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A Hybrid Hyper-Mutation Immune Clone Algorithm Based on Antibodies Cluster

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Abstract: Based on the inspiration of immune system, a new multi-objective optimization algorithm is presented. The proposed approach adopts a cluster mechanism in order to divide the antibodies into subpopulations for the stage of selection and reproduction. In the immune clone selection process, a hybrid hyper-mutation operator is introduced to improve the variety of antibodies and affinity maturation, thus it can quickly obtain the global and local optima. The convergence and time complexity of the algorithm is analyzed in this paper. The multi-objective optimization simulation results illustrated that the efficiency of the proposed algorithm and verified it's remarkable quality of the global and local convergence reliability.

Keywords: Hybrid Hyper-Mutation, Cluster, Immune, Optimization

1 Introduction

Many problems in the real world can be formulated as optimization problems, which often have a global optimum and many local optima. An evolution way that inspired form life system modeling was used to solve this questions, such as genetic algorithms. But it also has some deficient like the problems of converges to a local optimum and convergence efficient. Recently, the artificial immune system and its mechanism have come to the researcher's attention to solve engineering problems. De Castro proposed a clonal selection algorithm based on the clone selection principle and the affinity maturation process[1]; Hasegawa proposed a multi-modal search algorithm by combining the immunological features and genetic action [2]; Tsukiyawa designed an improved immune algorithm used in optimization and had good performance [3]; Timmis developed an immune network and hybrid genetic algorithm for Function Optimization[4][5][6]. All this research demonstrate that immune principles can lead to the development of powerful computational tools in real world. In this paper an improved version of the immune algorithm was present, it's realization and performance analysis was introduced. We used it for multi-modal function optimization and the result illustrates that it has a remarkable performance.

2 Algorithm Description

The algorithm is population based, like any typical evolutionary algorithm. Each individual of the population is a candidate solution belonging to the fitness landscape of a given computational problem. We expand the single population to multi-population by performing antibody cluster. In each subpopulation, realize the parallel sub-space search by performing competition clone and selection. We also introduce hybrid mutation, antibody elimination and supplement operators in each subpopulation in order to improve mature progenies and suppress the similar antibodies except the max affinity. Thus the remainder individuals have better fitness than the initial population; finally we

introduce the newcomers which yield a broader exploration of the search space, which can preserve the obtained local solutions from destroyed and expand the search space to find global precise solution .

2.1. Antibody Cluster Process

In general, we define N original population Ab , S is the shape-space and $Ab \in S^{N\times L}$, Thus we can construct the initial cluster as Figure 1.

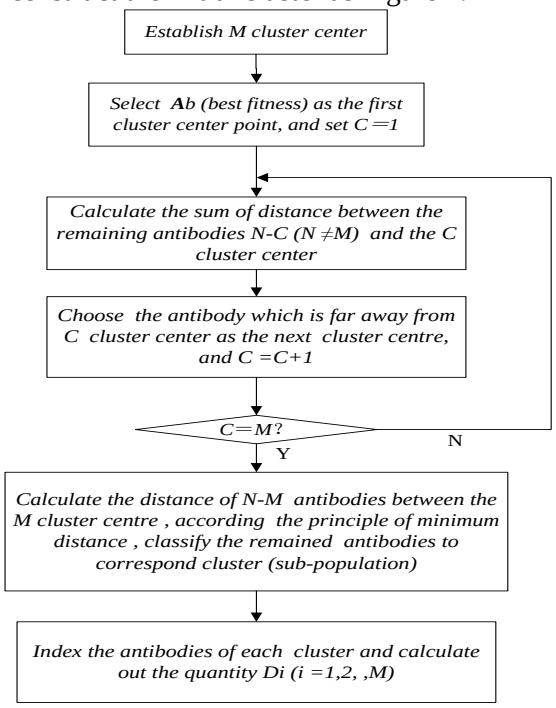


Figure 1: The cluster process of antibodies

After clustering, we can get the antibody group .Each cluster represents a sub-population and has D_i antibodies. So we introduce the competition selection mechanism in each sub-populations and put currently best antibody that has the max fitness and represents the cluster center into elite set. Through those operator, The similar antibodies will be put into the same cluster , which be selected and reproduced in the local elite set to realize the affinity maturation.

