An Artificial Immune System Algorithm for CDMA Multiuser Detection over Multi-Path Channels

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ABSTRACT
Based on the Antibody Clonal Selection Theory of immunology, we put forward a novel clonal selection algorithm for multiuser detection in Code-division Multiple-access Systems. By using the clonal selection operator, the new algorithm can carry out the global search and the local search in many directions rather than one direction around the same individual simultaneously. After discussing the main characters of the new algorithm, especially the convergence and complexity, the performance of the proposed receiver, named by CAMUD, is evaluated via computer simulations and compared to that of other suboptimal schemes as well as to that of Optimal Multiuser detector (OMD) and conventional detector in CDMA systems over Multi-Path Channels. When compared with the OMD scheme, the CAMUD is capable of reducing the computational complexity significantly. On the other hand, when compared with standard genetic algorithm and improved genetic algorithm, theoretical analysis and Monte Carlo simulations show that the CAMUD with same complexity has optimal performance in eliminating MAI and "near-far" resistance. The simulations also show that the CAMUD performs quite well even when the number of active users and the length of the transmitted packet are considerably large.

Categories and Subject Descriptors
I.2.8 [**Artificial Intelligence**]: Problem Solving, Control Methods, and Search – *Heuristic methods.*

General Terms: Algorithms, Design.

Keywords
Artificial immune systems, Clonal Selection, Multiuser Detection, Code-division Multiple-access Systems, Genetic algorithm.

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1. INTRODUCTION
An organism is a complicated nonlinear system. The information processing function of the organism is fulfilled by three subsystems, neural system, immune system and excretory system in different time and space. Just like evolutionary algorithms, artificial immune systems make use of the mechanism of vertebrate immune system in terms of the model of information processing, and construct new intelligent algorithms for providing some novel methods to solve problems. These methods have stable foundation of biology, provide new ideas of intelligent information processing by simulating the biological intelligence, and have high applicability as feeble methods, for example, it's available for any function, especially the functions that have no expressions, or have expressions but can't be computed accurately. Artificial immune system provides the evolutionary learning mechanism like noise enduring, non-teacher learning, self-organization, and memory, and combine with some advantages of other systems like classifier, neural network and machine reasoning, so its research production refers to many fields like control, data processing, optimization learning and fault detection, and it has been a research hotspot after the neural network, fuzzy logic and evolutionary computation [3].

In recent years, Direct-Sequence Code-division Multiple-access (DS-CDMA) systems have emerged as one of prime multiple-access solutions for 3G and future wide-band wireless systems [8]. In the DS-CDMA framework, multiple-access interference (MAI) existing at the received signal creates "near-far" effects and constitutes the main limitation of DS-CDMA systems. Multiuser detection (MUD) techniques can efficiently suppress MAI and substantially increase the capacity of CDMA systems, so it has gained significant research interest since the Optimal MUD (OMD) was proposed by Verdu [13]. But the computational complexity of OMD increases exponentially with the growth of user number. Aazhang, Paris, and Orshak [1] described a neural network for multi-used detection. Other approaches have included

probabilistic neural networks [6], Hopfield networks [9], and genetic algorithms [12]. All of them are capable of reducing the computational complexity significantly and getting good performances. Antibody Clonal Selection Theory is very important

for the immunology. The idea attracts such great attentions that some new algorithms based on Antibody Clonal Selection Theory have been proposed successively [4][10][11].

A novel clonal selection algorithm for Multiuser Detection (CAMUD) based on Antibody Clonal Selection Theory is presented in this paper, and the main characters of the new algorithm, such as convergence and complexity, are discussed. Based on the antibody-antibody affinity, antibody–antigen affinity and their dynamic allotting memory units along with the scale of antibody populations, CAMUD can combine the stochastic searching methods with evolutionary searching based on the probability. Furthermore, by using clonal selection operator, the algorithm can integrate the global searching and local searching. In order to show the new algorithm's advantages, the performances of the CAMUD is evaluated via computer simulations and compared with that of SGA and improved GA[7] as well as with that of the OMD and conventional detector in DS-CDMA Systems over Multi-Path Rayleigh Fading Channels. Theoretic analysis and Monte Carlo simulations show that the CAMUD is capable of reducing the computational complexity significantly and taking on optimal performance in eliminating MAI and "near-far" resistance and greatly improving the system capacity, i.e. when the number of active users and the length of the transmitted packet are relatively large, the proposed CAMUD detector performs quite well too. It also shows that the new algorithm is intended to integrate the local searching with the global and the probability evolution searching with the stochastic searching and has a faster global convergence speed.

