

Convergence of Elitist Clonal Selection Algorithm Based on Martingale Theory

Lu Hong, Joarder Kamruzzaman

Abstract—In recent years, progress has been made in the analysis of global convergence of clonal selection algorithms (CSA), but most analyses are based on the theory of Markov chain, which depend on the description of the transition matrix and eigenvalues. However, such analyses are very complicated, especially when the population size is large, and are presented for particular implementations of CSA. In this paper, instead of the traditional Markov chain theory, we introduce martingale theory to prove the convergence of a class of CSA, called elitist clonal selection algorithm (ECSA). Using the submartingale convergence theorem, the best individual affinity evolutionary sequence is described as a submartingale, and the almost everywhere convergence of ECSA is derived. Particularly, the algorithm is proved convergent with probability 1 in finite steps when the state space of population is finite. This new proof of global convergence analysis of ECSA is more simplified and effective, and not implementation specific.

Index Terms—Clonal selection algorithm; Elitist strategy; Martingale theory; Almost everywhere convergence

I. INTRODUCTION

ARTIFICIAL immune algorithm (AIS) inspired by biological immune mechanism is a new intelligent computation for solving complex problems. AIS has become a new leading edge research direction after the artificial neural networks, fuzzy systems, evolutionary computation [1]-[3]. Clonal selection algorithm (CSA) is one of the most popular and important algorithms in AIS. Consequently it has attracted growing interest of computational intelligence experts and scholars. Currently, the studies of CSA have revealed many interesting findings, but these results are mainly focused on algorithmic implementations, improvements and engineering applications, but the theoretical research exploring the characteristics of CSA and its convergence behavior is yet inadequate [4]. To assess whether an algorithm can effectively solve a class of problems, one must first start from convergence analysis. An algorithm has no practical value if the algorithm is not guaranteed to converge or not convergent within acceptable

computation time [5].

Existing convergence conclusions of CSA were mainly derived from the Markov chain and the ergodicity of mutation operators when the time tends to infinity, and basically were convergence in probability [6]. There are direct, accurate advantages when using Markov chain model to describe the evolution process of algorithms [7]. Though CSA described by Markov chain model has those advantages, due to the limitations of finite state Markov chain theory, the model can only be used for the description of the usual binary or special non-binary clonal selection algorithm. In addition, the convergence results obtained by these methods generally refer to the corresponding Markov chain that tends to follow a stationary distribution, which is different from the common convergence defined in optimization area. Moreover, it does not guarantee that the algorithm will necessarily be convergent with probability 1 to the global optimal solution [8]. Perhaps even greater limitation of those studies lies in the fact that they were established on the basis of particular implementations of the CSA, or discussed in a relatively weak sense of convergence. They belong to the weak law of large numbers category, and the means and methods of analysis have considerable limitations. The universal proof of clonal selection algorithm convergence theory has not yet been offered [9].

To improve the performance of CSA in terms of better convergence behavior and solution, many researchers have proposed elitist selection strategy for generating new population during the evolution process. Such class of CSA algorithms is known as elitist clonal selection algorithm (ECSA), which is the most widely used CSA in the current literature. In this paper, instead of the traditional Markov chain theory, we employ martingale theory to study the convergence of ECSA. The best individual affinity evolutionary sequence is transformed into a submartingale. Based on the submartingale convergence theorem, the almost everywhere convergence of the ECSA is analyzed. Our proof of convergence is valid irrespective of any particular implementation of ECSA.

The paper is structured as follows. The basic principles of clonal selection mechanism and the design scheme of the elitist clonal selection algorithm are presented in Section 2. In Section 3, the definitions of almost everywhere convergence and submartingale convergence theorem are introduced. After that, the submartingale theory proof method to ECSA and our main results are proposed. Finally, the conclusions and some possible work for future research are presented in Section 4.

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II. ELITIST CLONAL SELECTION ALGORITHM (ECSA)

Clone selection principle is one of the best-known mechanisms of biological immunology [10]. The basic idea of the algorithm is that antigens are required as objective function, and antibodies as the possible models of function optimization solutions. The affinity of the antibody and antigen corresponds to the function value of feasible solution. Only those cells recognizing antigens will be clonal expanded and selected relative to those not recognize the antigens. Those selected cells are subject to affinity maturation process. Clonal selection algorithm itself has these characteristics, which suggest that the algorithm has great potential for a variety of optimization problems and can be expected to be widely used in the field of optimization [11].

