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Bacterial colony foraging optimization

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ARTICLE INFO

Article history:

Received 23 November 2012

Received in revised form

14 March 2013

Accepted 17 April 2013

Available online 16 February 2014

Keywords:

Bacterial foraging

Chemotaxis

Self-adaptation

Cell-to-cell communication

Global optimization

ABSTRACT

This paper proposes a novel bacterial colony foraging (BCF) algorithm for complex optimization problems. The proposed BCF extend original bacterial foraging algorithm to adaptive and cooperative mode by combining bacterial chemotaxis, cell-to-cell communication, and a self-adaptive foraging strategy. The cell-to-cell communication enables the historical search experience sharing among the bacterial colony that can significantly improve convergence. With the self-adaptive strategy, each bacterium can be characterized by focused and deeper exploitation of the promising regions and wider exploration of other regions of the search space. A rigorous performance analysis is given where the proposed algorithm is benchmarked against four state-of-the-art reference algorithms using both a classical and a composition test function suites. The individual and collective bacterial foraging behaviors of the proposed algorithmic model are also studied. Statistical analysis of all these tests highlights the significant performance improvement due to the beneficial combination and shows that the proposed algorithm outperforms the reference algorithms.

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1. Introduction

Nature serves as a rich source of concepts, principles, and mechanisms for designing artificial computational systems to solve complex engineering problems. In optimization domain, researchers have developed many effective stochastic techniques that mimic the specific structures or behaviors of certain creatures. For examples, genetic algorithm (GA), originally conceived by Holland [1], represent a fairly abstract model of Darwinian evolution and biological genetics; ant colony optimization (ACO), proposed by Marco Dorigo [2,3], is developed based on the foraging behaviors of real ant colonies; particle swarm optimization (PSO), proposed by Kennedy and Eberhart [4,5], glean ideas from social behaviors of bird flocking and fish schooling. These algorithms have been found to perform better than the classical heuristic or gradient-based methods, especially for optimizing the nondifferentiable, multimodal and discrete complex functions. Currently, these nature-inspired paradigms have already come to be widely used in many areas.

In recent years, the computational models of chemotaxis (i.e. the bacterial foraging behavior) have attracted more and more attention, due to its research potential in engineering applications.

A few models have been developed to mimic bacterial foraging behavior and have been applied for solving some practical problems [6–8]. Among them, bacterial foraging optimization (BFO) is a successful population-based numerical optimization algorithm that mimics the foraging behavior of *E. coli* bacteria [8]. Until now, BFO has been applied to some engineering problems, such as optimal control [9], optimal power flow [10], color image enhancement [11] and machine learning [12]. However, classical BFO algorithm suffers from two major drawbacks: (1) as a bacterial colony evolves, the fixed run-length unit of each bacterium may lead them trap in local optima or oscillate about the optima; and (2) there is no information sharing among the bacterial colony. Thus, experimentation with complex and multimodal benchmark functions reveals that the BFO algorithm possesses a poor convergence behavior and its performance heavily decreases with the growth of search space dimensionality and problem complexity.

Several BFO variants have been developed to improve its optimization performance. In [13], Tripathy and Mishra proposed an improved BFO algorithm using two approaches: (1) in order to speed up the convergence, the average value is replaced by the minimum value of all the chemotactic cost functions for deciding the bacterium's health; and (2) for swarming, the distances of all the bacteria in a new chemotactic step are evaluated from the globally optimal bacterium to these points and not the distances of each bacterium from the rest of the others. Mishra [14] proposed a fuzzy bacterial foraging (FBF) algorithm using Takagi–Sugeno type fuzzy inference scheme to select the optimal chemotactic step size in BFO. The FBF algorithm was

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shown to outperform both classical BFO and a genetic algorithm when applied to the harmonic estimation problem. Kim et al. proposed a hybrid approach involving GA and BFO for function optimization [15]. The proposed algorithm outperformed both GA and BFO over a few numerical benchmarks and a practical PID controller design problem. Biswas et al. proposed a synergism of BFOA with the particle swarm optimization [16]. The new algorithm, named by the authors as bacterial swarm optimization (BSO), was shown to perform in a statistically better way as compared to both of its classical counterparts over several numerical benchmarks.

Three improved versions of BFO, namely the cooperative bacterial foraging optimizer (CBFO), adaptive bacterial optimization, and multi-colony bacterial foraging optimization (MCBFO), have been described in our previous works [29,30,34]. In [29], instead of simply considering chemotaxis behavior of single bacterium, MCBFO also introduced the communication strategies employs by natural multi-colony bacterial community in order to coordinate pattern emerges, which is lacking from the mentioned chemotaxis inspired algorithms. Then the MCBFO was evaluated on the static RFID network planning problem in comparison with GA and PSO. In [30], by employing the adaptive foraging strategies, two proposed ABFO algorithms are able to adjust the run-length unit parameter dynamically during algorithm execution in order to balance the exploration/exploitation tradeoff. In [34], the proposed CBFO applied two cooperative approaches to the original BFO, namely the serial heterogeneous cooperation on the implicit space decomposition level and the serial heterogeneous cooperation on the hybrid space decomposition level.