2.2. Hybrid Mutation Operators

Hybrid mutation operator, which consist of Gaussian mutation and Cauthy mutation. Traditional Gaussian mutation can making a search in the area surrounding the cell with high probability and has an outstanding ability of local searching, but it is easily to fall down local optimum. In the ability of escaping, Cauthy mutation should be obviously higher than Gaussian's. So adopt a Cauthy mutation to the operator to enhance its global convergence probability.

1. Gaussian mutation operator

$$\begin{aligned} \sigma_i^j &= \sigma_i^j \times \exp(\tau_1 \times \mathrm{N}(0,1) + \tau_2 \times \mathrm{N}_j(0,1)) \\ Ab_i^j &= Ab_i^j + \sigma_i^j \times \mathrm{N}_j(0,1) \\ \tau_1 &= \left(\sqrt{2\times\sqrt{L}}\right)^{-1}, \tau_2 = \left(\sqrt{2\times L}\right)^{-1} \end{aligned} \quad (2.1)$$

Where $\sigma_i = \{\sigma_1, \sigma_2, \cdots, \sigma_L\}$, $i = 1,2,\cdots,N_c$, $j = 1,2,\cdots,L$, parameter σ_i^j is the mutation step of antibody Ab_i^j , τ_1 and τ_2 is the whole step and the individual step respectively.

2. Cauthy mutation operator

$$\begin{aligned} \sigma_i^j &= \sigma_i^j \times \exp(\tau_1 \times \eta(0,1) + \tau_2 \times \eta_j(0,1)) \\ Ab_i^j &= Ab_i^j + s_i^{j\prime} \; h_j(0,1) \end{aligned} \quad (2.2)$$

Where $i = 1,2,\cdots,N_c$, $j = 1,2,\cdots,L$, $\eta(0,1)$ $\eta_j(0,1)$ r epresent the random variable of Cauthy distributing.

2.3. The Distance Between Antibodies

In order to be able to will antibody successfully clustering, need to calculate the distance between the antibodies. This article introduces the information entropy to measure binary coding antibodies distance According to the entropy of the definition, the similar two antibodies are their average information entropy smaller, And both the less similar, both the average information entropy is bigger. So can adopt two antibodies between the average information entropy to define two antibodies, and the distance between the dis_{uv} .

$$dis_{uv} = \frac{1}{L} \sum_{j=1}^{L} \sum_{i=1}^{2} - p_{ij} \log_X p_{ij} \quad (2.3)$$

2.4. Algorithm Realization

In the algorithm, where the single population can be expanded to multi-population with the center of the n initial individuals and realize the parallel sub-space search by performing competition clone and selection. It enhanced the variety of antibody and affinity maturation rate.By performing the hybrid hypermutation on the antibodies, we can find more outstanding antibody with higher probability through the course of affinity maturation. In order to balance the process of exploration and exploitation we suppress the similar antibodies except the max affinity gradually with the iteration. Thus the remainder individuals have better fitness than the initial population. On the other hand, the antibody supplement operation can add newcomers with a certain amount to improve the variety of group of antibodies.

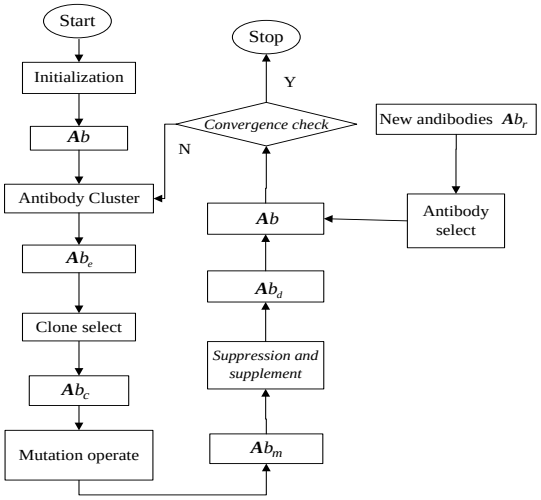


Figure 2: Algorithm Realization

2.5. Algorithm Analysis

The transformation of the states in the algorithm can be described as following stochastic process: where N_s is the new individuals which are added randomly.

