

A Novel Bacterial Foraging Optimizer with Linear Decreasing Chemotaxis Step

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Abstract—Bacterial foraging optimization (BFO) is a relatively new bio-heuristic algorithm which is based on a metaphor of social interaction of *E. coli* bacteria. Although the algorithm has successfully been applied to many kinds of real word optimization problems, experimentation with complex problems reports that the basic BFO algorithm possesses a poor performance. Thus a novel bacterial foraging optimizer with linear decreasing chemotaxis step (BFO-LDC) algorithm is proposed in the present paper. The performance of the proposed BFO-LDC is amply demonstrated by applying it for four classical test functions and comparing it with basic BFO. And the results obtained show this proposed algorithm greatly improves the efficiency of basic BFO algorithm.

Keywords—optimization; bacterial foraging; chemotaxis

I. INTRODUCTION

In 2002, a new natural heuristic optimization algorithm based on foraging behavior of bacteria was introduced [1, 2], which was known as bacterial foraging optimization (BFO) algorithm. Recently, the BFO algorithm has successfully been used in many practical applications. In 2007, H. N. Chen et al. proposed the multi-colony bacteria foraging optimization to solve complex RFID network planning problem [3]. In 2008, B. Niu presented a lifecycle model (LCM) to simulate bacterial evolution from a finite population of *E. coli* bacteria [4]. In addition, BFO algorithm has been employed to improve the proportional-integral derivative (PID) controller performance [5, 6], and also many other applications such as adaptive control [7], harmonic signal estimation [8], optimal power flow [9], stock market prediction [10]. However, experimentation with complex problems reveals that the BFO algorithm possesses a poor convergence behavior and its performance heavily depends on the chemotaxis step length of a virtual bacterium in a trial solution of the optimization problem.

In order to improve the searching performance of the basic BFO, of which chemotaxis step length was set to a constant, we proposed a novel bacterial foraging optimizer with linear decreasing chemotaxis step (BFO-LDC) in the present paper,

which allows each bacterium keeps a good balance between exploration and exploitation during algorithmic execution by decreasing its run-length unit linearly. To evaluate the performance of BFO-LDC, extensive studies based on a set of four well-known benchmark functions have been carried out. We also compared the test results with those of basic BFO respectively. The simulation results are very impressive. The BFO-LDC algorithm shows remarked performance improvement over the basic BFO.

The following section gives a short introduce to the BFO algorithm including its different motile behaviors. Section 3 describes our proposed improved BFO algorithm. The in-depth analysis of the influence of the chemotaxis step length parameter on the bacterial behavior is also presented here. Section 4 presents the performance of the BFO-LDC with comparison of basic BFO. This section gives a detailed analysis of the experimental results are obtained. Finally the conclusions and future research scopes are presented in Section 5.

II. BACTERIAL FORAGING OPTIMIZATION

Literature [1] introduces the *E. coli* bacterium has a control system that enables it to achieve a complex type of search and avoidance behavior. Evolution has designed this control system. It is robust and clearly very successful at meeting its goals of survival when viewed from a population perspective. In addition the control system dictates that bacterial foraging process can be subdivided into four motile behaviors namely chemotaxis, swarming, reproduction, and elimination and dispersal.

- 1) Chemotaxis: This process simulates the movement of an *E. coli* cell through swimming and tumbling via flagella. Biologically an *E. coli* bacterium can move in two different ways. It can swim for a period of time in the same direction or it may tumble, and alternate between these two models of operation for a run lifetime. Supposed $\theta^{i(j,k,l)}$ represents the i th bacterium at j th chemotactic k th reproductive and

l th elimination and dispersal step. $C(i)$ is the size of the step taken in the random direction specified by the tumble (run length unit). Δ indicates a vector in the random direction whose elements lie in $[-1, 1]$. Then in computation chemotaxis the movement of the bacterium may be represented by:

$$\theta'(j+1,k,l) = \theta'(j,k,l) + C(i) \frac{\Delta(i)}{\sqrt{\Delta^T(i)\Delta(i)}} \quad (1)$$

- 2) *E. coli* bacterium has a specific sensing, actuation and decision-making mechanism. As each bacterium moves, it releases attractant to signal other bacteria to swarm towards it. Meanwhile, each bacterium releases repellent to warn other bacteria to keep a safe distance from it. BFA simulates this social behavior by representing the combined cell-to-cell attraction and repelling effect as:

$$\begin{aligned} J_{cc}(\theta, P(j,k,l)) &= \sum_{i=1}^S J_{cc}^i(\theta, \theta^i(j,k,l)) \\ &= \sum_{i=1}^S \left[-d_{attract} \exp(-w_{attract} \sum_{m=1}^p (\theta_m - \theta_m^i)^2) \right] \\ &\quad + \sum_{i=1}^S \left[h_{repellent} \exp(-w_{repellent} \sum_{m=1}^p (\theta_m - \theta_m^i)^2) \right] \end{aligned} \quad (2)$$

