A novel multiobjective optimization algorithm based on bacterial chemotaxis

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ARTICLE INFO

ABSTRACT

In this article a novel algorithm based on the chemotaxis process of *Echerichia coli* is developed to solve multiobjective optimization problems. The algorithm uses fast nondominated sorting procedure, communication between the colony members and a simple chemotactical strategy to change the bacterial positions in order to explore the search space to find several optimal solutions. The proposed algorithm is validated using 11 benchmark problems and implementing three different performance measures to compare its performance with the NSGA-II genetic algorithm and with the particle swarm-based algorithm NSPSO.

1. Introduction

Most real-world optimization problems require making decisions involving two or more goals that typically are in contradiction with each other. When these goals are the minimization or maximization of functions they are typically referred to multiobjective optimization (MO). From the 1950s, in the area of operational research, a variety of methods known as classical has been developed for the solution of multiobjective optimization problems (MOP). These methods are based on formal logic or mathematical programming. Some of the most representative classical methods are linear programming, the weighted sum method and the goal programming method (Dantzig and Thapa, 1997). As an alternative to classical methods, a variety of techniques inspired on natural processes has emerged in the last two decades.

The emulation of nature has inspired scientists in various fields through the history of mankind. Recently, due to advances in computing and the emergence of new ideas based on the behavior of living organisms and natural processes, the techniques inspired in nature have gained increasing interest motivated by two basic aspects (De Castro and Von Zuben, 2004):

(1) Traditional methods have proven to be unable to adequately handling complex problems, characterized by the lack of complete mathematical models and the manipulation of a large number of variables.
(2) To a variety of engineering problems there is a similar version in nature.

Among bio-inspired optimization techniques, the most known are genetic algorithms (AGs). The pioneering work in the practical application of the fundamentals of AGs to MO is the vector evaluated genetic algorithm (VEGA) (Schaffer, 1984). At present, the most popular genetic algorithm for solving MOP is the nondominated sorting genetic algorithm II (NSGA-II) (Deb et al., 2002). Another bio-inspired approach is the so-called particle swarm optimization (PSO), which was recently implemented in the solution of MOP using algorithms such as nondominated sorting particle swarm optimizer (NSPSO) (Li, 2003), multi-objective particle swarm optimization (MOPSO) (Coello et al., 2004), and time variant multi-objective particle swarm optimization (TV-MOPSO) (Kumar et al., 2007). Another interesting biological process that has been already implemented as an optimization technique is the bacterial chemotaxis. About this novel technique Amos et al. (2007) exposed the potential of implementing bacterial chemotaxis as a distributed optimization process, recognizing that in natural colonies, it is the interaction and communication between bacteria the mechanism that enables them to develop biologically advantageous patterns.

2. Multiobjective optimization problems (MOP)

A multiobjective optimization problem is defined as the problem of finding a vector of decision variables that satisfies

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some restrictions and optimizes a vector function, which elements represent the values of the functions. A MOP may be formulated as follows (Deb, 2001):

$$
\begin{aligned}
\text{Maximize/minimize}: \quad & f_m(x) && m = 1, 2, ..., M \\
\text{Subject to}: \quad & g_j(x) \geq 0 && j = 1, 2, ..., J \\
& h_k(x) = 0 && k = 1, 2, ..., K \\
& x_i^L \leq x_i \leq x_i^U && i = 1, 2, ..., n
\end{aligned}
$$

where x is the vector of decision variables $x = (x_1, x_2, ..., x_n)^T$ and $f_m(x)$ are the m objective functions. The values x_i^L and x_i^U represent, respectively, the minimum and the maximum acceptable values for the variable x_i. These values define the boundary of the search space. The J inequalities g_j and the K equalities h_k are known as constraint functions.

For MOP, instead of a single optimal, there is a set of optimal solutions known as Pareto optimal front (POF). Any solution of this set represents a balance between the objective functions; therefore, it is not possible to say that there is other solution in the search space which is superior to this one when all objectives are considered. In the minimization MOP, Pareto optimality can be mathematically defined as follows (Chinchuluun and Pardalos, 2007):

Pareto optimality: A point $x^* \in S$ with $f(x^*)$ is called (globally) Pareto optimal (or nondominated), if and only if there exists no point $x \in S$ such that $f_i(x) \leq f_i(x^*)$ for all $i = 1, 2, ..., m$ and $f_l(x) < f_l(x^*)$ for at least one index $l \in \{1, 2, ..., m\}$, where S is the feasible region.

