SIS epidemic model-based optimization

Guang-qiu Huang *

School of Management, Xi'an University of Architecture and Technology, Xi'an 710055, China

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A B S T R A C T

To solve complicated function optimization problems, a function optimization algorithm is constructed based on the Susceptible–Infective–Susceptible (SIS) epidemic model, the function optimization algorithm is called SIS algorithm, or SISA in short. The algorithm supposes that some male and female organisms exist in an ecosystem; each individual is characterized by a number of features; an infectious disease exists in the ecosystem and infects among individuals, the infection rule is that female individuals infect male individuals or male individuals infect female individuals, the disease attacks a part of features of an individual. The infected individuals can be cured; the cured individuals can be infected again after a period of time. The physique strength of an individual is decided synthetically by the infection, cure and susceptibility of certain features. The S–I operator is used to transfer feature information from male to female or female to male, the I–S operator is used to transfer feature information from male to male or female to female, the I–S operator and S–S operator are used to transfer feature information among individuals without sex difference. The individuals with strong physique can continue to grow, while the individuals with weak physique stop growing. Results show that the algorithm has characteristics of global convergence and high convergence speed for the complicated functions optimization problems, especially for high dimensional function optimization problems.

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1. Introduction

Consider a complicated function optimization problem:

$$\min f(\boldsymbol{X})$$
$$\text{s.t.} \begin{cases} g_i(\boldsymbol{X}) \geq 0, & i = 1, 2, \ldots, I \\ h_i(\boldsymbol{X}) = 0, & i = 1, 2, \ldots, E \\ \boldsymbol{X} \in S \subset R^n \end{cases} \tag{1}$$

where R^n is an n-dimensional Euclidean space; $\boldsymbol{X} = (x_1, x_2, \ldots, x_n)$ is an n-dimensional decision vector; S is a search space, or solution space; $f(\boldsymbol{X})$ is objective function; $g_i(\boldsymbol{X}) \geq 0$ is the ith inequality constraint, $i = 1, 2, \ldots, I$, I is the number of inequality constraints; $h_i(\boldsymbol{X}) = 0$ is the ith equality constraint, $i = 1, 2, \ldots, E$, E is the number of equality constraints. There are not any special limit conditions for objective function $f(\boldsymbol{X})$, constraint $g_i(\boldsymbol{X})$ and $h_i(\boldsymbol{X})$.

It is very difficult for traditional optimization techniques to solve the optimization problem; some population-based intelligent optimization algorithms have been developed to solve it. The existed intelligence optimization algorithms are as follows: Genetic Algorithm (GA) [1], Ant Colony Algorithm (ACA) [2], Particle Swarm Optimization (PSO) [3], Artificial Fish Swarm Algorithm (AFSA) [4], Biogeography-based Optimization (BBO) [5], Differential Evolution (DE) [6,7], Evolution Strategy (ES) [8,9] and so on. These algorithms do not require generally special restrictions on objective function and constraints, so they have broad applicability.

WANG Lei, PAN Jin and JIAO Li-cheng propose the immune algorithm (IA) with analogies to the concept and theory of immunity in biotic science [10], the core of the algorithm lies on constructing the immune operator that is realized by vaccination and immune selection, IA is proved theoretically convergent. LI Mao-jun, LUO An and TONG Tiao-sheng constitute several artificial operators producing new

* Tel.: +86 2982201532.
E-mail address: huangnan93@163.com

antibodies in IA [11], and then IA becomes the artificial immune algorithm (AIA). AIA succeeds to the mechanism of the survival of the fittest.

The vast majority of achievements of AIA are based on Burnet's clone selection theory [12]. Based on the theory, Dr. De Castro proposes a clone selection algorithm [13], its core uses the proportion duplication operator and the proportion variation operator, but this algorithm cannot express diversity quite well and is very difficult to be implemented. Based on a deep research into the immunity selection mechanisms, JIAO Licheng and DU Haifeng propose many kinds of high-level immunity clone selection algorithms such as the self-adaptive multi-clone programming algorithm, the self-adaptive dynamic clone algorithm, the immunity superiority clone algorithm and so on [14].

However, individuals involved in AIA are genes, the immune operator is constructed through the two operations: vaccine selection and vaccination; construction of an immune operator must be associated with actual optimization problems to be solved. AIA has not form a universal algorithm frame as yet, most proposed AIAs focus on basically improvements of other intelligent optimization algorithms, especially the evolutionary algorithms. Actually, there are only several immune operators in AIA, if other operators need to be constructed, the profound immune knowledge on life sciences is needed, and hence it is very difficult for researchers who are not good at the immune knowledge in life sciences. When dimension of an optimization problem is very high, the performance of AIA decreases greatly. Moreover, AIA cannot take into account state transitions among susceptibility, infection, morbidity and cure for any individuals.