$$T: Ab(k) \xrightarrow{cluster} Ab'(k) \xrightarrow{clone} Ab_c(k) \xrightarrow{hybridmutation} Ab_m(k) \xrightarrow[selection]{} Ab_d(k) \cup N_s \xrightarrow[supplement]{suppress} Ab(k+1) \quad (2.4)$$

Markov chain offers an appropriate model to analyze the probability convergence properties. It is obviously that the transformation from the state $Ab(k)$ to $Ab(k+1)$ constitutes a Markov chain. The state $Ab(k+1)$ has nothing to do with the state earlier and depends only on $Ab_d(k) \cup N_s$, So the stochastic process $\{A(n), n \geq 1\}$ is still a Markov chain. The population serial $\{A(n), n \geq 0\}$ of this algorithm is a finite state Markov chain. In the algorithm, the initial population size is n and the antibodies are clustered to m sub-populations. $s_i \in S$, where S_i expresses the number of states in S . f is the fitness function of the variable X, namely $s^* = \{x \in X \mid f(x) = \max f(x)\}$ .So we can defined this algorithm completely convergence with probability one:

$$\lim_{k\to\infty} \sum_{s_i \in s^*} p\{A_k^i\} = 1 \quad (2.5)$$

Proof: Define $p_{ij}(k), (i, j \in I)$ is transfer probability of the stochastic process $\{A(k)\}$, and $I = \{i \mid s^i \in s^*\}$, where

$p_{ij}(k) = p\{A_{k+1}^j / A_k^i\} \geq 0$; namely $p\{A_k^i\}$ is p_i^k, $p_k = \sum_{i\in I} p_i(k)$, by the property of Markov chain we have

$$p_{k+1} = \sum_{s_j \in s} \Big| \sum_{s_i \in s^*} p_i(k) p_{ij}(k) = \sum_{i \in I, j \notin I} p_i(k) p_{ij}(k) + \sum_{i \in I, j \in I} p_i(k) p_{ij}(k)$$

$$\because \sum_{i\in I, j\notin I} p_i(k) p_{ij}(k) + \sum_{i\in I, j\in I} p_i(k) p_{ij}(k) = \sum_{i\in I} p_i(k) = p_k$$

$$\therefore \sum_{i\in I, j\notin I} p_i(k) p_{ij}(k) = p_k - \sum_{i\in I, j\in I} p_i(k) p_{ij}(k)$$

$$\therefore 0 \leq p_{k+1} \leq p_k - \sum_{i\in I, j\in I} p_i(k) p_{ij}(k) \leq p_k \leq 1$$

where we get $P_{k+1} \leq P_k$, we conclude that $\lim_{k\to\infty} p_k = 0$, therefore ,

$$1 \geq \lim_{k\to\infty} \sum_{s_i \in s^*} p_i(k) \geq \lim_{k\to\infty} \sum_{i\in I} p_i(k) = 1 - \lim_{k\to\infty} p_k = 1$$

.

So we can say that this algorithm is completely convergent with probability one .

Because of the antibody cluster operators, the N antibodies of population are divided to M sub-populations. In each local clusters, we can parallel perform clone selection, mutation and suppression operation. The time complexity of the algorithm during each cycle is $O((N+L)\times M \times D^2)$, which the clonal selection and mutation part is $O(D^2)$, the cluster part is $O(M)$, and the similarity suppression part is $O(N+L)$, where N, L is the number of antibodies during one cycle and may be different for each cycle.