Where $J_{cc}(\theta, P(j,k,l))$ is the cost function value to be added to the actual cost function to be minimized to present a time varying cost function, S is the total number of bacteria, p is the number of parameters to be optimized which are present in each bacterium, and $d_{attract}, w_{attract}, h_{repellent}, w_{repellent}$ are different coefficients that are to be chosen properly.

- 3) **Reproduction:** The health status of each bacterium is calculated as the sum of the step fitness during its life, that is $\sum_{j=1}^{N_c} J(i, j, k, l)$. All bacteria are sorted in reverse order according to health status. Only the first half of population survives and a surviving bacterium split into two bacteria, which are placed in the same location. Thus the population of bacteria keeps constant.
- 4) **Elimination and Dispersal:** For the purpose of improving the global search ability, elimination-dispersal event is defined after N_{re} steps of reproduction. The bacteria are eliminated and dispersal to random positions in the optimization domain according to the probability P_{ed} . This elimination-dispersal event helps the bacterium avoid being trapped into local optima. The number of the event is denoted as N_{ed} .

III. BACTERIAL FORAGING OPTIMIZATION WITH LINEAR DECREASING CHEMOTAXIS

While introducing the concept of chemotaxis step (C), Kevin M. Passino observed that a better performance would be obtained if a reasonable C value were chosen and supported his statement with a single case study. In fact, a large C value facilitates an exploration of the whole search space while a small C value facilitates an exploitation of the promising areas. One of the major driving forces of BFO algorithm performance is the chemotaxis step length of a virtual bacterium in a trial solution of the optimization problem.

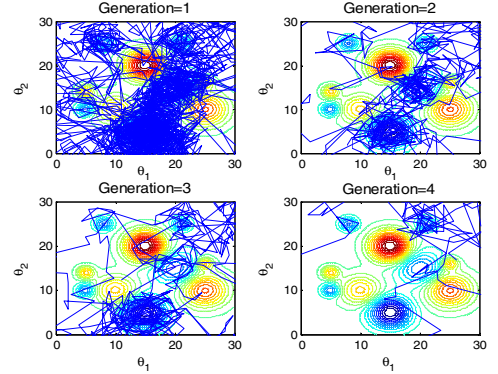


Fig. 1. Bacterial trajectories with $C = 1.5$

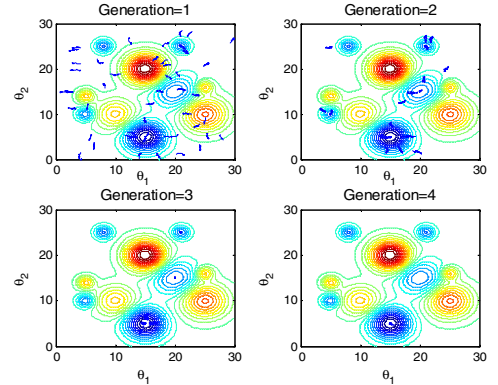


Fig. 2. Bacterial trajectories with $C = 0.01$

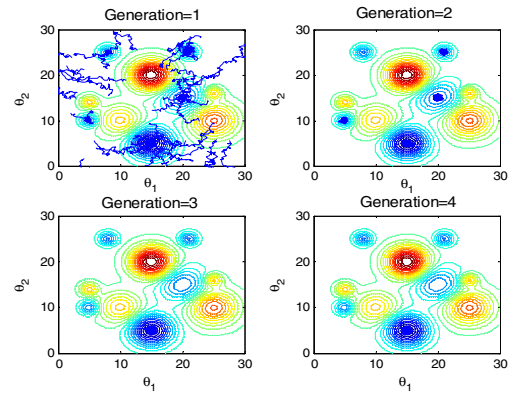


Fig. 3. Bacterial trajectories with $C = 0.1$

To illustrate the importance of C value, a two-dimensional fitness function in [1] is adopted as the benchmark function. The parameter settings are the same as [1]. A comparison of the bacterial motion trajectories using different chemotaxis step is shown in Fig 1, Fig 2 and Fig 3, respectively. Seen from the figures, it can be concluded that when C is too large ($C=1.5$) bacteria may miss the global optimum by swimming without stop (Fig 1). While C is too small ($C=0.01$), it takes a long time to find the global optimum (Fig 2). A proper chemotaxis step length ($C=0.1$) is responsible for finding a good result with a rapid search speed (Fig 3).