Clonal selection algorithm based on this mechanism has been widely used in many areas of optimal control, data processing, intrusion detection and fault diagnosis, and has become another research focus in the artificial immune computation. The CLONALG algorithm proposed by De Castro in 2002 is a typical clonal selection algorithm in recent years [12], which marks the beginning of intelligent algorithm based on immune mechanism to solve the optimization problem. Since then, the researchers proposed a wide variety of clonal selection algorithms from different angles of clone selection principle, most of which were based on the elitist remains strategy [13]-[17]. The antibody with highest affinity in current population does not participate in cloning and mutation operations, and directly replace the one with the lowest affinity after these operations. This strategy is the basic condition to ensure the convergence of an algorithm.

For convenience, the basic steps of a class of elitist clone selection algorithm are given in details.

Step 1. $i = 0$, Randomly generating an initial set of antibodies $\vec{X}(0) = \{X_1, X_2, \dots, X_N\}$, the length of the antibody is L , binary coded, the number of antibodies is N ;

Step 2. Calculating each antibody's affinity $f(X_i)$ in the antibody set $\vec{X}(i)$.

Step 3. Selecting the antibody with highest affinity in $\vec{X}(i)$, and sending it directly into the next generation and replace the antibody with the lowest affinity;

Step 4. Conducting cloning operation, mutation operation to the remaining $N - 1$ antibodies in $\vec{X}(i)$ and generating a new antibody set $\vec{X}(i+1)$.

Step 5. Generating d new antibodies randomly, and replacing d antibodies with lowest affinity in $\vec{X}(i+1)$.

Step 6. $i = i + 1$, Repeating Step (2) - (6), until the end condition is met.

The flow chart of elitist clone selection algorithm is given in Fig 1.

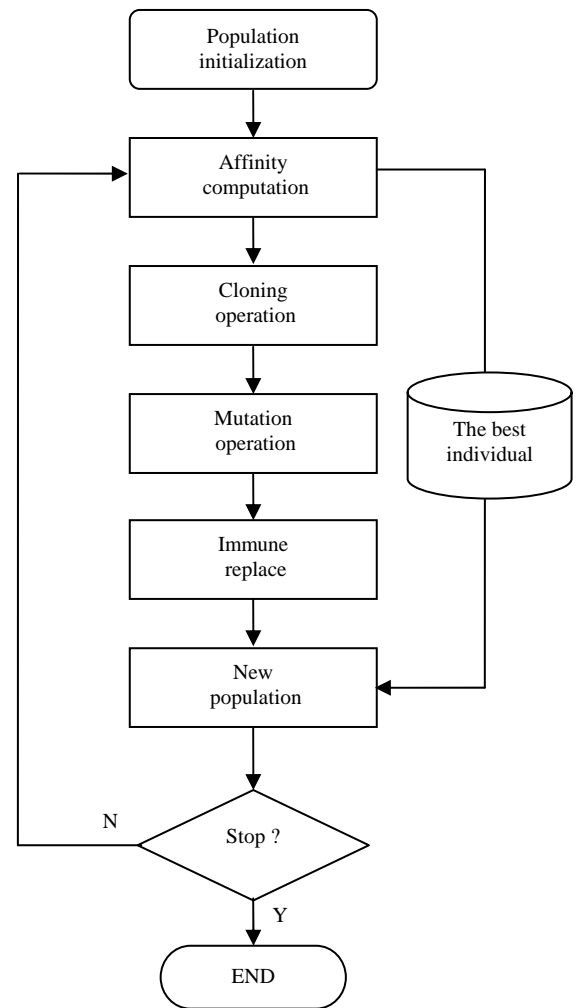


Fig.1 Flow Chart of Elitist Cloning Selection Algorithm

III. ALMOST EVERYWHERE CONVERGENCE ANALYSIS OF ECSA

We substitute traditional ergodic analysis, by using stochastic processes martingale theory, whereby the martingale characteristic of the best individual affinity of the population is analyzed and the almost everywhere convergence of ECSA is deduced. Furthermore, it is proved that the algorithm is global convergent with probability 1 in a finite number of steps when the state space is finite. This method offers a new tool for theoretical analysis of clonal selection algorithm [18].