2. PROBLEM STATEMENTS

Consider a base-band digital DS-CDMA network with K active users operating with a coherent BPSK modulation format. The CDMA signal received at the output of the sensor can be expressed as:

$$\boldsymbol{r}(t)=\sum_{i=0}^{M-1}\sum_{k=1}^{K}A_k b_k(i)s_k(t-iT_{\mathrm{b}})+\boldsymbol{n}(t)=\boldsymbol{S}(t,\boldsymbol{b})+\boldsymbol{n}(t) \quad (1)$$

here $\boldsymbol{n}(t)$ is the additive white noise vector whose standard deviation is σ, T_{b} is the symbol interval, M is the number of data symbols transmitted in a packet, A_k is the signal's amplitude of the k^{th} user, $b_k(m)$ is the m^{th} coded modulated symbol of the k^{th} user and $b_k(m)\in\{\pm 1\}$, $s_k(t)$ is the k^{th} user's signature sequence.

The matched filter output corresponding to the m^{th} bit of the k^{th} user is given by:

$$y_k(m)=\int_{-\infty}^{\infty}\boldsymbol{r}(t)s_k(t-mT_b-\tau_k)dt \quad (2)$$

If set

$\boldsymbol{y}(m)=[y_1(m),y_2(m)\cdots,y_K(m)]^{\mathrm{T}}$,

$\boldsymbol{b}(m)=[b_1(m),b_2(m),\ldots,b_K(m)]^{\mathrm{T}}$, $\boldsymbol{A}(m)=\mathrm{diag}(\boldsymbol{A}_1,\boldsymbol{A}_2,...,\boldsymbol{A}_K)$,

$\boldsymbol{n}(m)=[n_1(m),n_2(m),\ldots,n_K(m)]^{\mathrm{T}}$ and $\boldsymbol{R}(q)=(\rho_{kl}(q))_{K\times K}$,

where $\rho_{kl}(q)=\int_{\tau_k}^{T+\tau_k}s_k(t-\tau_k)s_l(t+qT-\tau_l)dt$ then

$$\boldsymbol{y}=\boldsymbol{RAb}+\boldsymbol{n} \quad (3)$$

Where

$\boldsymbol{y}=[\boldsymbol{y}(m),\boldsymbol{y}(m+1)\cdots,\boldsymbol{y}(m+M-1)]^{\mathrm{T}}$,

$\boldsymbol{b}=[\boldsymbol{b}(m),\boldsymbol{b}(m+1),\ldots,\boldsymbol{b}(m+M-1)]^{\mathrm{T}}$,

$\boldsymbol{A}=diag(\boldsymbol{A}(m),\boldsymbol{A}(m+1),...,\boldsymbol{A}(m+M-1))$

and $\boldsymbol{n}=[\boldsymbol{n}(m),\boldsymbol{n}(m+1),\ldots,\boldsymbol{n}(m+M-1)]^{\mathrm{T}}$.

The Optimal MUD produces an estimate for the information vector transmitted at the discrete-time instant m, based on the maximization of the logarithm of the likelihood function. In the asynchronous multi-path case it holds that

$$\hat{\boldsymbol{b}}_{\mathrm{optimal}}=\arg\max_{\substack{b_k^{(m)}\in\{-1,\,1\}\\ 1\le k\le K,\,1\le m\le M}}\left\{2\Re\left\{\boldsymbol{b}^T\boldsymbol{Ay}\right\}-\boldsymbol{b}^T\boldsymbol{AHAb}\right\} \quad (4)$$

Where $\boldsymbol{H}=\boldsymbol{G}^{\mathrm{H}}\left\{\boldsymbol{R}\circ[\boldsymbol{\Phi}^{\mathrm{H}}\boldsymbol{\Phi}]\right\}\boldsymbol{G}$.

Note that, for the above problem to be solved by the Viterbi algorithm[15], its computational complexity will increase exponentially with the growth of the number of users and the packet length. If the number of users and the packet length is relatively large, the computational effort required for the solution of (4) becomes prohibitively large for real-time implementations due to the NP-complete nature of the optimization problem.

In order to reduce the complexity, we proposed a novel detector based on a clonal selection algorithm in the following section.

3. PRESENTATION OF THE ALGORITHM

The Antibody Clonal Selection Theory was proposed as the basic features of an immune response to an antigen stimulus [2]. It establishes the idea that cells are selected when they recognize the antigens and proliferate. The antigen can selectively react to the antibody, which is a native production and spreads on the cell surface in the form of peptides. The reaction leads to cell proliferating clonally and the colony has the same antibody. The clonal selection is a dynamic process of the immune system stimulated by the self-adapting antigen.

