

An Effective Bacterial Foraging Optimization Based on Conjugation and Novel Step-Size Strategies

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An Effective Bacterial Foraging Optimization Based on Conjugation and Novel Step-Size Strategies

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Abstract—Bacterial Foraging Optimization (BFO) is an effective metaheuristic algorithm that has been widely applied to the real world. Despite outstanding computing functionality, BFO algorithms can barely avoid premature convergence induced by easy trapping in local optima. To improve the computing functionality of BFO algorithm, this paper presents an improved BFO algorithm that employs a novel step-length evolution strategy. Also, the improved BFO algorithm adopts Lévy flight strategy proposed in LPBFO and the conjugation strategy proposed in BFO-CC. By combining the three strategies associatedlly, the proposed Conjugated Novel Step-size BFO algorithm(CNS-BFO) strikes an outstanding balance between exploitation and exploration, effectively mitigating the problem of premature convergence in BFO algorithm. Experimental results comparing with several similar algorithms on 8 benchmark functions are conducted to demonstrate the efficiency of the proposed CNS-BFO algorithm.

Keywords-BFO; Lévy flight; conjugation; adaptive step size

I. INTRODUCTION

Metaheuristic algorithm, the so-called nature-inspired algorithm, has drawn considerable attention since inception. Because of its efficacy in tackling optimization and computation problems (especially multi-minimum and multi-constraints problems), metaheuristic algorithm is among the most popular algorithms for researchers. Compared to traditional algorithms, metaheuristic algorithm is much more capable of solving discontinuous and multi-modal problems[1]. Due to its advantages in solving realistic problems, metaheuristic algorithm is incessantly studied and modified to get better performance.

Metaheuristic algorithms are generally divided into singlesolution metaheuristic algorithms and population-based metaheuristic algorithms in terms of the way they search for best solutions[2]. single-solution metaheuristic algorithms center on improving single candidate solution. A typical example of single-solution metaheuristic algorithms is simulated annealing algorithm(SA)[3], which simulates the heating and cooling process to control temperature and energy in order to find approximate global optima. Population-based metaheuristic algorithms center on improving multiple candidate solutions. The most popular population-based metaheuristic algorithms include particle swarm optimization algorithm (BFOA)[4], bacterial foraging optimization algorithm (BFOA)[5], ant colony optimization algorithm (ACOA)[6], genetic algorithm (GA)[7], differential evolution algorithm (DEA)[8] and so on. Xiaojun Qiu and Hong Wang* College of Management Shenzhen University Shenzhen, Guangdong, China, 518060 Email: ms.hongwang@gmail.com

The nature-inspired algorithms are derived from natural phenomena and biological behaviors. For example, particle swarm optimization algorithm[4] is inspired by swarm characteristics of birds seeking foods, and genetic algorithm[7] simulates the process of natural selection and genetic construction.

Performance of population-based metaheuristic algorithms is mostly determined by the process of exploitation and exploration[9], which focus on converging to best candidate solution and adding diversification separately. Exploitation is introduced to perform local search so as to speed up convergence, while usually leading to premature convergence in which the algorithm can get stuck in local optima. In contrast to exploitation, exploration centers on seeking various solutions by broadening search area to provide sufficient candidates for the solution, while usually slowing down the convergence and wasting computational efforts[10]. Lopsided emphasis on either search process can lead to the inefficacy of an algorithm, and hence researchers have exerted enormous efforts in balancing the exploration and exploitation in proposed metaheuristic algorithms[11].

Bacterial foraging optimization algorithm is proposed by Passino in 2002[5]. Under observation, researchers found that Escherichia coli approach nutrients by steps and that the bacteria in unhealthy conditions can be starved and die. Based on the observation, Passino constructed four basic processchemotaxis, swarming, reproduction, and elimination in the original BFO algorithm. Since the inception of BFO algorithm, it is broadly employed in all sorts of fields, including robotic cells[12], power generation[13], sensor network[14], image segmentation[15], and so on.

Numerous novel BFO algorithms have been proposed in recent years. Hybridization of BFO algorithm with other metaheuristic algorithm attracts much attention from researchers. Researchers proposed hybrid BFO algorithms combined with all sorts of algorithms, such as GABFO[16], BSO[17], and DEBFO[18]. By taking full advantages of other algorithms, hybrid algorithm shows extraordinary advantages in specific fields, such as PID controller tunings[19], economic dispatch problems[20] and so on.

Structure modifications of BFO are also proposed by researchers. To reduce computational time, researchers have re-designed construction of BFO algorithm, such as structure-redesign-based BFO (SRBFO) proposed by Niu et al. in 2014[21], and IMBFOA proposed by Ocaña in 2016[22]. Recently, coevolutionary structure-redesigned-based BFO is modeled by Niu et al. and achieve satisfactory performance[23]. The redesigns of algorithm structures effectively save computational efforts of BFO algorithm.

