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A population-based artificial immune system for numerical optimization

Maoguo Gong *, Licheng Jiao, Xiangrong Zhang

Key Lab of Intelligent Perception and Image Understanding of Ministry of Education of China, Institute of Intelligent Information Processing, Xidian University, Xi'an 710071, PR China

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ABSTRACT

Many immue-inspired algorithms are based on the abstractions of one or several immunology theories, such as clonal selection, negative selection, positive selection, rather than the whole process of immune response to solve computational problems. In order to build a general computational framework by simulating immune response process, this paper introduces a model for population-based artificial immune systems, termed as PAIS, and applies it to numerical optimization problems. PAIS models the dynamic process of human immune response as a quaternion (***G***, ***I***, ***R***, ***Al***), where ***G*** denotes exterior stimulus or antigen, ***I*** denotes the set of valid antibodies, ***R*** denotes the set of reaction rules describing the interactions between antibodies, and ***Al*** denotes the dynamic algorithm describing how the reaction rules are applied to antibody population. Some general descriptions of reaction rules including the set of clonal selection rules and the set of immune memory rules are introduced in PAIS. Based on these reaction rules, a dynamic algorithm, termed as PAISA, is designed for numerical optimization. In order to validate the performance of PAISA, nine benchmark functions with 20–10,000 dimensions and a practical optimization problem, optimal approximation of linear systems are solved by PAISA, successively. The experimental results indicate that PAISA has high performance in optimizing some benchmark functions and practical optimization problems.

1. Introduction

Biological inspiration can successfully be transferred into novel computational paradigms, as shown in the development and successful use of concepts such as artificial neural networks, evolutionary algorithms, swarm algorithms and so on. Many bio-inspired algorithms are based on populations of agents trained to perform some task or optimization. The most obvious one is the area of evolutionary algorithms, based on analogy to populations of organisms breeding and selecting to become "fitter" [41].

The human immune system (HIS) is a highly evolved, parallel and distributed adaptive system. The information processing abilities of HIS provide important aspects in the field of computation. This emerging field is referring to as the immunological computation, immunocomputing or artificial immune systems (AIS) [11,43]. AIS can be defined as computational systems inspired by theoretical immunology and observed immune functions, principles and models, which are applied to problem solving [12]. AIS have received a significant amount of interest from researchers and industrial sponsors in recent years. Some of the first work in applying HIS metaphors was undertaken in the area of fault diagnosis [32]. Later work applied HIS metaphors to the field of computer security [17], which seemed to act as a catalyst for further investigation of HIS as a metaphor in anomaly detection [26,43], pattern recognition [6,19,44,45], optimization [10,13,16,20,33] and some other related areas [8,15,24,28–30]. The first immune optimization algorithm may be the work of Fukuda et al. [18] that included an abstraction of clonal selection to solve computational problems [21]. But the AIS for optimization have been popularized mainly by de Castro and Von Zuben's CLONALG [13]. CLONALG can perform multi-modal optimization while delivering good approximations of a global optimum. Garrett [20] has presented an attempt to remove all the parameters from clonal selection algorithm. The work of Cutello et al. [9,10] introduced different hypermutation and aging operators into clonal selection to face hard problems including numerical optimization problems. These algorithms encoded the parameters into individuals where each individual represents a search point in the space of potential solutions. A large number of parameters would result in a large search space [7]. Nowadays, there is no report about AIS algorithms effectively solving numerical optimization problems with more than 100 parameters.

These immune-inspired optimization algorithms are mainly based on the abstraction of the clonal selection principle [5]. HIS relies on the prior formation of an incredibly diverse population of

* Corresponding author. Tel.: +86 29 88202661; fax: +86 29 88201023.
E-mail addresses: gong@ieee.org (M. Gong), lchjiao@mail.xidian.edu.cn (L. Jiao).