It is impossible and unnecessary for us to apply the biology definitions and the biology process mechanically. For problem (4), assume that K active users share the same channels and the packet length is M, in order to describe the algorithm well, we just define the glossary as follows.

Definition 1. Antigen

In AIS, antigen usually means the problem and its constraints. Especially, for the multiuser detection problem, the antigen is defined as follows:

$$f(\boldsymbol{b})=2\Re\left\{\boldsymbol{b}^T\boldsymbol{Ay}\right\}-\boldsymbol{b}^T\boldsymbol{AHAb} \quad (5)$$

where $\boldsymbol{b}=\left\{\ [b_1^{(1)},b_2^{(1)}\cdots,b_K^{(1)}]\ ,\cdots,\ [b_1^{(M)},b_2^{(M)}\cdots,b_K^{(M)}]\ \right\}$, $b_k^{(m)}\in\{-1\ ,\ 1\}$ is the variants to be optimized.

Definition 2. Antibody

Antibodies represent candidates of the problem, defining the limited-length character string

$\boldsymbol{b} = \{\ [b_1^{(1)}, b_2^{(1)} \cdots, b_K^{(1)}]\ , \cdots,\ [b_1^{(M)}, b_2^{(M)} \cdots, b_K^{(M)}]\ \} \in \boldsymbol{I}$ is the antibody coding, where $b_k^{(m)} \in \{-1\ ,\ 1\}$ and $\boldsymbol{I}$ denotes the antibody space.

Definition 3. Antibody-Antigen Affinity

Antibody-Antigen Affinity is the reflection of the total combination power locates between antigen and antibodies. In AIS, it generally indicates values of objective functions or fitness measurement of the problem. In this paper, we set the antigen f as the antibody-antigen affinity.

If the antibody population at time k is represented by the time-dependent variable $\boldsymbol{B}(k) = \{\boldsymbol{b}_1(k), \boldsymbol{b}_2(k) \cdots \boldsymbol{b}_n(k)\}$, then the main operations are defined as follows.

Definition 4. Clone Operation

In the immunology, clone is the process of antibody proliferation. In AIS, the clonal operation to the antibody population is defined as:

$$\boldsymbol{Y}(k) = T_{\mathrm{c}}^{\mathrm{C}}(\boldsymbol{B}(k)) = [T_{\mathrm{c}}^{\mathrm{C}}(\boldsymbol{b}_1(k))\quad T_{\mathrm{c}}^{\mathrm{C}}(\boldsymbol{b}_2(k)),\quad \cdots,\quad T_{\mathrm{c}}^{\mathrm{C}}(\boldsymbol{b}_n(k))]^{\mathrm{T}} \tag{6}$$

where $\boldsymbol{Y}_i(k) = T_{\mathrm{c}}^{\mathrm{C}}(\boldsymbol{b}_i(k)) = I_i \times \boldsymbol{b}_i(k)$, $i = 1, 2, \cdots, n$, I_i is a q_i dimensional identity row vector. The process is called the q_i clone of antibody $\boldsymbol{b}_i$, namely $q_i(k) = \hbar(n_{\mathrm{c}}, \boldsymbol{\Theta}_i)$, where $\boldsymbol{\Theta}_i$ stands for the affinity function of antibody $\boldsymbol{b}_i$ and other antibodies, and n_{c} is the clonal scale.

Definition 5. Clonal Mutation Operation

According to the mutation probability p_{m}, the antibody populations are mutated as follows:

$$\boldsymbol{Z}_i(k) = \{z_{ij}(k)\} = \{T_{\mathrm{m}}^{\mathrm{C}}(\boldsymbol{y}_{ij}(k))\} = \{(-1)^{random \le p_m}\, \boldsymbol{y}_{ij}(k)\} \tag{7}$$

$(-1)^{random \le p_m}\, \boldsymbol{y}_{ij}(k)$ means each number of the antibody $\boldsymbol{y}_{ij}(k)$ multiplies -1 with probability p_{m}.

Definition 6. Clonal Selection Operation

$\forall i = 1,2,\cdots n$, if there are mutated antibodies

$$\boldsymbol{b}_i'(k) = \max\{\boldsymbol{Z}_i(k)\} = \{z_{ij}(k) \mid \max f(z_{ij}(k))\quad j = 1, 2, \cdots, q_i\}$$

, the probability of $\boldsymbol{b}_i'(k)$ taking place of $\boldsymbol{b}_i(k) \in \boldsymbol{B}(k)$ is:

$$p_{\mathrm{s}}^{\mathrm{k}}\left(\boldsymbol{b}_i(k) = \boldsymbol{b}_i'(k)\right) = \begin{cases} 1 & \text{when } f(\boldsymbol{b}_i(k)) < f(\boldsymbol{b}_i'(k)) \\ 0 & \text{when } f(\boldsymbol{b}_i(k)) \ge f(\boldsymbol{b}_i'(k)) \end{cases} \tag{8}$$

