A Modified Immune Network Optimization Algorithm

Lu Hong, Joarder Kamruzzaman

***Abstract*— This study proposes a modified artificial immune network algorithm for function optimization problems based on idiotypic immune network theory. A hyper-cubic mutation operator was introduced to reduce the heavy computational cost of the traditional opt-AINet algorithm. Moreover, the new symmetrical mutation can effectively improve local search. To maintain population diversity, we also devised an immune selection mechanism based on density and fitness. The global convergence of the algorithm was deduced through the method of pure probability and iterative formula. Simulation results of benchmark function optimization show that the modified algorithm converges more effectively than other immune network algorithms.**

***Index Terms*—Artificial immune algorithm, Idiotypic immune network, Hyper-cubic mutation, Convergence**

I. INTRODUCTION

BIOLOGICAL immune systems has the ability of learning, memory and recognition antigen, and the characteristics of adaptive, distributed and diversity. Inspired by biological immune mechanism, a variety of artificial immune algorithms have been developed to solve problems in machine learning, fault diagnosis, system modeling, computer security, and other fields of engineering [1]–[2]. Artificial immune algorithm is an optimization search algorithm that is bionic and intelligent. It imitates biological immunology and the mechanism of gene evolution. At present, proposed immune algorithms mainly include clonal selection algorithm, negative selection algorithm, and immune network algorithm [3]–[4]. The immune network algorithm is based on immune network theory and is generally represented by the opt-AINet algorithm, which was proposed by De Castro in 2002 [5]. This algorithm was inspired by idiotypic network theory and can describe some of the dynamic characteristics of the immune system. Moreover, it possesses several unique features, including dynamically varied population sizes, local and global search, and the capability to maintain any number of optima. Thus, this algorithm is among the most widely applied artificial immune optimization methods in problems of pattern recognition and multimodal optimization. However, the immune network algorithm is limited with respect to large-scale complicated optimization problems, including additional parameters, heavy computational cost, sensitivity to population size, and slow convergence rate. Furthermore, the algorithm does not fully reflect the regulation mechanism of immune networks, and it is rarely analyzed in terms of mathematical theory [6–7].

In the current study, we present a modified immune network algorithm (MINA) based on opt-AINet. This algorithm evaluates objective functions without negating the valuable characteristics of the original algorithm. We also introduce a hyper-cubic cloning mutation operator and a specific immune selection mechanism. The globle convergence of the algorithm is deduced by adopting the pure probability and iterative formula method. MINA is then compared with other immune network algorithms to verify its effectiveness.

The paper is structured as follows. The basic principle of idiotypic immune network theory is presented in Section 2. The design scheme of the MINA for optimization is detailed in Section 3. The globle convergence of the modified algorithm are discussed in Section 4. The experimental results for a set of test functions and the comparisons with other algorithms are explained in Section 5. Finally, conclusions and recommendations for future research are provided in Section 6.

II. IDIOTYPIC IMMUNE NETWORK THEORY

In 1974, Jerne introduced idiotypic immune network theory [9], which asserts that antibodies in the biological immune system have the uniqueness of being recognized by other antibodies. The uniqueness of antibodies can be seen as an epitope, and its role is to be recognized by other antibodies. Moreover, antibodies are identified by antigens through the receptors on the surface of the antibodies, which are called paratopes. Thus, antibodies can recognize one another and form an idiotypic immune network, as shown in Fig. 1.

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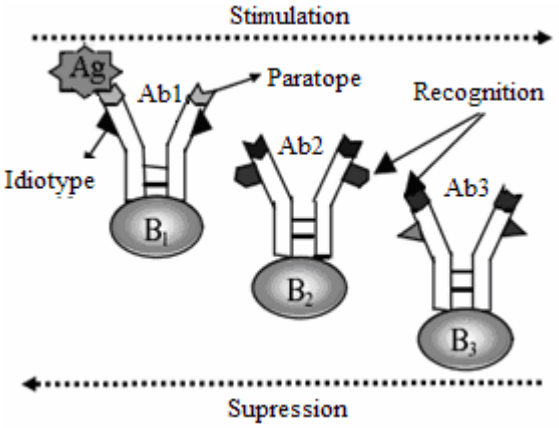

Fig. 1. The principle of idiotype immune network.