In most cases it is not easy to find analytical expressions for the line or curve that contains the POF; thus, commonly optimal solutions points and the objective functions values in them are calculated. In order to find optimal solutions, there are two goals that any multiobjective optimization algorithm (MOA) seeks to achieve (Deb, 1999): (1) Guide the search towards the global Pareto optimal region; (2) Maintain the population diversity in the Pareto optimal front.

In this work a novel algorithm based on bacterial chemotaxis and communication exchange in bacterial colonies is developed to solve MOP. The proposed algorithm is validated using 11 benchmark problems. Three different performance measures were also implemented to compare the performance of the proposed algorithm with the NSGA-II genetic algorithm and with the particle swarm-based algorithm NSPSO.

3. Bacterial chemotaxis

Chemotaxis is a cell movement in response to gradients of chemical concentrations present in the environment. This movement and the chemical substances involved in it are used by bacteria as a survival strategy that allows them to search for nutrients and avoid noxious environments.

A bacterium is a prokaryotic unicellular organism. Its structure is basically conformed by a central body of microscopic size that can take many different forms (Young, 2006) and whose size can vary from 0.01 μm^3 to a volume 10^{10} times bigger (Rappe et al., 2002; Angert et al., 1993). Many bacteria are endowed with a series of rotating flagella in its cell surface that act as propellants, allowing them to swim at a speed of 10–35 $\mu m/s$ (Eisenbach et al., 2004). In addition to the appropriate structure to move in an autonomous way, bacteria have potent receivers (chemoreceptors) located at the cell surface, capable of detecting temporal-space changes of chemical concentrations in the environment that surrounds them. In this way, when an external perturbation is detected, bacteria use their memory (Segall et al., 1986) to make a temporal-space comparison of the gradients found. Depending on the external conditions sensed, bacteria change their movement from a random walk to a biased random walk.

This work was based on chemotaxis process of one of the most studied bacterium, the (E. coli). This is a bacterium present in human intestine that has 8–10 left-handed helix configured flagella placed randomly on its cell body. These flagella used for locomotion, can rotate at high speeds (270 r.p.s.) (Kudo et al., 1990), stop momentarily and change the direction of rotation in a controlled manner (Eisenbach et al., 2004). As a result of the flagella helix configuration, when they all move counterclockwise act as propellants moving the bacterium gently forward in an almost rectilinear movement called swim. Otherwise, if the flagella rotate clockwise, they destabilize, propelling the bacterial body in different directions at the same time, so the bacterial body tumbles randomly. Using different combinations of swim and tumble, varying the length and duration of these movements, bacteria explore the environment during their lifetime.

The chemotactical strategy of E. coli can be summarized as follows (Passino, 2002):

If a bacterium finds a neutral environment or an environment without gradients, it alternately tumbles and swims.
If a bacterium finds a nutrient gradient, the bacterium spend more time swimming and less time tumbling, so the directions of movement are "biased" toward increasing nutrient gradients.
If a bacterium finds a negative gradient or noxious substances, it swims to better environments or run away from dangerous places.

4. Bacterial chemotaxis as optimization process

Chemotaxis is a strategy of movements optimized by nature. The chemotactical behavior of bacteria as an optimization process was modeled for the first time by Bremermann (1974) in the early 1970s. Two decades later, was proposed an algorithm based on Bremmerman's work and was applied to maximize a profit function for fed-batch bioreactors (Montague and Wardb, 1994). Also inspired by Bremmerman's work, Müller et al. (2002) developed an algorithm and applied it to the solution of inverse airfoil design.

In 2002, a new optimization algorithm based on foraging behavior of bacteria was introduced by Passino (2002). This novel algorithm which is known as bacterial foraging optimization algorithm (BFOA), considers not only the chemotactical strategy but also other stages of bacterial foraging behavior as swarming, reproduction and elimination and dispersal; besides communication between bacteria acquires great influence on the entire process, getting closer to the concept that foraging is a phenomenon of a bacterial colony rather than an individual behavior. In subsequent publications of Passino with other authors (Liu and Passino, 2002; Gazi and Passino, 2002; Passino, 2005), have been made tests of convergence and stability analysis of this technique. Since its initial publication but especially in the last 3 years, new modified versions of BFOA have been proposed (De Castro and Von Zuben, 2004; Tang and Wu, 2006; Biswas, 2007; Chen, 2007); also the original algorithm and some of the modified versions have been successfully implemented to solve various kinds of engineering problems. In Mishra (2005) it is presented as an application for harmonic estimation problem in power systems; in Kim and Cho (2006) the algorithm is used for tuning the PID controller of an AVR; an optimal power flow solution is proposed in Li et al. (2007); in Wu et al. (2007) it is shown as an application of job shop scheduling benchmark problems; in Lin et al. (2007) the parameters of membership