Applied Soft Computing 31 (2015) 274–292

Contents lists available at ScienceDirect

Applied Soft Computing

journal homepage: www.elsevier.com/locate/asoc

An improved multi-objective bacteria colony chemotaxis algorithm and convergence analysis

Lu Zhi-gang*, Zhao Hao, Xiao Hai-feng, Wang Hao-rui, Wang Hui-jing

Key Lab of Power Electronics for Energy Conservation and Motor Drive of Hebei Province, Yanshan University, 066004, China

ARTICLE INFO

Article history:
Received 26 June 2013
Received in revised form
16 December 2014
Accepted 24 February 2015
Available online 16 March 2015

Keywords:
Multi-objective optimization
Bacterial chemotaxis
Adaptive grid
Convergence analysis

ABSTRACT

In this paper, a novel algorithm based on the bacterial colony chemotaxis (BCC) algorithm is developed to solve multi-objective optimization problems. The main objective of the paper is to improve the performance of BCC. Hence, the main work is to add three improvements, which are improved adaptive grid, oriented mutation based on grid and adaptive external archive, in order to improve the convergence performance on multi-objective optimization problems and the distribution of solutions. This paper also presents a first and simple convergence analysis of the general Pareto-based MOBCC. The proposed algorithm is validated using 12 benchmark problems and four performance measures are implemented to compare its performance with the MOBCC algorithm, the NSGA-II algorithm, and the MOEA/D algorithm. The simulation results confirmed the effectiveness of the algorithm.

1. Introduction

It is common that problems with two or more (often conflicting) objectives to be simultaneously optimized in real-world applications. Such problems are called multi-objective optimization problems (MOP). MOP are optimization problems that optimize more than one objective function in a specific area and are to find solutions that contain a vector of decision variables and satisfy the restrictions. A multi-objective optimization problem can be formulated as follows [1]:

$$\begin{aligned} &\text{Minimize/Maximize}: && f_i(x) && i = 1, 2, \ldots, N \\ &\text{Subject to}: && g_j(x) \le 0 && j = 1, 2, \ldots, J \\ & && h_k(x) = 0 && k = 1, 2, \ldots, K \end{aligned}$$

where $x = (x_1, x_2, \ldots, x_n)$ is the vector of decision variables; $f_i(x)$ are the i objective functions which satisfy the J inequalities $g_j(x)$ and the K equalities $h_k(x)$ constraint functions.

Different from single objective optimization problem (SOP), it is impossible to get a single optimal for multi-objective optimization problems. MOP contains a set of optimal solutions which are non-dominated and balanced between several objective functions, that is Pareto optimal front (POF). The traditional ways can not deal with these complex problems sufficiently for the lack of integral mathematical models and the ability to handle a large number of variables. Now there have been a lot of elitist algorithms to solve multi-objective optimization problems, such as non-dominated Sorting Genetic Algorithm (NSGA-II) [2], Strength Pareto Evolutionary Algorithm (SPEA-II) [3], Multiple Objectives Particle Swarm Optimization (MOPSO) [4], and bacterial chemotaxis (BC) [5].

Many people also have researched on the algorithms for real-world application. Niknam et al. [6] developed multi-objective new fuzzy self-adaptive particle swarm optimization (MNFSAPSO) to overcome local optima problems and he also proposed an Evolutionary Algorithm using the Modified Teaching-Learning-Algorithm [7] and the two algorithms are used to solve multi-objective optimization problems in distribution network with renewable energy sources. Chen [8,9] proposed bacterial colony foraging optimization (BCFO) algorithm for complex optimization problems and it is applied to a real-world application of dynamic RFID network optimization.

Recently, bacterial colony chemotaxis (BCC) optimization algorithm has attracted more and more attention. Bremermann [10] pioneered chemotaxis algorithm in 1974. Basing on the research of Berg, Brown and Bremermann, Müller et al. [11] developed BC optimization algorithm in 2002, which is an environmental chemical attractant inspired optimization algorithm that performs similar to standard evolutionary algorithm but worse than evolution strategies with enhanced convergence properties. However, it opened up a new research field. Li et al. [12] introduced the colony to improve the basic BC algorithm, proposing bacterial colony chemotaxis (BCC) optimization algorithm. Guzmán [5] firstly applied the

* Corresponding author. Tel.: +86 13803358585.
E-mail address: zhglu@ysu.edu.cn (Z.-g. Lu).

http://dx.doi.org/10.1016/j.asoc.2015.02.046
1568-4946/

BC algorithm to solve multi-objective optimization problems and got better result than the NSGA-II genetic algorithm and the particle swarm-based algorithm NSPSO. Cheng et al. [13] developed MOBCC algorithm to figure out Multi-objective optimization problems and it performed well. Lu et al. [14] improved multi-objective optimization bacterial colony chemotaxis with Lamarckian constraint handling method to solve low-carbon emission/economic power dispatch.

BC is a simple and robust algorithm. In BC algorithm, every bacterium searches the optimal value according to its own judgment. Bacteria use their own memory to make a temporal space comparison of the gradients found, and decide the length and duration of their next movement. As the length and duration are computed by probability distributions, it indicates that they are able to escape from local optimal solutions and find the global optimal value. BCC is proposed based on BC, which adds communication features to the basic algorithm. BCC performs better on convergence ability and computation speed than BC. As it is different in the realization principle from other traditional algorithms, and is promising in multi-objective optimize problems, we study and make some improvements on its performance in this paper.