Antibodies can recognize not only external invasive antigens, but also other antibodies. However, antibodies are suppressed during recognition, and the interaction network within the immune system reaches a dynamic equilibrium. Hence, the stimulation level of B cells (antibodies) not only depends on the affinity between the antibody and the antigen but also on the matching degree between antibodies. If stimulation levels exceed a certain threshold, the B cells produce new antibodies through cloning and super mutation. Otherwise, these cells die immediately and are replaced by those produced in the marrow. Thus, the mutation rate of an antibody is inversely proportional to its fitness during mutation. In particular, the mutation process of antibodies involves a continuous enhancement in affinity and a gradual maturation. These characteristics of immune network not only maintain the diversity of the antibody population effectively but also facilitate self-organization and regulation in the biological immune system [10]–[11].

III. Modified Immune Network Algorithm

In 2002, De Castro and Von Zuben proposed the opt-AINet network model [5]. Briefly, opt-AINet is an incomplete weighted connection diagram. This algorithm was originally intended for data mining, pattern recognition, and multimodal optimization [12]; it can perform local and global searches and adjust population size dynamically. Specifically, this algorithm conducts local searches based on cloning, mutation, and antibody selection. It performs global exploration by inserting random points and modifying population size.

The performance levels of opt-AINet and other algorithms were compared in [13]. The results show that opt-AINet successfully determined the global optimum of the test functions used but that the required computational cost was much higher than those of the other algorithms. The study concluded that this heavy computational cost may be related to population increase. However, the possibility that the exploration of local optima causes population growth has not been studied further [14].

Hence, the current study proposes a modified MINA to reduce computational cost and to improve the convergence of opt-AINet in processing problems related to complicated function optimization.

The MINA algorithm is designed in detail as follows:

(1) Chaotic Initialization: An initial population of N antibodies should be generated using the logistic formula.

(2) When the stopping criterion is unsatisfied,

(2.1) Fitness calculation: The fitness of each antibody should be calculated.

(2.2) Antibody clone: Clones should be generated for each antibody.

(2.3) Antibody mutation: Each clone mutates with the aid of the hyper-cubic mutation operator. The parent antibody is retained.

(2.4) Clonal selection: N cells with maximum fitness from N mutation sets are selected from each clone set based on density and fitness for the next generation. The ideal n antibodies are copied to the memory set.

(2.5) Immune suppression: The antibody with a poor fitness value is deleted as determined according to Euclidean distance and the fitness difference between two antibodies. The antibody with an improved fitness value is preserved in the memory set.

(2.6) Immune replacement: d antibodies with poor fitness values are replaced with new, randomly generated members with high fitness values (diversity introduction).

(2.7) The best antibody is determined from the memory set before proceeding to step 2.

The main operators of MINA are detailed as follows:

A. Chaotic Initialization

To reflect the chaotic nature of the biological immune system and to generate the initial population, we adopt a chaotic initialization operator. L chaotic variables are computed using the following logistic formulas:

$$x_k^{n+1} = \mu x_k^n \left(1 - x_k^n\right), \; x^n \in [0,1]. \tag{1}$$

Where $k = 1, 2, \ldots, L$, $n = 1, 2, \ldots, N-1$ and $\mu = 4$. k is the serial number of chaotic variables. We assume that $n = 0$ and that the L chaotic initial values x_k^0 vary randomly. The values of L chaotic variables x_k^n are then calculated using the logistic equation. The other $N-1$ antibodies are obtained in the same manner.

B. Antibody Clone

The opt-AINet algorithm is very sensitive to the change of the number of clones. Therefore, each individual in the antibody population is cloned to a fixed number. Each antibody then possesses $2n$ clones that are equally displaced over each dimension. n denotes the number of dimensions.

C. Hyper-cubic Mutation

To increase the probability of exceeding the local optimum, a hyper-cubic mutation operator is introduced into the algorithm [15]. The mutation operation in Step 2.3 is conducted using the following method:

Each individual antibody copies two clones for each problem dimension. These clones are symmetrically displaced from the original antibody under distance k .

$$k = 0.01 * \exp\left(-f^*\right)\left(1 + Gauss(0,1)\right), \tag{2}$$

where f^* is the normalized fitness of the original antibody, and $Gauss(0,1)$ is the random Gaussian variable. The clones are evaluated over the objective function, and the ideal point from each dimension is determined to estimate

the ideal hypercube vertex as defined by the $2n$ clones. An additional clone is generated from the estimated best value, as depicted in Fig. 2.