Let $\vec{X}(t)$ be the population at generation t , and S be the state space of antibody. The best individual affinity of the population $\vec{X}(t)$ is denoted by $f^*(\vec{X}(t))$. The global optimal set is denoted by $M = \{f^*; \forall X \in S, f^* \geq f(X)\}$.

Let us give the formal definition of some terms as follows:

Definition 1: The sequence $\{X(t), t \geq 0\}$ is almost everywhere convergence, if and only if

$$P\left\{\lim_{t \rightarrow \infty} \left[f^* \left(\bar{X}(t) \right) \subset M \right] \right\} = 1.$$

Definition 2: Let $\{X(t), t \geq 0\}$ be a stochastic sequence defined in probability space (Ω, ξ, P) , and $\{\xi(t)\}$ be an increasing σ -field of ξ . Then $\{X(t), t \geq 0\}$ is a submartingale, if it meets the following conditions:

- (1) $\{X(t)\}$ adapts to $\{\xi(t)\}$;
- (2) $E[X(t)] < +\infty, \forall t$;
- (3) $E[X(t+1) | \xi(t)] \geq X(t), \forall t$.

Based on the analysis of ECSA, the convergence of the algorithm is studied by using the feature of the best individual affinity function. If the conditional expectation of the best individual affinity function of new population with respect to current population is equal or greater than the best individual affinity function of current population, then the best individual affinity function can be transformed into a submartingale and used to analyze the convergence of ECSA. This can be formulated in the following theorem.

Theorem 1: The population sequence of ECSA is denoted as $\{\bar{X}(t), t \geq 0\}$, and $\xi(t) = \xi(\bar{X}(0), \bar{X}(1), \dots, \bar{X}(t))$ is measurable least σ -algebra. Then $\{f^*(\bar{X}(t)), t \geq 0\}$ is a submartingale, that is

$$E\left[f^* \left(\bar{X}(t+1) \right) | \xi(t) \right] \geq f^* \left(\bar{X}(t) \right), t \geq 0.$$

Proof: For $\{\bar{X}(t), t \geq 0\}$ is a Markov process, from above analysis, we can obtain:

$$\begin{aligned} & E\left[f^* \left(\bar{X}(t+1) \right) | \xi(t) \right] \\ &= E\left[f^* \left(\bar{X}(t+1) \right) | \bar{X}(0), \bar{X}(1), \dots, \bar{X}(t) \right] \\ &= E\left[f^* \left(\bar{X}(t+1) \right) | \bar{X}(t) \right] \\ &= \sum_{\bar{Y}} f^* \left(\bar{Y} \right) P\left\{ \bar{X}(t+1) = \bar{Y} | \bar{X}(t) = \bar{X} \right\} \\ &\geq f^* \left(\bar{X}(t) \right) \end{aligned}$$

i.e., $\{f^*(\bar{X}(t)), t \geq 0\}$ is a submartingale.

Let T_m be the operator of ECAS and $P'_{T_m} \{ \bar{X}, \bar{Y} \}$ the transition probability from population \bar{X} to \bar{Y} at generation t .

Theorem 2: Under Theorem 1, let $r_t^* = \min_{\bar{X}, \bar{Y}} P'_{T_m} \{ \bar{X}, \bar{Y} \}$,

$t \geq 0$, while $\sum_{t=1}^{\infty} r_t^* = \infty$, we have

- (1) $P\left\{ \lim_{t \rightarrow \infty} \left[f^* \left(\bar{X}(t) \right) \subset M \right] \right\} = 1$;
- (2) $P\left\{ \bigcup_{k=1}^{\infty} \bigcap_{t=k}^{\infty} \left[f^* \left(\bar{X}(t) \right) \subset M \right] \right\} = 1$.