Definition 7. Clonal Death Operation

After the Clonal Selection Operation, the new population is:

$$\boldsymbol{B}(k+1) = \{\boldsymbol{b}_1(k+1), \boldsymbol{b}_2(k+1), \cdots, \boldsymbol{b}_i'(k+1), \cdots, \boldsymbol{b}_n(k+1)\} \tag{9}$$

where $\boldsymbol{b}_i'(k+1) = \boldsymbol{b}_j(k+1) \in \boldsymbol{B}(k+1)$ $i \ne j$ and $f(\boldsymbol{b}_i'(k+1)) = f(\boldsymbol{b}_j(k+1))$, in which $\boldsymbol{b}_j(k+1)$ is one of the best antibodies in $\boldsymbol{B}(k+1)$. Whether $\boldsymbol{b}_i'(k+1)$ should be canceled or not depends on the clonal death proportion *T%*.

Then the novel clonal selection algorithm can be implemented as Figure 1.

begin
Enact the halt conditions and algorithm parameters;
initialize $\boldsymbol{B}(0) = \{\boldsymbol{b}_1(0), \boldsymbol{b}_2(0), \cdots \boldsymbol{b}_n(0)\} \in \boldsymbol{I}^{\mathrm{n}}$; k = 0;
calculate affinity of $\boldsymbol{B}(0)$:
$\{f(\boldsymbol{B}(0))\} = \{f(\boldsymbol{b}_1(0)), f(\boldsymbol{b}_2(0)), \cdots f(\boldsymbol{b}_n(0))\}$;
while not satisfy the halt conditions, **do**
$k := k + 1$;
generate $\boldsymbol{B}(k)$ from $\boldsymbol{B}(k-1)$ by Clonal Operation, Clonal Mutation Operation, Clonal Selection Operation and Clonal Death Operation;
calculate the affinity of $\boldsymbol{B}(k)$;
end
end

Figure 1. The Clonal Selection Algorithm for MUD.

4. ANALYSIS OF THE ALGORITHM

4.1 The Convergence of the Algorithm

Definition 8. $\boldsymbol{I}^{\mathrm{n}^*}$ is called the satisfactory antibody population space if $\boldsymbol{I}^{\mathrm{n}^*} = \{\boldsymbol{B} \in \boldsymbol{I}^{\mathrm{n}} \mid \vartheta(\boldsymbol{B}) \ge 1\}$.

This definition denotes that there is at least one best antibody in the satisfactory antibody population space. And $\overline{\boldsymbol{I}}^{\mathrm{n}^*} = \boldsymbol{I}^{\mathrm{n}} - \boldsymbol{I}^{\mathrm{n}^*}$ is called the normal antibody population space.

The process of clonal selection is a stochastic and memonic state transfer. The mathematic model of CAMUD can be described as a Markov Chain.

Definition 9. For random state $\boldsymbol{B}_0$, if

$$\lim_{k\to\infty} p\{\boldsymbol{B}(k) \cap \boldsymbol{b}^* \ne \varnothing \mid \boldsymbol{B}(0) = \boldsymbol{B}_0\} = \lim_{k\to\infty} p\{\boldsymbol{B}(k) \in \boldsymbol{I}^{\mathrm{n}^*} \mid \boldsymbol{B}(0) = \boldsymbol{B}_0\} = 1$$

always legitimacy, namely

$$\lim_{k\to\infty} p\{\vartheta(\boldsymbol{B}(k)) \ge 1 \mid \boldsymbol{B}(0) = \boldsymbol{B}_0\} = 1 \tag{10}$$

then we called the $\boldsymbol{B}_0$ can be convergent to $\boldsymbol{I}^{\mathrm{n}^*}$ with probability of 1.

Theorem 1. The algorithm of CAMUD is convergent with probability of 1.