The Susceptible–Infective–Susceptible (SIS) epidemic model, which is constructed according to KM Assumptions proposed by Kermack and Mckendrick in 1927, describes dynamic behaviors between susceptible and infectious individuals by some nonlinear dynamics methods [15]. The model describes an infectious disease not from the view of pathological knowledge of the infectious disease, but using a general transmission mechanism of the infectious disease to describe its spreading process, analyze the changing laws of infected individuals and reveal its dynamic characteristics.

In recent years, The SIS epidemic model is supported by extensive researches and applications [16–22]. In other scientific fields, the model gets wide applications. LI Guang-zheng and SHI Ding-hua study the stochastic SIS model of epidemic spreading on small-world network [23]. Based on the BA scale-free network's rich-club phenomenon and breadth first search, JI Peng and GE Hong-wei propose a search immunization strategy (RPBSI algorithm) which requires only local degree information [24]; the algorithm can lead to the eradication of the epidemic by immunizing a smaller fraction of the nodes than the acquaintance immunization in BA scale-free network and scientific collaboration networks. DING Xue-feng, MA Liang and DING Xue-song study the virus propagation characteristics, which depend on the topology of the entire network and presents a mathematical model of virus propagation to derive the epidemic threshold value and the relative conditions [25]. HU Jin-hua and YING Rui-yao use the SIS epidemic model to give a general framework of quantitative analysis on dynamic transfer of rural surplus labor in China [26]. WANG Vei-hong builds a theoretical model for the analysis of horizontal cross-border financial crisis propagation, i.e. a regression model with network propagation effect in it, and establishes also a dynamic evolution model that can better describe the process of financial crisis propagation with the help of SIS model borrowed from epidemiology [27]. YANG Meng, FU Xin-chu and WU Qing-chu study the global stability of the SIS epidemic model with infective medium on complex heterogeneous networks [28].

Because the SIS epidemic model has a good description on transmission laws of infectious diseases among individuals, it has good advantages to describe information exchange among many alternative solutions of optimization problem (1). Therefore the model will have certain special superiority to solve complicated function optimization problems like optimization problem (1). Based on this idea, the paper presents a new algorithm for function optimization based on the SIS epidemic model; we call it SIS Algorithm or SISA in short. The evolution operators presented in SISA do not need to be associated with actual optimization problems to be solved, SISA has universal evolutionary operators; because the SIS epidemic model does not need the support of pathological knowledge, SISA does not need the support of pathological knowledge also. Research results show that SISA has strong search capabilities and global convergence and is suitable to solve complicated functions optimization problems, especially high dimensional function optimization problems.

2. Design of SISA based on the SIS epidemic model

To enable SISA to be fit for many kinds of optimization problems, objective function $f(\boldsymbol{X})$ of optimization problem (1) is rewritten as follows:

$$F(\boldsymbol{X}) = \begin{cases} f(\boldsymbol{X}) & \forall i \in \{1, 2, \ldots, I\}, \ g_i(\boldsymbol{X}) \geq 0; \quad \forall j \in \{1, 2, \ldots, E\}, \ h_j(\boldsymbol{X}) = 0; \quad \boldsymbol{X} \in S \\ F_{\max} & \text{otherwise} \end{cases} \tag{2}$$

where $F_{\max}$ is a very large real number used to punish the alternative solutions that does not satisfy constraints of optimization problem (1).

2.1. KM assumptions

Kermack and Mckendrick used some nonlinear dynamics methods to build a mathematical model of infectious diseases; we refer to this model as a KM model. This model is based on the following three basic assumptions, known as KM Assumptions [15]:

Assumption A. The number of individuals in an ecosystem is constant and does not change over time.

Assumption B. Owing to the influence of an infectious disease, the rate that the number of susceptible individuals changes over time is proportional to the product of the number of susceptible individuals and the number of infected individuals.

Assumption C. The rate transferring from a class formed by infected individuals to another class formed by recovered individuals is proportional to the number of infected individuals.

Based on the three assumptions, individuals in an ecosystem are divided into two categories:
Class S: the category of susceptible individuals, namely all the non-infected individuals in an ecosystem, these individuals are vulnerable to be infected if they make effective contact with the infected ones.