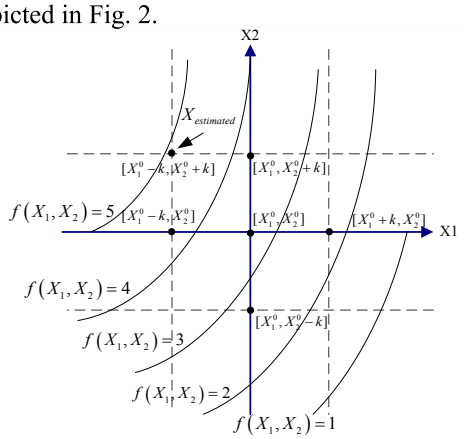

Fig. 2. Hyper-cubic maturation and best vertex estimation for a two-dimensional maximization problem

Therefore, the number of clones for each subpopulation is no longer a random parameter. However, it is fixed at $2n+1$.

D. Immune Selection

The principle of idiotypic networks suggests that B cells are stimulated and suppressed not only by non-self antigens but also by other interacted B cells, according to Jenre [9]. To maintain population diversity, we introduce a new selection mechanism based on density and fitness into MINA.

The affinity between two antibodies can be defined as follows:

$$\begin{cases} ED(X_i, X_j) = \sqrt{\sum_{k=1}^{L}(X_{ik} - X_{jk})^2} \le \varepsilon \\ \left| f(X_i) - f(X_j) \right| \le \omega \end{cases}. \quad (3)$$

Where $f(X_i)$ and $f(X_j)$ represent the fitness values of antibodies X_i and X_j, respectively; ε and ϖ are positive threshold values; and $ED(\cdot)$ corresponds to the Euclidean distance. If Equation (3) is satisfied, the two antibodies are similar. The density (D_i) of antibody X_i can be defined with the following equation:

$$D_i = \frac{Sim(X_i)}{N}. \quad (4)$$

Where $Sim(X_i)$ is the number of antibodies similar to X_i and N is the population size of the antibody.

Based on the activation and suppression regulations of antibodies in the immune system, the selection probability of individual X_i can be defined as follows:

$$p(X_i) = \frac{f(X_i)\exp\left(-\frac{D(X_i)}{\upsilon}\right)}{\sum_{j=1}^{N} f(X_j)\exp\left(-\frac{D(X_j)}{\upsilon}\right)}. \quad (5)$$

Where υ is the regulation factor; $D(X_i)$ is the density of antibody X_i ; and $f(X_i)$ is the fitness value of antibody X_i.

The formula reflects the uncertainty of antibody selection and of the dynamic adjustment mechanism of idiotypic immune network theory. Therefore, MINA can not only maintain the high affinity between individuals, but it also generates a diverse population.

IV. Convergence Analysis of MINA

Convergence result obtained by traditional Markov chain model generally refers to the corresponding Markov chain tending to a stationary distribution. Moreover, it differs from the general definition of convergence in optimization [16]. Furthermore, the Markov chain typically undergoes numerous states. As a result, the performance of the transition matrix is very difficult to analyze. To simplify the algorithm considerably, we substitute traditional ergodic analysis with the method of pure probability and an iterative formula in the global convergence analysis of MINA.

For convenience, some parameters are defined as follows:

Ω : Antibody space

$S = \Omega^N$: Population space

$P(\bullet)$: Probability distribution

$\Gamma_t : \Omega^N \to \Omega^N$: Operator of MINA

$\vec{X}(t) = \Gamma_t\left(\vec{X}(t-1)\right)$: Markov chain of MINA in space Ω^N

$M = \{X; \forall Y \in S, f(X) \ge f(Y)\}$: Global optimal set

Some terms are formally defined as follows:

Definition 1. If sequence $\left\{\vec{X}(t), t \ge 0\right\}$ is the probability convergent to the global optimal solution set, then $\lim_{t\to\infty} P\left\{\left[\vec{X}(t) \cap M \ne \varnothing\right]\right\} = 1$ and we denote $\vec{X}(t) \to M\,(P.W)$.

Based on the previous analysis, MINA can be described as a random search sequence $\left\{\vec{X}(t), t \ge 0\right\}$ and expressed as follows:

$$\vec{X}(t+1) = T_r T_s\left(T_m\left(\vec{X}(t)\right) \oplus \vec{X}(t)\right) T_g^d(\Omega). \quad (6)$$

Where T_r is the immune suppression operator; T_s is the immune selection operator; T_m is the hyper-cubic mutation operator; and T_g^d is the immune replace operator.