Proof: If $P_0(k) = P\{\vartheta(\boldsymbol{B}(k)) = 0\} = P\{\boldsymbol{B}(k) \cap \boldsymbol{b}^* = \varnothing\}$, according to Bayes's Theorem [14], we can draw that

$$\begin{aligned} P_0(k+1) &= P\{\vartheta(\boldsymbol{B}(k+1)) = 0\} \\ &= P\{\vartheta(\boldsymbol{B}(k+1)) = 0 \mid \vartheta(\boldsymbol{B}(k)) \ne 0\} \times P\{\vartheta(\boldsymbol{B}(k)) \ne 0\} \\ &+ P\{\vartheta(\boldsymbol{B}(k+1)) = 0 \mid \vartheta(\boldsymbol{B}(k)) = 0\} \times P\{\vartheta(\boldsymbol{B}(k)) = 0\} \end{aligned} \tag{11}$$

From the property of the clonal operations, the following equation holds:

$$P\left\{\vartheta\left(\boldsymbol{B}(k+1)\right)=0\middle|\vartheta\left(\boldsymbol{B}(k)\right)\neq 0\right\}=0 \quad (12)$$

So

$$P_0(k+1)=P\left\{\vartheta\left(\boldsymbol{B}(k+1)\right)=0\middle|\vartheta\left(\boldsymbol{B}(k)\right)=0\right\}\times P_0(k) \quad (13)$$

If $\zeta=\min_k P(k), \quad k=0,1,2\cdots$ then

$$P\left\{\vartheta\left(\boldsymbol{B}(k+1)\right)\geq 1\middle|\vartheta\left(\boldsymbol{B}(k)\right)=0\right\}\geq\zeta>0 \quad (14)$$

So

$$P\left\{\vartheta\left(\boldsymbol{B}(k+1)\right)=0\middle|\vartheta\left(\boldsymbol{B}(k)\right)=0\right\}=1-P\left\{\vartheta\left(\boldsymbol{B}(k+1)\right)\neq 0\middle|\vartheta\left(\boldsymbol{B}(k)\right)=0\right\}=$$
$$1-P\left\{\vartheta\left(\boldsymbol{B}(k+1)\right)\geq 1\middle|\vartheta\left(\boldsymbol{B}(k)\right)=0\right\}\leq 1-\zeta<1$$

From equation (13) we find that

$$0\leq P_0(k+1)\leq(1-\boldsymbol{\zeta})\times P_0(k)\leq(1-\boldsymbol{\zeta})^2\times P_0(k-1)\cdots\leq(1-\boldsymbol{\zeta})^{k+1}\times P_0(0)$$

Notes that $\lim_{k\to\infty}(1-\boldsymbol{\zeta})^{k+1}=0$, $1\geq P_0(0)\geq 0$, so

$$0\leq\lim_{k\to\infty}p_0(k)\leq\lim_{k\to\infty}(1-\zeta)^{k+1}P_0(0)=0 \quad (15)$$

So $\lim_{k\to\infty}p_0(k)=0$, now we can draw the conclusion that

$$\lim_{k\to\infty}P\left\{\boldsymbol{B}(k)\cap\boldsymbol{b}^*\neq\Phi\middle|\boldsymbol{B}(0)=\boldsymbol{B}_0\right\}=1-\lim_{k\to\infty}P_0(k)=1 \quad (16)$$

Thus, the algorithm of CAMUD is convergent with probability of 1. We succeed in proving theorem 1.

Although it is believed that the algorithm could converge to the global optimal with probability 1 in theory, in practice, just like other EAs, it is difficult to calculate its convergent speed accurately. As a result, assuring convergence with probability 1 in definite generations is very difficult.

4.2 The Complexity of the New Algorithm

The problem of Optimal Multi-user Detection is a NP-complete optimization problem. The dimension of the search space is $K\times M$. When solved with Viterbi algorithm, its computational complexity will be $O(2^{K\times M})$. If the number of users and the packet length are relatively large, the computational effort becomes prohibitively large for real-time implementations.

In our algorithm, the computation complexity is decided by two elements: one is the terminated generation of evolution *ga* and the other is the computational complexity per generation *N*. Therefore, the complexity will be $O(N\times ga)$. Let *ga* be equal to αMK, where a is a constant. We also find that if the algorithm parameters, such as population size, clone scale, mutation probability and clonal death proportion are fixed then the computational complexity per generation is $O(KM)$, so the complexity of the new algorithm is $O((KM)^2)$.

In this contribution, we succeeded in reducing the complexity of the Optimal MUD, which performs $O(2^{K\times M})$ search, by employing the sub-optimal CAMUD, which performs only $O((K\times M)^2)$ search.

4.3 Analysis of the Algorithm Parameters

There are four parameters to be settled at initialization: the size of the antibody population n, the clone scale n_c, the mutation probability p_m and the clonal death proportion *T%*. n and n_c directly affect the computational complexity of the algorithm. Given n and n_c large enough, the diversity of the population can be enhanced and the prematurity can be avoided to some extent with a high convergence speed. But the computational complexity will also be very large. It is important to emphasize that the performance of the algorithm determined by the parameters p_m and *T%*. In order to evaluate the impact of p_m and *T%*, we have run the same set of experiments 1000 times in different circumstances.