In the basic bacterial foraging algorithm the chemotaxis step length C is a constant. By this way, it is hard to keep a right balance between global search and local search ability and thus influence accuracy and speed of the search.

We proposed a simple scheme to adapt the chemotaxis step size with a view to improving its convergence behavior without imposing additional requirements in terms of numbers of evaluations. The size of the step length adjusted in the reproduction and elimination-process, which ensures the bacteria moving global optimum quickly at the beginning, and the global optimum accurately in the end.

In our proposed method we used a linearly varying chemotaxis step length over iterations, in which the chemotaxis step length starts with a high value C_{\max} and linearly decreases to C_{\min} at the maximal number of iterations. The mathematical representations of the BFO method are given as shown in

$$C(j) = C_{\min} + \frac{iter_{\max} - iter}{iter} (C_{\max} - C_{\min}) \quad (3)$$

where $iter_{\max}$ is the maximal number of iterations, $iter$ is the current number of iterations, j is the j th chemotaxis step. With $C_{\min} = C_{\max}$, the system becomes a special case of fixed chemotaxis step length, as the basic proposed BFO algorithm. From hereafter, this BFO algorithm will be referred to as bacterial foraging optimizer with linear decreasing chemotaxis (BFO-LDC).

IV. EXPERIMENT AND RESULT

The performance of the proposed BFO algorithm is tested for four well-known benchmark functions which have been extensively used to compared both BFO-type and non-BFO-type bio-heuristic algorithm. TABLE I lists the four classical functions and their variable bounds for BFO-LDC.

TABLE I. CLASSICAL TEST FUNCTION AND VARIABLE BOUND

| Function Name | Function Equation | Variable Bound |
|---------------|---|----------------|
| Sphere | $f_1(x) = \sum_{i=1}^n x_i^2$ | [-100, 100] |
| Rosenbrock | $f_2(x) = \sum_{i=1}^n 100 \times (x_{i+1} - x_i^2)^2 + (1 - x_i)^2$ | [-30, 30] |
| Rastrigin | $f_3(x) = \sum_{i=1}^n 100 \times (x_{i+1} - x_i^2)^2 + (1 - x_i)^2$ | [-5.12, 5.12] |
| Griewank | $f_4(x) = \frac{1}{4000} \sum_{i=1}^n x_i^2 - \prod_{i=1}^n \cos(\frac{x_i}{\sqrt{i}}) + 1$ | [-600, 600] |

As in [1], for each function, $S=50$, $N_c=1000$, $N_{re}=5$, $N_{ed}=2$, $N_s=4$, $P_{ed}=0.25$. The dimension size and the maximum number of iterations are set to 15 and 10000 for all functions. In BFO-LDC, a linearly decreasing chemotaxis step length is used which started at C_{\max} and ended at C_{\min} , and their values are shown in TABLE II. All experiments were repeated 10 runs.

TABLE II. PARAMETER SETTINGS FOR BFO-LDC

| f | N_c | N_{re} | N_{ed} | C_{\max} | C_{\min} | N_s |
|-------|-------|----------|----------|------------|------------|-------|
| f_1 | 1000 | 5 | 2 | 0.2 | 0.01 | 4 |
| f_2 | 1000 | 5 | 2 | 0.2 | 0.01 | 4 |
| f_3 | 1000 | 5 | 2 | 0.1 | 0.01 | 4 |
| f_4 | 1000 | 5 | 2 | 0.6 | 0.001 | 4 |

Figs. 4-7 show the comparison of the convergence curves of basic BFO and BFO-LDC during 10000 generations for f_1 , f_2 , f_3 and f_4 respectively. From these figures, BFO-LDC kept on optimizing towards a better fitness, whereas the BFO stagnated and flattened out with no further improvement. The results indicate superiority in terms of speed of convergence for our proposed BFO-LDC algorithm for the four classical test functions, without sacrificing accuracy, especially the most complex optimization problem function f_4 .

The stimulation results for which the proposed BFO-LDC algorithm and basic BFO for four benchmark problems are shown in TABLE III-IV. For each function, our improved BFO algorithm obtains better results with the comparison of basic BFO.