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B cells and T cells [1]. The specificity of both the B-cell receptors and T-cell receptors, that is, the epitope to which a given receptor can bind, is created by a remarkable genetic mechanism. Each receptor is created even though the epitope it recognizes may never have been present in the body. If an antigen with that epitope should enter the body, those few lymphocytes able to bind to it will do so. If they also receive a second co-stimulatory signal, they may begin repeated rounds of mitosis. In this way, clones of antigen-specific lymphocytes (B and T) develop providing the basis of the immune response. This phenomenon is called clonal selection [1,3,5]. In fact, besides the clonal selection, during the initial expansion of clones, some of the progeny cells neither went on dividing nor developed into plasma cells. Instead, they reverted to small lymphocytes bearing the same B-cell receptor on their surface that their ancestors had. This lays the foundation for a more rapid and massive response the next time the antigen enters the body, i.e. immune memory. The majority immune-inspired optimization algorithms mentioned above are concentrated on the clonal selection while the immune memory is only a concomitant which is simply modeled as the elitist selection.

In order to build a general computational framework by simulating the whole process of immune response, this paper introduces a model for population-based artificial immune systems, termed as PAIS. PAIS models the above dynamic process of human immune response as a quaternion ($\boldsymbol{G}$, $\boldsymbol{I}$, $\boldsymbol{R}$, $\boldsymbol{Al}$), where $\boldsymbol{G}$ denotes exterior stimulus or antigen, $\boldsymbol{I}$ denotes the set of valid antibodies, $\boldsymbol{R}$ denotes the set of reaction rules describing the interactions between antibodies and $\boldsymbol{Al}$ denotes the dynamic algorithm describing how the reaction rules are applied to antibody population. PAIS can be considered as a general architecture of population-based artificial immune systems rather than an immune algorithm. Many immune phenomena, such as clonal selection, immune memory, negative selection, passive selection, can be modeled as corresponding reaction rules and added to the set of reaction rules $\boldsymbol{R}$. Based on the PAIS, our final aim is to build a self-adaptive dynamic system by simulating all the possible interactions between antibodies during immune response. Then the PAIS can automatically select reaction rules depending on antigen $\boldsymbol{G}$, and thereby the pending problems could be solved automatically. In order to solve numerical optimization problems, the set of clonal selection rules and the set of immune memory rules are introduced. Consequently, a dynamic algorithm based on these heuristic rules is designed, which can effectively solve numerical optimization problems even when the number of variable parameters is as many as 10,000.

The rest of the paper is organized as follows: Section 2 describes the population-based AIS model. Section 3 describes the experimental study on nine benchmark functions. Section 4 describes the experimental study on the optimal approximation of linear systems. Finally, concluding remarks are presented in Section 5.

2. A population-based artificial immune system

HIS incorporates mechanisms that enable antibodies (lymphocytes) to learn the structures of specific foreign proteins. Essentially, HIS evolves and reproduces antibodies that have high affinities for specific antigens. In this paper, we introduce a model for population-based artificial immune systems, termed as PAIS. PAIS models the dynamic process of human immune response as a quaternion ($\boldsymbol{G}$, $\boldsymbol{I}$, $\boldsymbol{R}$, $\boldsymbol{Al}$) [25], where $\boldsymbol{G}$ denotes exterior stimulus or antigen, $\boldsymbol{I}$ denotes the set of valid antibodies, $\boldsymbol{R}$ denotes the set of reaction rules describing the interactions between antibodies and $\boldsymbol{Al}$ denotes the dynamic algorithm describing how the reaction rules are applied to antibody population.

2.1. Quaternion model of PAIS

Among the four elements of the PAIS model ($\boldsymbol{G}$, $\boldsymbol{I}$, $\boldsymbol{R}$, $\boldsymbol{Al}$), antibody space $\boldsymbol{I}$ and dynamic algorithm $\boldsymbol{Al}$ depend on the antigen $\boldsymbol{G}$, and the practical design of reaction rules in set $\boldsymbol{R}$ depend on the antigen $\boldsymbol{G}$ and the representation method of antibodies.

2.1.1. Antigen $\boldsymbol{G}$

In immunology, an antigen is any substance that causes immune system to produce antibodies against it. In PAIS, antigens refer to the pending problems. Taking optimization problem (P) for example

$$(P)\ \begin{cases} \text{minimize} & f(\boldsymbol{x}) \\ \text{subject to} & g_i(\boldsymbol{x})<0 \quad i=1,2,\ldots,p \\ & h_j(\boldsymbol{x})=0 \quad j=p+1,p+2,\ldots,q \end{cases} \tag{1}$$

where $\boldsymbol{x}=(x_1,x_2,\ldots,x_m)$ is called the decision vector, antigen is the function of objective function $f(\boldsymbol{x})$, i.e. $G(\boldsymbol{x})=g(f(\boldsymbol{x}))$. Similar to the effect of antigen in immunology, it is the initial factor of artificial immune response.