I. Influence of p_m

The mutation probability $p_m\in[0,1]$. In order to evaluate the impact of p_m, we have run the same set of experiments 1000 times in 3 different circumstances as follows:

Case 1: It is assumed that the number of synchronous users is 10 over Gaussian channels, and the Gold sequences of length 31 were used as code sequences. Signal-to-Noise (*SNR*) is 10 dB. All users have the same power. We will terminate the search at the 15th generation and the individual associated with the highest fitness value at this point will be result. The impact of p_m in Case 1 is shown in Figure 2(a). Our performance metric is the average Bit Error Ratio (*BER*).

Case 2: It is assumed that the number of asynchronous users is 4 over Gaussian channels, the packet length is 5, and the Gold sequences of length 31 were used as code sequences. *SNR*=4 dB. All users have the same power. We will terminate the search at the 30th generation and the individual associated with the highest fitness value at this point will be the detected results. The impact of p_m in case 2 is shown in Figure 2(b).

Case 3: It is assumed that the number of asynchronous users is 10 over Gaussian channels, the packet length is 10, and the Gold sequences of length 31 were used as code sequences. *SNR*=10 dB. All users have the same power. We will terminate the search at the 150th generation and the individual associated with the highest fitness value at this point will be the detected results. The impact of p_m in case 3 is shown in Figure 2(c).

More similar experiments showed that the best results were obtained when $p_m\approx 1/(K\times M)$.

II. Influence of *T%*

The clonal death proportion $T\%\in[0,1]$. In order to evaluate the impact of *T%*, we assumed that the number of asynchronous users is 10 over a Gaussian channel, the packet length is 10, and Gold sequences of length 31 were used as code sequences. SNR=10 dB. All users have the same power. Terminate the search at the 150th generation. The impact of *T%* is shown in Figure 2(d).

More similar experiments showed that the best results were obtained when $T\%\approx 50\%$.

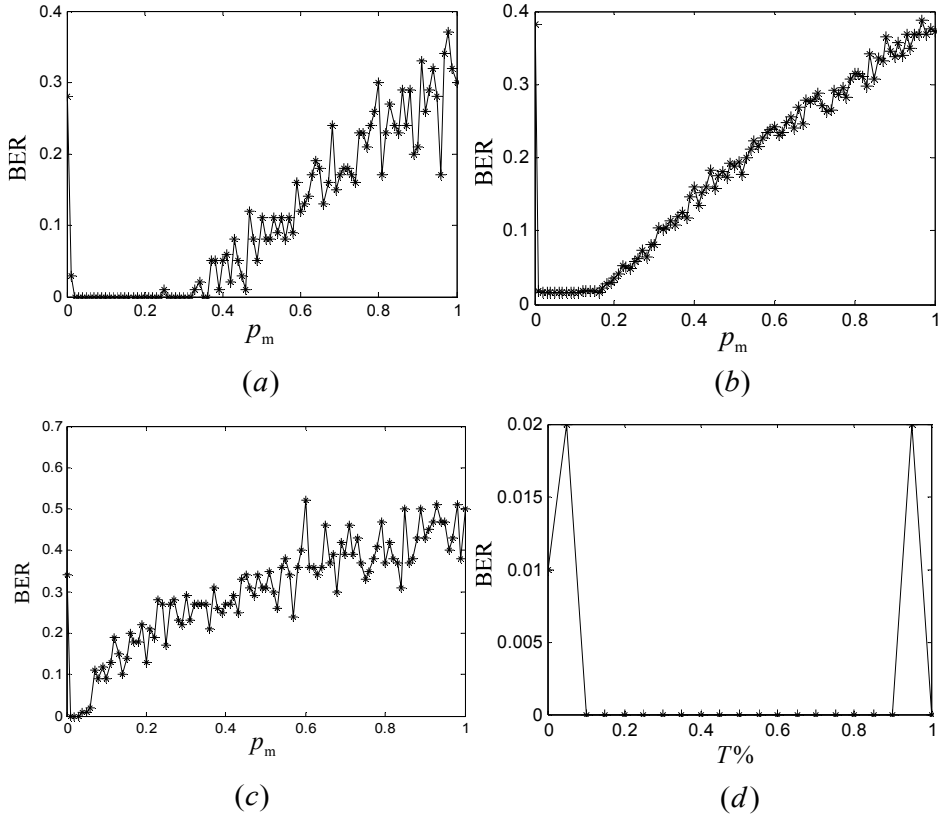

Figure 2. The influence of the algorithm parameters. (a) The influence of p_m when K=10, SNR=10 dB. (b) The influence of p_m when K=4, M=5, SNR=4 dB. (c) The influence of p_m when K=10, M=10, SNR=10 dB. (d) The influence of *T*% when K=10, M=10, SNR=10 dB.