Building on the success of our preliminary work on bacterial foraging algorithms, this paper aims to demonstrate convincingly that the self-adaptive and communication approaches are both effective strategies and can be utilized to help scaling up the performance of bacterial foraging algorithms for solving complex optimization problems with high dimensionality. That is, this paper extend the classical BFO to a novel bacterial colony foraging (BCF) optimization model by applying two enhanced manipulated steps, namely a PSO-based cell-to-cell communication and a self-adaptive foraging strategy that mimics the area concentrated search (ACS) [20] behaviors in nature. In the proposed BCF model, each artificial bacterium can climb the nutrient gradient based on not only its own experience but also the knowledge of the others; also, each bacterium can strike a balance between the exploration and the exploitation of the search space during its evolution, by adaptively tuning the magnitude of its chemotactic step size.

Several experiments were performed to evaluate the performance of the proposed algorithm. The first test-suite contains ten classical benchmark functions, namely the Sphere, Rosenbrock, Ackley, Rastrigin, Griewank, Weierstrass, Sphere_noise, Noisy, Rotated hyper-ellipsoid, and Noncontinuous Rastrigin's function functions. Moreover, this work used a novel composition test function suite developed by Liang et al. [17]. This benchmark set is made up by six composed functions, which were especially designed to test optimization algorithms providing many desirable properties, namely shifted, non-continuous, rotated, and narrow global basin of attraction. The proposed BCF algorithm has been compared with its classical counterpart, the classical BFO algorithm [8], the very popular swarm-intelligence algorithm known as PSO [4,5], a hybrid optimization technique that synergistically couples BFOA with PSO that called BSO [16], and a standard real-coded genetic algorithm (GA) [18] over both classical and composition test suites with respect to the statistical performance measures of solution quality and convergence speed.

The proposed BCF and its application on global optimization problem described in this paper enhance our previously proposed methods in the following aspects:

- The proposed BCF combines bacterial chemotaxis with cell-to-cell communication based cooperation. This combination

successfully casts the bacterial foraging algorithm into cooperative foraging fashion and remarkably improves the convergence speed of the bacterial colony.

- By introducing a self-adaptive foraging strategy, namely the area concentrate search (ACS), the previous bacterial foraging optimization model has been extended to an adaptive scheme in this paper. This adaptive scheme can effectively maintain the bacterial colony diversity in the search process.

The rest of the paper is organized as follows. In Section 2, we outline the classical BFO in sufficient details. In Section 3, the proposed BCF algorithm will be introduced and its implementation details will be given. In Section 4, the experiment studies of the proposed BCF and the other algorithms are presented with descriptions of the benchmark functions, experimental settings, and experimental results. Finally, conclusions are drawn in Section 5.

2. Classical bacterial foraging optimization

Bacterial foraging optimization algorithm is inspired by an activity called “chemotaxis” exhibited by bacterial foraging behaviors. Motile bacteria such as *E. coli* and *salmonella* propel themselves by rotation of the flagella. To move forward, the flagella rotates counterclockwise and the organism “swims” (or “runs”), while a clockwise rotation of the flagellum causes the bacterium to randomly “tumble” itself in a new direction and swim again [19]. Alternation between “swim” and “tumble” enable the bacterium to search for nutrients in random directions. Swimming is more frequent as the bacterium approaches a nutrient gradient. Tumbling, hence direction changes, is more frequent as the bacterium moves away from some food to search for more. Basically, bacterial chemotaxis is a complex combination of swimming and tumbling that keeps bacteria in places of higher concentrations of nutrients. Chemotaxis can also be considered as the optimal foraging decision making capabilities of bacteria.

2.1. BFO model

The original BFO system consists of four principal mechanisms, namely chemotaxis, swarming, reproduction, and elimination-dispersal [8]. We briefly describe each of these processes as follows:

2.1.1. Chemotaxis

In the original BFO, a unit walk with random direction represents a “tumble” and a unit walk with the same direction in the last step indicates a “run”. Suppose $\theta^i(j, k, l)$ represents the i th bacterium at j th chemotactic, k th reproductive, and l th elimination-dispersal step. $C(i)$ is the chemotactic step-size for this bacterium during each run or tumble (run-length unit). Then in each computational chemotactic step, the movement of the i th bacterium can be represented as

$$\theta^{i(j+1, k, l)} = \theta^i(j, k, l) + C(i) \frac{\Delta(i)}{\sqrt{\Delta^T(i)\Delta(i)}} \quad (1)$$

where $\Delta(i)$ is the direction vector of the j th chemotactic step. When the bacterial movement is run, $\Delta(i)$ is the same with the last chemotactic step; otherwise, $\Delta(i)$ is a random vector whose elements lie in $[-1, 1]$.

With the activity of “run” or “tumble” taken at each step of the chemotaxis process, a step fitness for each bacterium, denoted as $J(i, j, k, l)$, will be evaluated.

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