textit{ and } Ab_i^{\#}(t) \textit{ not the best antibody}; \\ 0, & \textit{if } \Delta f \geq 0 \textit{ and } Ab_i^{\#}(t) \textit{ is the best antibody}, \end{cases} \tag{11}$$

where $\Delta f = f(Ab_i(t+1)) - f(Ab_i^{\#}(t))$, $a > 0$ *is a value related to the diversity of the antibody population. higher the diversity is, the higher the value of a is.*

Definition 7 ***The terminal criterion*** *E is quantitatively described by a limited number of iterations or the best solution that cannot be improved in a certain number of iterations, or a combination of both. A termination criterion can be:*

$$\mid f^* - f^{best} \mid < \varepsilon; \quad OR: \mid f^* - f^{best} \mid < \varepsilon \mid f^* \mid, \textit{ if } 0 < \mid f^* \mid < 1, \tag{12}$$

where f^* *is the optimal value of the objective function;* f^{best} *is the best value of the objective function in the current generation.*

3. Logic Flow of the HSIEA

From the fundamentals described in the previous section, the logic flow and procedures of the HSIEA can be developed and are shown in Figure 2.

4. Numerical Experimentation

Two benchmark test functions are investigated in this section to demonstrate the HSIEA: Michalewicz's function denoted by f_1 and the rotated hyper-ellipsoid function denoted by f_2:

$$f_1 = \sum_{i=1}^{5} \sin(x_i) \sin\left(\frac{i \cdot x_i^2}{\pi}\right)^{20}, \; x_i \in [0, \pi], \tag{13}$$

$$f_2 = -\sum_{i=1}^{5} \left(\sum_{j=1}^{i} x_j\right)^2, \; x \in [-65.536, 65.536]. \tag{14}$$

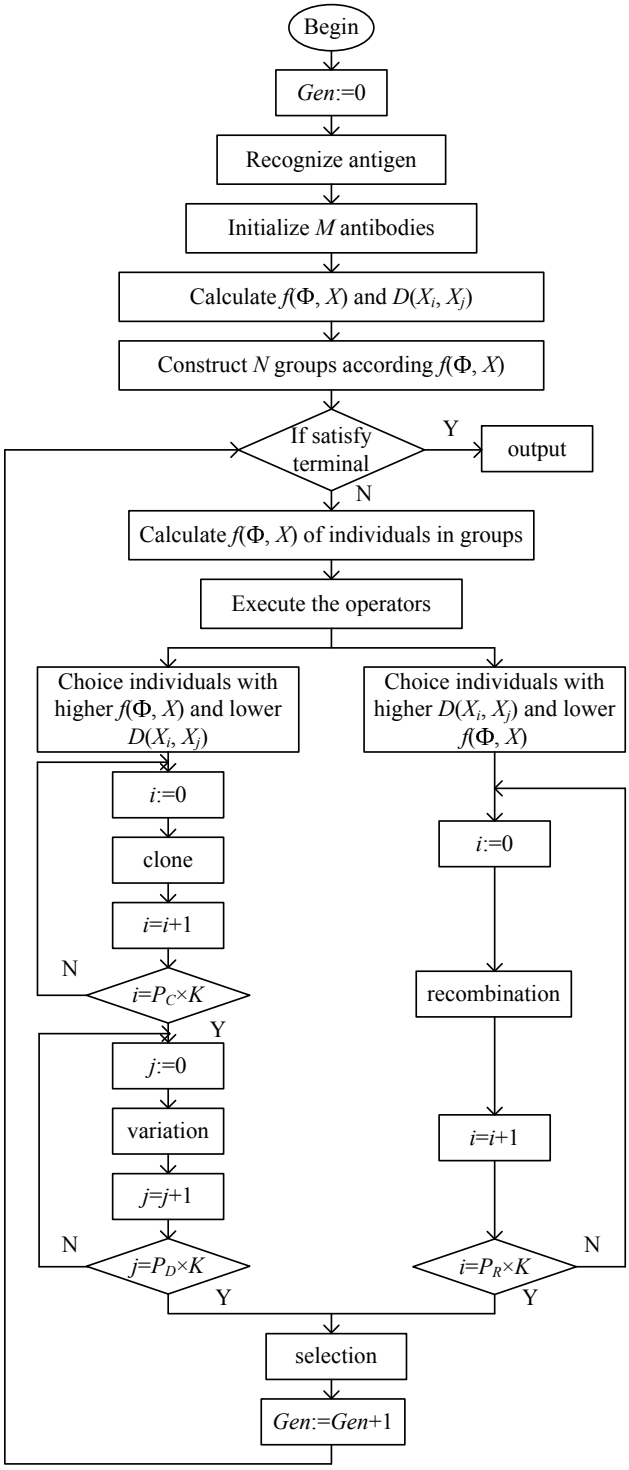

Figure 2. *Flowchart of the HSIEA*

For the Michalewicz's function f_1, there are 5! local optima and the global minimum is $f_{1min} = -4.687$. The rotated hyper-ellipsoid function f_2 has a global minimum $f_{2min} = 0$ at $x_i = 0$, $i = 1, \cdots, 5$.