5. EXPERIMENTAL RESULTS

In this section, we present some simulation results and comparison that demonstrate the potential of our algorithm. The performance of the CAMUD is evaluated via computer simulations and compared with that of standard genetic algorithm (GAMUD) and improved genetic algorithm [7] (IAMUD) as well as with that of the optimal Multi-user Detector (OMD) and conventional matched filters detector (MFD) in DS-CDMA systems over Multi-Path Rayleigh Fading Channels.

It is assumed that the number of users is *K* and the packet length is *M*, Gold sequences of length 31 are used as code sequences. The signal to noise ratio of the *k*th user is defined as $SNR_k = A_k^2 / \sigma^2$. For CAMUD, IAMUD and GAMUD, we will terminate the search at the *Y*th generation and the individual associated with the highest fitness value at this point will be the detected results. In this paper, we let $Y = 1.5 \times K \times M$. In GAMUD and IAMUD, the size of population is 25, the selection probability $P_r = 0.4$, the cross probability $P_c = 0.6$ and the mutation probability $p_m = 0.05$. In CAMUD, the size of antibody population is 5, clonal scale is 5, clonal death proportion $T\% = 50\%$ and mutation probability $P_m = 1/(K \times M)$. In that case, the computational complexities of CAMUD, IAMUD and GAMUD are pretty much the same ting.

We have taken each experiment based on 10000 bits signals and our performance metric is the average Bit Error Ratio (BER).

We consider a DS-CDMA system with a uniform linear phased antenna array over Rayleigh fading Channels. The number of multi-path channels is 3 and the number of receive antennas is 4. The direction of arrival (DOA) θ_{kl} is a uniformly distributed random variable between $[-\frac{\pi}{2}, \frac{\pi}{2}]$. The relative time delay τ_{kl} is a uniformly distributed random integer variable between [0, 31]. The channel fading gain α_{kl} is a Rayleigh distributed random complex variable.

I. Comparisons with the Optimal Multiuser Detector

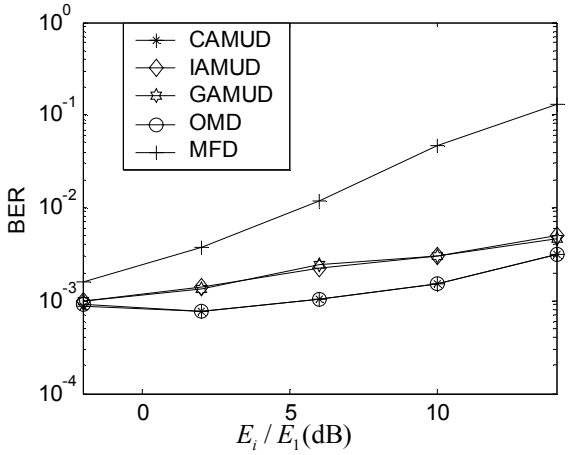

Figure 3. The performance comparison with OMD.

If the number of users and the packet length are relatively large in CDMA systems, the computational effort required for the Viterbi algorithm becomes prohibitively large for real-time implementations due to the NP-complete nature of the optimization problem. In order to gain the results of the OMD, we assumed that K=3, M=3, SNR=10 dB. The first user is the desired user while other users are the multiple access interference sources, i.e. other users are disturbing users with the same power. The ratio between the power of disturbing user E_i $(i = 2,3)$ and the power of desired user E_1 denotes the ratio of 'near-far'. We have taken the experiments based on 10000 bits signals. The BER versus E_i / E_1 obtained by CAMUD, IAMUD, GAMUD, OMD and MFD are shown in Figure 3.

II. The performance in "near-far" resistance

It is assumed that *K*=10, *M*=10, *SNR*=10 dB. The first user is the desired user, and other users are disturbing users and have the same power. The ratio between the power of disturbing user E_i $(i = 2 \sim 10)$ and the power of desired user E_1 denotes the ratio of 'near-far'. We have taken the experiments based on 10000 bits signals. The BER versus E_i / E_1 obtained by CAMUD, IAMUD, GAMUD and MFD are shown in Figure 4(a).

III. The performance in suppressing noise's disturbing

It is assumed that *K*=10, *M*=10. All users have the same power. Changing the value of *SNR* from 2 to 18, We have taken the experiments based on 10000 bits signals. The BER versus *SNR* obtained by CAMUD, IAMUD, GAMUD and MFD are shown in Figure 4(b).