Let

$$\begin{cases} \alpha_t^M = P\left(\vec{X}(t+1) \cap M = \varnothing \mid \vec{X}(t) \cap M \ne \varnothing\right) \\ \beta_t^M = P\left(\vec{X}(t+1) \cap M \ne \varnothing \mid \vec{X}(t) \cap M = \varnothing\right) \end{cases}.$$ We can then generate the following theorem.

Theorem 1. If sequences $\{\alpha_t^M\}$ and $\{\beta_t^M\}$ satisfy the following properties:

(1) $\sum_{t=1}^{\infty} \beta_t^M = \infty$; (2) $\lim_{t\to\infty} \frac{\alpha_t^M}{\beta_t^M} = 0$,

then the random sequence $\left\{\vec{X}(t), t \ge 0\right\}$ is probability convergent to the satisfied solution set M. We then determine $\lim_{t\to\infty} P\left(\vec{X}(t) \cap M \ne \varnothing\right) = 1$. Given the space limitations, we do not prove this theorem in this paper; rather, we will discuss the proof in our full-length paper.

According to Theorem 1, the convergence of sequence $\left\{\vec{X}(t), t \geq 0\right\}$ and parameters α_t^M and β_t^M are very closely related.

To confirm the probability convergence of MINA, we must generate the following:

$\forall \vec{X}(t), \vec{Y}(t) \in S$, $\exists \sigma > 0$. We then obtain

$$r_t^* = \min\left(P\left(T_m\left(\vec{X}(t) \to \vec{Y}(t)\right)\right)\right) > \sigma > 0, \quad (7)$$

where r_t^* is the minimum mutation rate.

Theorem 2. For any initial distribution, MINA converges to global optimal solution set M in probability.

Proof. Let $\vec{X}(t) = \{X_i, 1 \leq i \leq N\}$ represent the antibody population at generation t and let X_N denote the best individual. At generation $t+1$, we obtain

$$\vec{X}(t+1) = \{Y_i, 1 \leq i \leq N\} = \left\{\vec{Y}_1, Y_{N-d}, \vec{Y}_2\right\}.$$

Where $\vec{Y}_1 = \{Y_1, Y_2, \cdots, Y_{N-d-1}\}$, $Y_{N-d} = X_N$, and $\vec{Y}_2 = T_g^d(S) = \{Y_{N-d+1}, Y_{N-d+2}, \cdots, Y_N\}$.

Hence,

$$P\left(\vec{X}(t+1) = \vec{Y} \mid \vec{X}(t) = \vec{X}\right) = \begin{cases} P\left(T_r T_s\left(T_m\left(\vec{X}\right) \oplus \vec{X}\right) = \vec{Y}_1\right) \circ P\left(T_g^d(\Omega) = \vec{Y}_2\right), & Y_{N-d} = X_N \\ 0, & Y_{N-d} \neq X_N \end{cases}. \quad (8)$$

Two cases must be considered with regard to state transition probability:

(1) If $\vec{X} \cap M \neq \varnothing, \vec{Y} \cap M = \varnothing$, we derive $P\left(\vec{X}(t+1) = \vec{Y} \mid \vec{X}(t) = \vec{X}\right) = 0$ from Equation (8). Then

$$P\left(\vec{X}(t+1) \cap M = \varnothing \mid \vec{X}(t) \cap M \neq \varnothing\right) = \sum_{\vec{X} \cap M \neq \varnothing} \sum_{\vec{Y} \cap M = \varnothing} P\left(\vec{X}(t+1) = \vec{Y} \mid \vec{X}(t) = \vec{X}\right) = 0. \quad (9)$$

(2) If $\vec{X} \cap M = \varnothing, \vec{Y} \cap M \neq \varnothing$, we obtain

$$P\left(T_g^d(\Omega) = \vec{Y}_2\right) \geq \left(\frac{|M|}{|\Omega|}\right)^d \quad (10)$$

$$P\left(T_r T_s\left(T_m\left(\vec{X}\right) \oplus \vec{X}\right) = \vec{Y}_1\right) = r_t^* \bullet \sum_{\vec{Z} \in S^N, \vec{Y}_1 \subset (\vec{Z} \oplus \vec{X})} P\left(T_s(\vec{Z} \oplus \vec{X}) = \vec{Y}_1\right). \quad (11)$$