3. Experiments

As an illustration, consider the case of the multi-modal function optimization.

$$f_1(x,y) = 0.5 - \frac{\sin^2\sqrt{(x^2+y^2)} - 0.5}{1.0 + 0.001(x^2+y^2)} \quad x,y \in [-10,10] \quad (3.1)$$

$$f_2(x,y) = 1 + x' \sin(4\pi x) - y' \sin(4\pi y + \pi) + \frac{\sin(6\sqrt{x^2+y^2})}{6\sqrt{x^2+y^2} + 10^{-15}}, \quad x,y \in [-1,1] \quad (3.2)$$

Table 1. The basic properties of the test function

Func	Global optimum	Local optima	The value of (x,y) when local global optimum	Number of global /local optima
f_1	1	0.990283	(0, 0)	1/(infinite)
f_2	2.118	2.077	$(\pm 0.64, \pm 0.64)$	4(32)

Table 1 shows the basic properties of this formula to execute the proposed algorithm. f_1 function has a large number of local optima. The global optimum is difficult to find because the value at the best local optimum differs from only about 10^{-3}. As the local optima are not punctual,

they form crowns around the global optimum. From the Figures 3 and 4, we can see that the Immune Clone Algorithm (ICA) in this paper was capable of locating the global maximum of the function and performing a better exploration of search space. The individuals of the population are uniformly spread over the surface of the local optima.

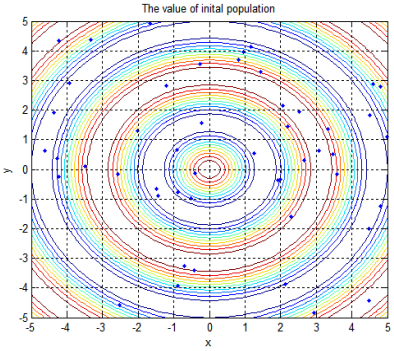


Figure 3: Distribution of the initial population

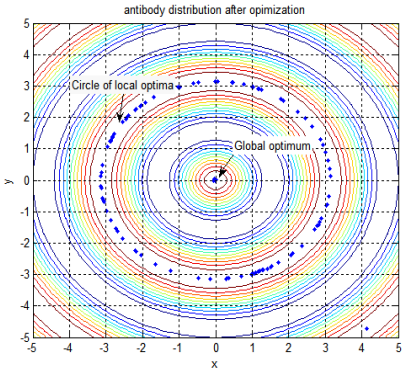


Figure 4: Optimization result after 100 iteration

Since the initial population is created randomly, the result is different in each time. We test the f_1 function repeatedly 30 times by ICA algorithm. where the results were compared to the SGA and AIA algorithm[9][10].

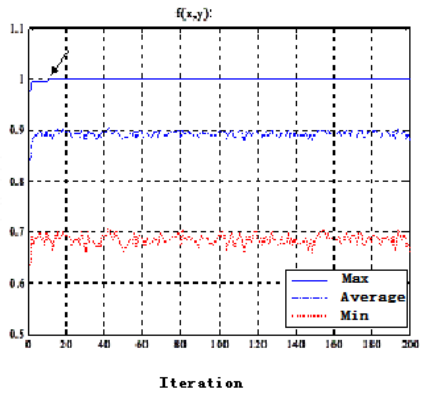


Figure 5: Fitness of the population

To be convenient for comparing, we choose the same number of initial population $N = 100$,the code length of each variable is 22 and the affinity threshold $s = 10^{-3}$. For this algorithm, the other parameters are chosen as following: cluster criterion $M = 15$; clone probability, $P_c = 0.1$; Gauss mutation probability $P_{mg} = 0.8$, Cauth mutation probability $P_{mc} = 0.6$, percentage of newcomers $P_n = 0.4$.