To make comparisons between the HSIEA and MEA, we consider the convergence speed, the quality of the solution, and the off-line performance [15]: $X_e^*(A) = \frac{1}{T}\sum_{t=1}^{T} f_e^*(Ab_i(t))$, where $f_e^*(Ab_i(t)) = \text{best}\{f_e(Ab_1(t)),\ f_e(Ab_2(t)), \cdots, f_e(Ab_i(t))\}$ is the best object function value or the best affinity at the t^{th} iteration, T is the number of iterations of the algorithm.

In our simulations, the initial number of individuals is set to be $M = 200$. The terminal number of iterations is 100 generations, and the terminal threshold $\varepsilon = 0.0001$. The number of successful optimizations is denoted by N_{TS}, and the number of failures is denoted by N_{TF}, respectively. We have $N_{TS} + N_{TF} = 100$.

The results are summarized in Table 1 and Figures 3 and 4. It is seen from these results that compared with the MEA, the HSIEA not only converges faster but also gives a better solution and off-line performance for both functions.

Table 1. *Results of the HSIEA and MEA (the threshold $\epsilon = 0.0001$).*

Test function	MEA			HSIEA			Real Solution
	N_{TS}	N_{TF}	Solution	N_{TS}	N_{TF}	Solution	
f_1 in (13)	0	100	−4.583	86	14	−4.679	−4.687
f_2 in (14)	0	100	1.296E+1	97	3	4.979E-10	0

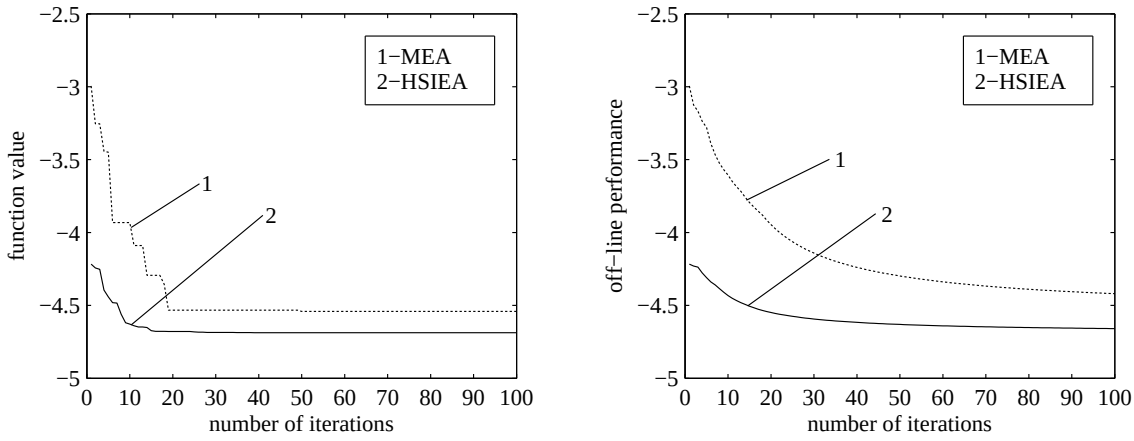

Figure 3. *Optimization of Michalewicz's function in Equation (13).*

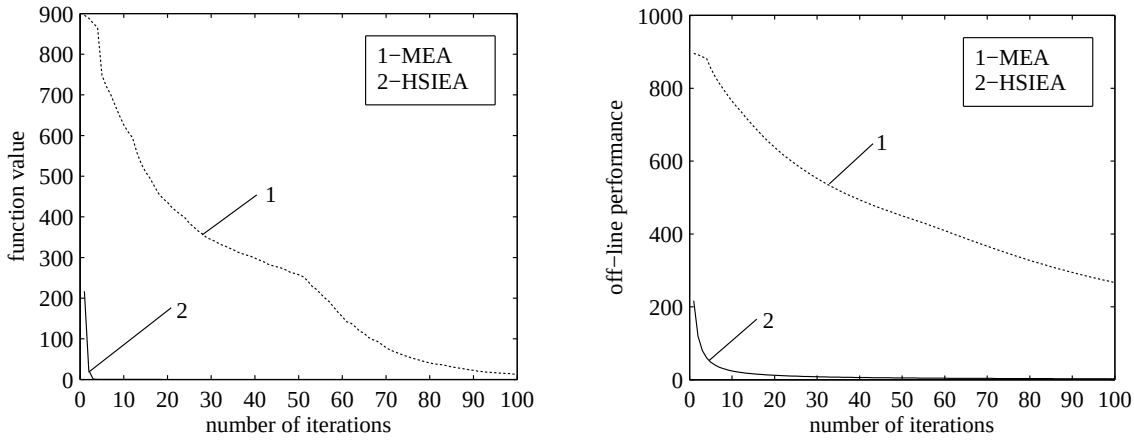

Figure 4. *Optimization of the rotated hyper-ellipsoid function in Equation (14).*

5. Conclusion

A new evolutionary algorithm, the HSIEA, has been developed in this paper. The algorithm inherits the advantages of the MEA method and also introduces the features of the artificial immune systems. Because of the introduction of the clonal selection principle, the HSIEA has used several new evolutionary operations such as antigen recognition, clone, variation, recombination, and selection in comparison with the MEA method. This makes the HSIEA fundamentally different from the MEA and other evolutionary algorithms. The effectiveness of the HSIEA approach has been demonstrated through three benchmark functions.

Acknowledgments.

Author G. Xie would like to thank the National Natural Science Foundation of China for its support under Grant Number 60975032.

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