If $\vec{Y}_1 \subset (\vec{Z} \oplus \vec{X})$, then

$$P\left(T_s(\vec{Z} \oplus \vec{X}) = \vec{Y}_1\right) = \prod_{Y_1 \in \vec{Y}_1} \frac{f(Y_1) e^{-\frac{D(Y_1)}{\upsilon}}}{\sum_{W \in (\vec{Z} \oplus \vec{X})} f(W) e^{-\frac{D(W)}{\upsilon}}} \geq \left(\frac{1}{N} e^{-\frac{1}{\upsilon}}\right)^{N-d-1}. \quad (12)$$

Based on Equations (7), (8), (10), and (11), we can obtain

$$P\left(\vec{X}(t+1) = \vec{Y} \mid \vec{X}(t) = \vec{X}\right) \geq \sigma \bullet \left(\frac{|M|}{|\Omega|}\right)^d \bullet \left(\frac{1}{N} e^{-\frac{1}{\upsilon}}\right)^{N-d-1} \equiv \varsigma \left(0 < \xi \leq 1\right). \quad (13)$$

Hence,

$$P\left(\vec{X}(t+1) \cap M \neq \varnothing \mid \vec{X}(t) \cap M = \varnothing\right) \geq P\left(\vec{X}(t+1) = \vec{Y} \mid \vec{X}(t) = \vec{X}\right) \geq \varsigma. \quad (14)$$

The proof is completed with Equations (7), (9), and (14).

V. Simulation and Results

To verify the convergence performance of MINA, we test the following three complex multimodal functions. The results are compared with those of traditional opt-AINet [5] and the novel immune clonal algorithm (NICA) [17].

(1) Levy No. 3 f_1:

$$f(x_1, x_2) = \sum_{i=1}^{5} i \cos\left[(i+1)x_1 + i\right] \times \sum_{j=1}^{5} j \cos\left[(j+1)x_2 + j\right]$$

$$-10 < x_1, x_2 < 10.$$

This function contains approximately 760 local minima and 18 global minima with the ideal function value $f^* = -176.542$.

(2) Levy No. 8 f_2:

$$f(x) = \sin^2(\pi y_1) + \sum_{i=1}^{n-1} (y_i - 1)^2 \left[1 + 10\sin^2(\pi y_{i+1})\right] + (y_n - 1)^2.$$

Where $y_i = 1 + \frac{x_i - 1}{4}$, $-10 \leq x_i \leq 10$, and $i = 1, 2, ..., n$. When $n = 3$ and $x^* = (1,1,1)^T$, the global minima is $f^* = 0$. Under this condition, we can obtain approximately 125 local minimum values.

(3) Levy No. 10 f_3:

$$f_3(x) = \sum_{i=1}^{n} \frac{x_i^2}{4000} - \prod_{i=1}^{n} \cos\left(\frac{x_i}{i^{1/2}}\right) + 1.$$

Where $n = 10$ and $x_i \in [-600, 600]$. Using this formula, we can conduct a complex high-dimensional test function and increase the number of local extreme values with the growth in problem dimension. When $x^* = (0, 0, \cdots, 0)$, the global minimum is $f^*(x) = 0$.

In all of the experiments, the parameters of MINA are chosen as follows:

$N = 100$, $\varepsilon = 0.01$, $\omega = 0.02$, $\mu = 4$, $\nu = 2$, $d = 20$. For opt-AINet and NICA, we follow the parameters in [5] and [17].

The experiments were run 30 times using MINA, NICA, and opt-AINet on each test function. We present the average performance in terms of mean value, computational time, and the percentage of successful convergence. Table I illustrates the performance levels of the three algorithms, and Fig. 3 compares the convergence results of the functions using these three algorithms.