TABLE III. NUMERICAL RESULTS FOR SPHERE FUNCTION

| | <i>Best</i> | <i>Worst</i> | <i>Mean</i> | <i>Std</i> |
|---------|-------------|--------------|-------------|-------------|
| BFO | 0.0637 | 0.1005 | 0.0800 | 0.0122 |
| BFO-LDC | 9.4411e-004 | 0.0014 | 0.0012 | 1.3828e-004 |

TABLE IV. NUMERICAL RESULTS FOR ROSENBRACK FUNCTION

| | <i>Best</i> | <i>Worst</i> | <i>Mean</i> | <i>Std</i> |
|---------|-------------|--------------|-------------|------------|
| BFO | 22.2595 | 107.3795 | 42.9600 | 29.8036 |
| BFO-LDC | 5.0536 | 11.4833 | 8.0572 | 2.2018 |

TABLE V. NUMERICAL RESULTS FOR RASTRIGIN'S FUNCTION

| | <i>Best</i> | <i>Worst</i> | <i>Mean</i> | <i>Std</i> |
|---------|-------------|--------------|-------------|------------|
| BFO | 37.1416 | 49.9942 | 45.1861 | 3.4579 |
| BFO-LDC | 18.4889 | 31.1916 | 25.0785 | 4.6219 |

TABLE VI. NUMERICAL RESULTS FOR GRIEWANK FUNCTION

| | <i>Best</i> | <i>Worst</i> | <i>Mean</i> | <i>Std</i> |
|--------|-------------|--------------|-------------|------------|
| BFO | 45.6331 | 99.1808 | 65.9662 | 17.8595 |
| BFOLDC | 0.0080 | 1.4884 | 0.1731 | 0.4624 |

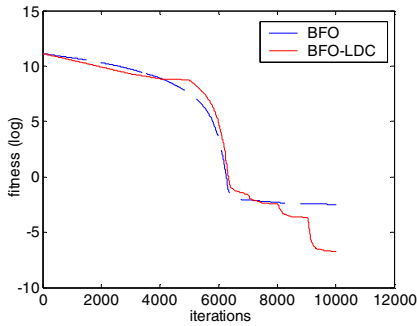


Fig. 4. Convergence curve of sphere function

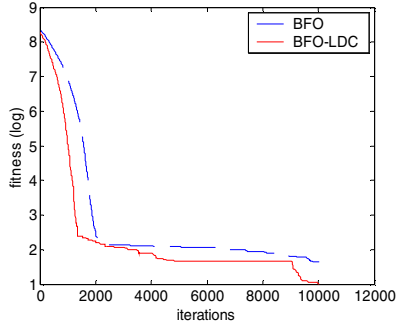


Fig. 5. Convergence curve of Rosenbrock function

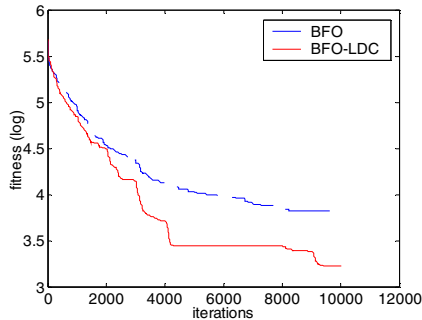


Fig. 6. Convergence curve of Rastrigin function

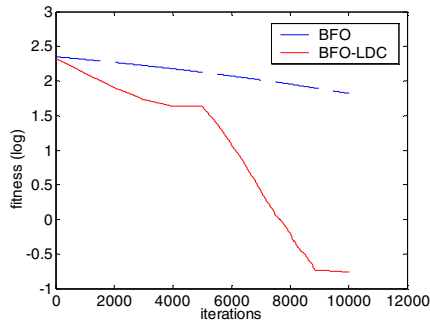


Fig. 7. Convergence curve of Griewank function

V. CONCLUSIONS

A new variant of BFO is proposed here which employs linear variation of chemotaxis step. This linear decreasing strategy is adopted so that the proposed BFO-LDC algorithm

can dynamically adjust the chemotaxis step size to keep right balance between an exploration of the whole search space and an exploitation of the promising areas. Finally the performances of the proposed BFO-LDC algorithm have been tested for a set of benchmark functions and then they have been compared with basic BFO algorithm. The performance comparisons indicated that this proposed method is capable of alleviating the problems of premature convergence in BFO.

However, only four benchmark problems have been applied to BFO-LDC and more benchmark tests must be investigated in the future. And then a number of other heuristic optimization algorithms may be used to compare with the proposed algorithm in subsequent studies, in addition to basic BFO. We are also setting about to explore other proposed methods (nonlinear strategy etc.) for chemotaxis step to improve the performance of BFO.

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