Table 2. The results of three algorithm

Algorithm	It	Ntrap	NIavg	NIl	NIm	threshold
SGA	200	23	173.9	134	197	10^{-3}
AIA	200	6	110.4	47	195	10^{-3}
ICA	200	0	43.2	16	77	10^{-3}

Note: It: Iterations;
Ntrap: Nomber of trap into local optima;
NIavg: Average iterations local global optimum;
NIl: The least iterations local global optimum;
NIm: The most iterations local global optimum

From table 2 we can learn that ICA has 100% convergence probability in 30 times, and the least number of iterations to local global optimum is 16 .Note that the algorithm proposed, on average, requires less number of iterations to local the global optimum than the SGA and AIA. As shown in Figure 6, f_2 was used to evaluate the performance of ICA compared to that of SGA[9] . It can see from Figure 7 that there are less peaks can be located by SGA algorithm. Moreover, most of them gather around some peaks with larger fitness. This leads to the premature convergence. Differently, the ICA algorithm is able to obtain a set of optimal solutions including the local optima and global optima. It is demonstrated that the solutions obtained by ICA have a better diversity than the SGA. As a result, the ICA can search for multiple quasi-optimal solutions simultaneously. It can be observed that ICA determined the global optimum faster than SGA from Figure 8. And also, that the SGA did not converge for the 90 iterations. But ICA got the global optimum after 50 iterations and got all the local peaks.

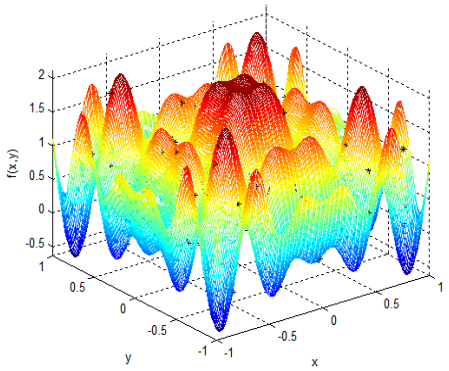
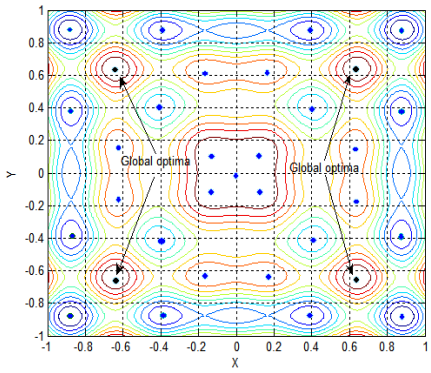
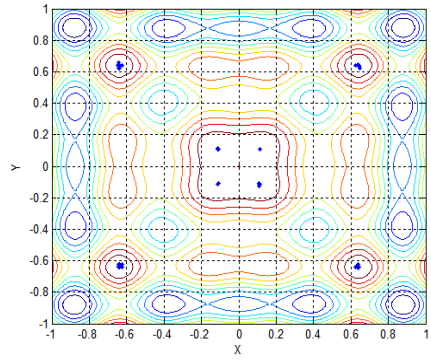


Figure 6: Distribution if the initial population



(a: ICA)



(b: SGA)

Figure 7: Optimization result after 100 iteration

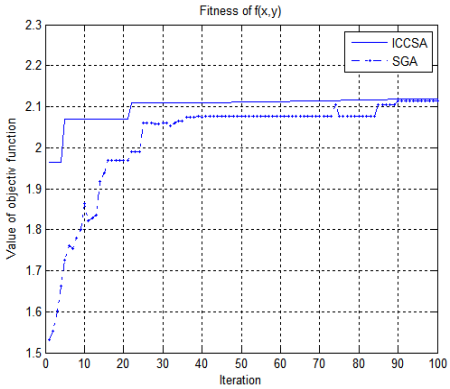


Figure 8: Fitness and final number of individuals in the population(Solid line: ICA; Dash line: SGA)

4. Conclusion

This paper proposed a modified version of immune clonal algorithm to solve multi-modal function optimization . In this work, a mechanism of cluster was introduced in the clonal selection process. Additional, compete expansion, clonal elimination, antibody hyper mutation and supplement operators were adopted to quickly obtain the global optimum and local optimum. It enhanced the variety of antibody and affinity maturation. Applied this algorithm in complicated function optimization and verified it has a remarkable quality of the global and local convergence reliability and convergence velocity. Demonstrate that these biological principles can lead to the development of powerful computational tools in real world.

Acknowledgements

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