Proof:

$$\text{Let } F_t = \left\{ \left(\bar{X}(t) = \bar{X} \right) \cap M = \emptyset \right\} = \left\{ f^* \left(\bar{X}(t) \right) \neq f^* \right\}.$$

Assuming $\bar{X}(t) = \bar{Y}_m$ satisfies $\left(\bar{X}(t) = \bar{Y}_m \right) \cap M \neq \emptyset$.

$$\text{Let } \mathcal{G} = \min \left\{ |f(X) - f(Y)|, f(X) \neq f(Y) \right\},$$

$$\text{then } f^* \left(\bar{Y}_m \right) - f^* \left(\bar{X} \right) \geq \frac{\mathcal{G}}{N}.$$

Due to the property of conditional expectation, we have

$$\begin{aligned} & E\left(f^* \left(\bar{X}(t+1) \right) \right) - E\left(f^* \left(\bar{X}(t) \right) \right) \\ &= E\left(E\left(f^* \left(\bar{X}(t+1) \right) | \bar{X}(t) \right) \right) - E\left(f^* \left(\bar{X}(t) \right) \right) \\ &= \sum_{\bar{X}} P\left\{ \bar{X}(t) = \bar{X} \right\} \left(E\left(f^* \left(\bar{X}(t+1) \right) | \bar{X}(t) = \bar{X} \right) - f^* \left(\bar{X}(t) \right) \right) \\ &= \sum_{\bar{X}} P\left\{ \bar{X}(t) = \bar{X} \right\} \sum_{\bar{Y}} P'_{T_m} \left\{ \bar{X}, \bar{Y} \right\} \left(f^* \left(\bar{Y} \right) - f^* \left(\bar{X} \right) \right) \\ &\geq \sum_{\bar{X} \cap M = \emptyset} P\left\{ \bar{X}(t) = \bar{X} \right\} P'_{T_m} \left\{ \bar{X}, \bar{Y}_m \right\} \left(f^* \left(\bar{Y}_m \right) - f^* \left(\bar{X} \right) \right) \\ &\geq \frac{\mathcal{G}}{N} P(F_t) r_t^* \end{aligned}$$

Summating the above inequality, then

$$f^* \geq E\left(f^* \left(\bar{X}(t+1) \right) \right) - E\left(f^* \left(\bar{X}(1) \right) \right) \geq \frac{\mathcal{G}}{N} \sum_{k=1}^t P(F_k) r_k^*, \text{ as}$$

$$t \rightarrow \infty, \sum_{t=1}^{\infty} P(F_t) r_t^* < \infty.$$

Where $\sum_{t=1}^{\infty} r_t^* = \infty$, therefore, as $t \rightarrow \infty, P(F_t) \rightarrow 0$. Namely,

$\lim_{t \rightarrow \infty} f^* \left(\bar{X}(t) \right) = f^*$, that is

$$P\left\{ \lim_{t \rightarrow \infty} \left[f^* \left(\bar{X}(t) \right) \subset M \right] \right\} = 1.$$

Since $\lim_{t \rightarrow \infty} f^* \left(\bar{X}(t) \right) = f^*$, when the state space S is finite,

i.e., $\{\bar{X}(t), t \geq 0\}$ only contains finite different values.

Hence, $\exists k$, when $t \geq k$, $f^* \left(\bar{X}(t) \right) = f^*$, consequently,

$$f^* \left(\bar{X}(t) \right) \subset M, \text{ i.e.,}$$

$$P\left\{ \bigcup_{k=1}^{\infty} \bigcap_{t=k}^{\infty} \left[f^* \left(\bar{X}(t) \right) \subset M \right] \right\} = 1.$$

From the above we can conclude the followings. (1) of theorem 2 shows that population affinity must tend to the optimal values if ECSA meets conditions, that is, ECSA is almost sure strong convergent; Conclusion (2) shows that the algorithm is globally convergent with probability 1 in a finite number of steps when the state space of population is finite.

IV. CONCLUSIONS

In this paper, the convergence of elitist clonal selection algorithm (ECSA) is studied using martingale theory. The best individual affinity evolutionary sequence of the algorithm is transformed into a submartingale, and based on the submartingale convergence theorem, the almost everywhere convergence of the ECSA is derived. Unlike the traditional theory of Markov chain, the new method can avoid solving complex transition matrix eigenvalues, and is

independent of the encoded form of the chromosome. This method makes the convergence analysis of ECSA more simplified and effective because of its unique advantage. However, it is to be noted that the method proposed in this paper are still under development and our future work will focus on further theoretical analysis, e.g., convergence rate of ECSA.

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