The main contributions of this paper are: proposing an improved multi-objective BCC algorithm based on grid (GMOBCC) to improve the convergence performance and uniformity of solutions; analyzing the convergence properties of the multi-objective BCC algorithm.

In this paper, three main modifications are introduced to improve the diversity and uniformity of nondominated solutions. Firstly, the improved adaptive grid strategy is applied to maintain the diversity and uniformity of nondominated solutions in the external archive. Secondly, the oriented mutation based on grid is proposed to generate more nondominated solutions in the sparse area of the current archive. Thirdly, the concept of adaptive archive is introduced, whose capacity can change along with the searching process. The last two methods are not only remedies to make up the loss of nondominated solutions caused by adaptive grid, but also efficient methods to generate more nondominated solutions to provide a good basic to maintain the diversity and uniformity of solutions.

To appraise its performance, the proposed algorithm is tested on 12 benchmark problems, and four different performance measures are implemented to compare its properties with those of MOBCC, NSGA-II [2], and MOEA/D [15].

This paper is organized as follows. Section 2 describes the basic bacterial chemotaxis model. Section 3 presents the GMOBCC algorithm. The convergence analysis of the multi-objective BCC algorithm is proved in Section 4. In Section 5, GMOBCC is applied on 12 testing functions and the results are compared with other optimization algorithms. Conclusions and some possible paths for future research are finally drawn in Section 6.

2. Multi-objective optimization problems and BCC algorithm

2.1. The basic BCC algorithm

The chemotactical behavior of bacteria is modeled by making the following assumptions according to Dahlquist et al. [16]. (1) The path of a bacterium is a sequence of straight-line trajectories joined by instantaneous turns, each trajectory being characterized by speed, direction, and duration. (2) All trajectories have the same constant speed. (3) When a bacterium turns, its choice of a new direction is governed by a probability distribution, which is azimuthally symmetric about the previous direction. (4) The angle between two successive trajectories is governed by a probability distribution. (5) The duration of a trajectory is governed by an exponentially decaying probability distribution. (6) The probability distributions for both the angle and the duration are independent of parameters of the previous trajectory (Fig. 1).

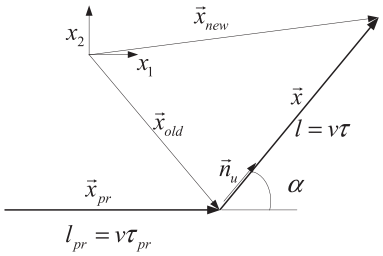

Fig. 1. 2-D path of a bacterium.

The 2-D model of the basic multi-objective BCC algorithm is presented as follows:

(1) Compute the velocity. The velocity is a constant value.

$$v = const \tag{1}$$

(2) Compute the duration τ. It is a random variable governed by an exponential probability density function.

$$P(X = \tau) = \frac{1}{T}\ell^{-\tau/T} \tag{2}$$

where the expectation $\mu = E(X) = T$ and the variance $\sigma^2 = Var(X) = T^2$.

The value T is given by

$$T = \begin{cases} T_0 & \text{if } (\vec{x}_{pre} \succ \vec{x}_{cur}) | (\vec{x}_{pre} \sim \vec{x}_{cur}) \\ T_0\left(1 + b \times \min\left(\left|\frac{f_{pr1}}{l_{pr}}\right|, \left|\frac{f_{pr2}}{l_{pr}}\right|\right)\right) & \text{if } \vec{x}_{pre} \prec \vec{x}_{cur} \end{cases} \tag{3}$$

where T_0 is the minimal mean time, $T_0 = \varepsilon^{0.03} \cdot 10^{-1.73}$; f_{pr} is the difference between the actual and the previous function value; $l_{pr} = x_{pr}$, where x_{pr} is the vector connecting the previous and the actual position in the parameter space; b is the dimensionless parameter, $b = T_0 \cdot (T_0^{-1.54} \cdot 10^{0.6})$.

(3) Compute the new direction. The probability density distribution of the angle α between the previous and the new direction is Gaussian and reads, for turning right or left, respectively:

$$P(X = \alpha, v = \mu) = \frac{1}{\sqrt{2\pi\sigma}} \exp\left[-\frac{\alpha - v}{2\sigma^2}\right] \tag{4}$$

$$P(X = \alpha, v = -\mu) = \frac{1}{\sqrt{2\pi\sigma}} \exp\left[-\frac{\alpha - v}{2\sigma^2}\right] \tag{5}$$

where $\alpha \in [0^\circ, 180^\circ]$ and the expectation value μ and the variance σ are determined by the formulation:

$$(\mu, \sigma) = \begin{cases} \begin{pmatrix} \mu = 62^\circ \\ \sigma = 26^\circ \end{pmatrix}, & \text{if } (f_{pre} \succ f_{cur}) | (f_{pre} \sim f_{cur}) \\ \begin{pmatrix} \mu = 62^\circ(1 - \cos(\theta)) \\ \sigma = 26^\circ(1 - \cos(\theta)) \end{pmatrix}, & \text{if } f_{pre} \succ f_{cur} \end{cases} \tag{6}$$

with:

$$\cos(\theta) = e^{-\tau_C \tau_{Pr}} \tag{7}$$

where τ_C is the correlation time, $\tau_C = (b/T_0)^{0.31} \cdot 10^{1.16}$, and τ_{Pr} the duration of the previous step.

(4) Compute the new location $\vec{x}_{new1}$.

$$\vec{x}_{new1} = \vec{x}_{pre} + v \cdot \tau \tag{8}$$

(5) Compute the nondominated center. As bacteria do share information among each other [15], its movement will be affected