2.1.2. Antibody space $\boldsymbol{I}$

In PAIS, B cells, T cells and antigen-specific lymphocytes are generally called antibodies. An antibody is a representation of a candidate solution of an antigen. The antibody $\boldsymbol{a}=a_1a_2\cdots a_l$ is the coding of variable $\boldsymbol{x}$, denoted by $\boldsymbol{a}=e(\boldsymbol{x})$, and $\boldsymbol{x}$ is called the decoding of antibody $\boldsymbol{a}$, expressed as $\boldsymbol{x}=e^{-1}(\boldsymbol{a})$. The representation of antibody $\boldsymbol{a}$ varies with antigen $\boldsymbol{G}$, can be binary string, real number sequence, symbolic sequence and characteristic sequence. In this study, we adopt real-coded presentation, i.e. $\boldsymbol{a}=e(\boldsymbol{x})=\boldsymbol{x}$.

Set $\boldsymbol{I}$ is called antibody space, where $\boldsymbol{a}\in\boldsymbol{I}$. An antibody population $\boldsymbol{A}=\{\boldsymbol{a}_1,\boldsymbol{a}_2,\ldots,\boldsymbol{a}_n\}$, $\boldsymbol{a}_k\in\boldsymbol{I}$, $1\leqslant k\leqslant n$, is an n-dimensional group of antibody $\boldsymbol{a}$, where the positive integer n is the antibody population size.

In order to explain the concepts of antibody and antibody population, we give a simple example as follows. For the optimization problem in Eq. (1), if a vector $\boldsymbol{x}_1=(0.5,\ 0.2,\ 4,\ 5)$ belongs to the feasible region, then $\boldsymbol{x}_1$ is a candidate solution of the optimization problem (P), the corresponding real-coded antibody is denoted by $\boldsymbol{a}_1=(0.5,\ 0.2,\ 4,\ 5)$. If $\boldsymbol{a}_1=(0.5,\ 0.2,\ 4,\ 5)$, $\boldsymbol{a}_2=(0.7,\ 0.6,\ 4,\ 7)$ and $\boldsymbol{a}_3=(0.2,\ 0.6,\ 6,\ 1)$ are three antibodies, then the set $\boldsymbol{A}=\{\boldsymbol{a}_1,\boldsymbol{a}_2,\boldsymbol{a}_3\}$ is an antibody population with size 3.

2.1.3. The set of reaction rules $\boldsymbol{R}$

The set $\boldsymbol{R}$ describes all the possible interactions between antibodies in antibody space $\boldsymbol{I}$. For antibody population $\boldsymbol{A}=\{\boldsymbol{a}_1,\boldsymbol{a}_2,\ldots,\boldsymbol{a}_n\}$, a rule $R\in\boldsymbol{R}$ can be expressed as

$$R(\boldsymbol{A})=R(\boldsymbol{a}_1+\boldsymbol{a}_2+\cdots+\boldsymbol{a}_n)=\boldsymbol{a}'_1+\boldsymbol{a}'_2+\cdots+\boldsymbol{a}'_m \tag{2}$$

where n, m are positive integers, the value of m depends on rule R, and the representation '+' is not the arithmetical operator, but only separates the antibodies on either side in Eq. (2). Eq. (2) shows that the n antibodies of $\boldsymbol{A}$ evolve into m antibodies on the right-hand side by the work of reaction rule R. For simulating biologic immune response in detail, it is necessary to design enough rules inspired by biologic immune system.

2.1.4. Dynamic algorithm $\boldsymbol{Al}$

$\boldsymbol{Al}$ is the algorithm simulating the process of antibody evolution and dominating interactions among antibodies during artificial immune response, including the format of the set $\boldsymbol{R}$ acting on antibody space $\boldsymbol{I}$, the calculation of antibody–antibody affinity and antibody–antigen affinity, the termination judgment and so on.