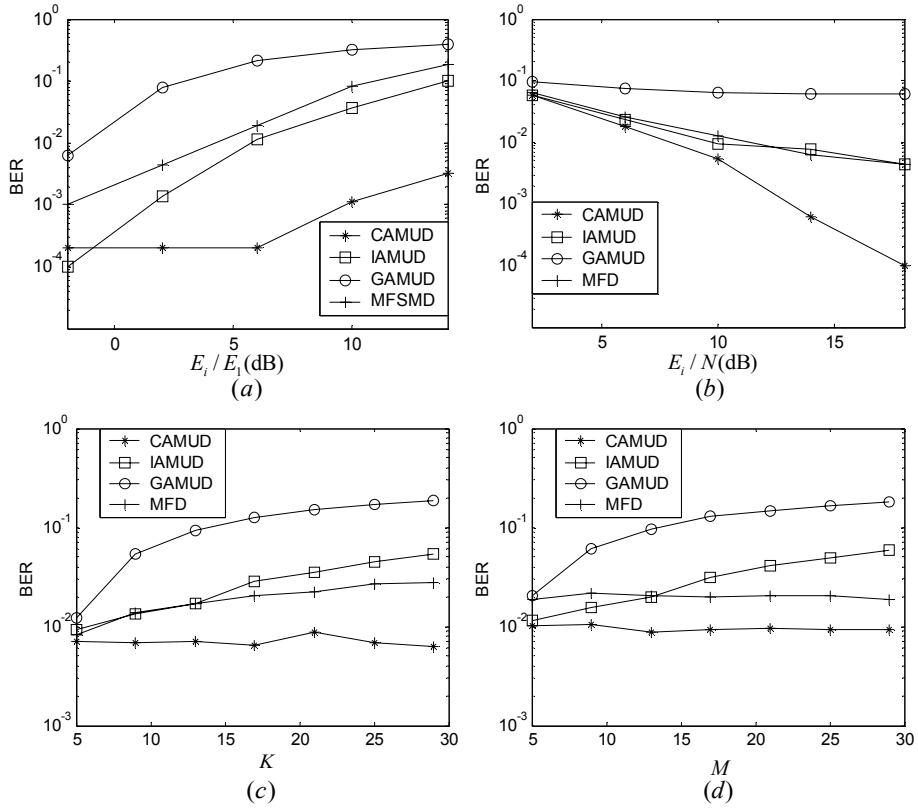

Figure 4. The performance comparisons among CAMUD, IAMUD, GAMUD and MFD over Rayleigh fading channels. (a) The BER versus E_i / E_1 when K=10, M=10, SNR=10 dB. (b) The BER versus *SNR* when K=10, M=10. (c) The BER versus K when M=10, SNR=10 dB. (d) The BER versus M when K=10, SNR=10 dB.

IV. The performance in accommodating users

It is assumed that *SNR*=10 dB, *M*=10, the number of users *K* is changed from 5 to 30, all users have the same power. We have taken the experiments based on 10000 bits signals. The BER versus *K* obtained by CAMUD, IAMUD, GAMUD and MFD are shown in Figure 4(c).

V. The performance in accommodating packet length

It is assumed that *SNR*=10 dB, *K*=10, the packet length *M* is changed from 5 to 30, all users have the same power. We have taken the experiments based on 10000 bits signals. The BER versus *M* obtained by CAMUD, IAMUD, GAMUD and MFD are shown in Figure 4(d).

Figure 3 shows that the performance of CAMUD is almost the same good as the Optimal Multiuser Detector. As can be seen from Figure 4(a), The MFD, GAMUD and IAMUD exhibited severe performance degradation when powers of the transmitting users are dissimilar. As we expect, the novel detector based on the clonal selection algorithm exhibits the best performance and seldom fails to produce the correct estimate for the transmitted symbols. When the cumulative BER achieved by MFD, GAMUD, IAMUD and CAMUD are evaluated versus the value of the *SNR* of all the users, Figure 4(b) shows that the CAMUD receiver achieves acceptable performance, whereas the performances of MFD, GAMUD and IAMUD are very poor. When the number of active users is large and the length of the transmitted packet is relatively large, the advantage of CAMUD can be seen in Figure 4(c) and Figure 4(d).

6. CONCLUDING REMARKS

In this paper, a novel MUD receiver based on a clonal Selection Algorithm was proposed. Theoretical analysis and Monte Carlo simulations show that the new algorithm could significantly reduce the computational complexity and achieve better performance in MAI suppression and "near-far" resistance over other algorithms such as the conventional detection, SGA and the improved GA. It greatly improves the system capacity in acceptable computational cost for practical implementation in CDMA systems. It also shows that the new algorithm is intended to integrate the local searching with the global and the probability evolution searching with the stochastic searching and has a faster global convergence speed.

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