TABLE I.
PERFORMANCE COMPARISON RESULTS OF THE THREE ALGORITHMS

	opt-AINet			NICA			MINA		
	Mean	Time(s)	Conv%	Mean	Time(s)	Conv%	Mean	Time(s)	Conv%
f_1	-172. 466	4.55	95	-175.220	3.64	96	-176.542	2.44	100
f_2	2.54×10^{-4}	8.28	90	6.57×10^{-6}	5.09	94	0	3.75	100
f_3	4.46×10^{-4}	14.33	86	2.49×10^{-5}	9.25	91	1.79×10^{-7}	6.83	96

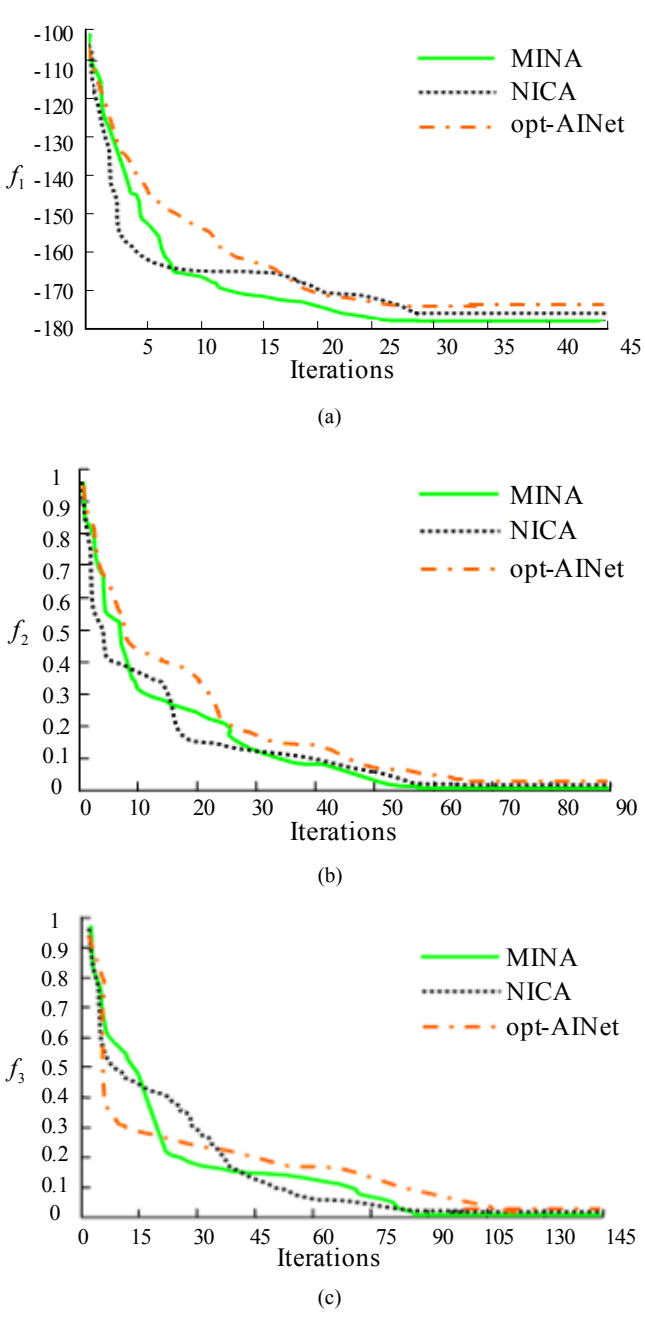

Fig. 3. Comparisons of convergence results using MINA, NICA, and opt-AINet

Table I presents the simulation results for MINA, NICA, and opt-AINet. These algorithms can generate the global maximum values of the three functions; however, MINA explores the search space more effectively than the other two algorithms. Moreover, it can detect almost all of the peaks of the functions at a faster convergence rate than the other two algorithms. MINA converged after 26, 55, and 88 iterations of the functions f_1, f_2 and f_3 respectively.

This finding can be attributed to hyper-cubic mutation and the use of the new immune selection operator. The former reduces the computational cost of the network algorithm, whereas the latter maintains population diversity and enhances global search capability. Hence, MINA can effectively solve complex problems of multimodal optimization.

VI. CONCLUSIONS

This study proposed a modified artificial immune network algorithm (MINA) based on idiotypic immune network theory for multi-modal optimization. This algorithm mainly differs from the original opt-AINet algorithm with respect to hyper-cubic mutation and the immune selection mechanism based on density and fitness. The modified algorithm not only retained the unique characteristics of opt-AINet, but it also considerably reduced the number of objective function evaluations required during optimization. The global convergence of the algorithm was deduced using the method of pure probability and iterative formula. MINA was applied to several test functions, and the results indicated that MINA can escape from the neighborhoods of local minima and can effectively locate the global optimum. However, the ideas and the algorithm proposed in this paper remain under development and further analysis and applications will be addressed in our future work.

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