Apart from hybridization of other algorithms and the modification of structure, researchers integrate communication mechanism in BFO algorithms. Social learning mechanism is incorporated in classical BFO algorithm by Yan et al. in 2012[24]; adaptive comprehensive learning mechanism (ALCBFO)[25] is introduced by L. Tan et al. in 2015 in order to keep balance between exploitation and exploration; novel chemotaxis and conjugation strategies (BFO-CC) are employed by Yang et al. in 2016[26] and contribute to the improvement of BFO algorithm. Recently, Pang B et al. proposed LPBFO[27], which incorporates Lévy flight to the reconstruction of BFO's step-size, making progress in addressing the limitation of premature convergence in BFO algorithm.

Besides, chemotaxis step improvement is thoroughly considered by researchers. Adaptive bacterial foraging optimization algorithm (ABFO) is proposed by Dasgupta et al. in 2009[28]. Linear decreasing BFO (BFO-LDC) and non-linear decreasing BFO (BFO-NDC) are modeled by Niu et al. in 2011[29]. Gravitation search strategy is combined with chemotactic step by Zhao et al. in the proposed effective BFO (EBFO)[30].

Despite huge efforts exerted by researchers, deficiencies of premature convergence and slow convergence speed remain unsolved. In order to further the improvement of BFO algorithm, the paper proposes a Conjugated Novel Step-size BFO algorithm(CNS-BFO) which employs a novel chemotaxis step-size evolution strategy. Moreover, the proposed CNS-BFO algorithm employes conjugation strategy proposed in BFO-CC algorithm and Lévy flight strategy proposed in LPBFO, significantly ameliorating the deficiency of premature convergence, improving the computational efficiency of BFO algorithm.

The rest of the contents is organized as the followings. Classical BFO algorithm is illustrated in section two. In section three, the paper introduces the proposed Conjugated Novel Step-size BFO algorithm. Experiments are conducted to test the performance of the CNS-BFO algorithm in section four. Finally, section five concludes the proposed CNS-BFO algorithm.

II. CLASSICAL BFO ALGORITHM

Bacterial foraging optimization proposed by Passino[5] in 2002 simulates behaviors of *E. coli* bacteria. To summarize, the classical bacterial foraging optimization algorithm consists of three basic behaviors: chemotaxis, reproduction, and elimination-dispersal. Subsections written below will demonstrate how the three behaviors work.

A. Chemotaxis

E. coli bacteria move towards places of abundant nutrients by rotating flagella. The rotation of flagella can be in either clockwise direction or counterclockwise direction. Counterclockwise direction rotation pushes the bacteria to move towards nutrients, while clockwise direction leads to bacteria's tumbling away from the current position for searching nutrients. By combining both actions, bacteria perform chemotaxis to approach nutrient.

Suppose bacterium *i* is denoted as $\theta^i(j, k, l)$, in which *j* denotes the *j*-th chemotaxis, *k* denotes the *k*-th reproduction, and *l* denotes the *l*-th elinimation& dispersal, the behaviors of the *i*-th bacterium can be demonstrated as follows:

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

where C(i) denotes the step size of chemotaxis and $\Delta(i)$ denotes random direction vector in which elements are within [-1,1] .

If the health status gets better after tumbling, bacteria will keep on swimming for several steps, in order to further approach optimal solutions.

B. Reproduction

After the stage of chemotaxis, each bacterium is assigned with different health status. The health status is evaluated by the summation of the fitness of each bacterium. The lower the total fitness value, the healthier the bacterium. The function for calculating health status can be demonstrated as follows:

$$J_{health} = \sum_{j=1}^{N_c} J(i, j, k, l)$$
⁽²⁾

where N_c denotes the number of chemotactic behaviors and J is the evaluated value of the position of the *i* bacterium at the *k* reproduction and the *l* ellimination. In classical BFO algorithm, only the first half bacteria ranked by health status can survive, with their offsprings supplant the other half of bacteria. Reproduction is designed to strenghthen local search ability of BFO while maintaining stable population of bacteria population. The function for reproduction can be demonstrated as follows:

$$\theta^{i+Sr}(j,k,l) = \theta^{i}(j,k,l) \tag{3}$$

where Sr is half of the population size.

C. Elimination & Dispersal

For fortifying the ability of global search, classical PSO algorithm introduces the mechanism of elimination & dispersal. After stages of chemotaxis and reproduction, bacteria will encounter death induced by adverse environment by a possibility P_{ed} . Bacteria will be dispersed to random positions within the search area. By introducing stage of elimination & dispersal, the diversity of bacteria increases and results in stronger global search ability.

III. CONJUGATED NOVEL STEP-SIZE BFO ALGORITHM

A. Lévy Flight Step Length Strategy

Levy distribution, proposed by Lévy Paul[31], is a special inverse-gamma distribution, whose formula can be expressed as $P_s = s^{-\lambda}$, in which s is a step size and λ is between

1 and 3. Subject to Lévy distribution, Lévy flight is a sort of random moving which can generate frequent small step sizes and occasional larger step sizes for bacteria. The traits of Lévy flight makes bacteria move with ununiformed step size, strengthening BFO's ability of exploitation and exploration at the same time: on the one hand, frequent small step sizes fortify the local search ability of bacteria, whereby the exploitation ability of the algorithm can be improved. On the other hand, occasional larger steps prevent bacteria from over concentrating on exploiting the current position, guiding bacteria to a broader search area, whereby the exploration ability of BFO can be strengthened.

The paper adopts the Lévy flight strategy modified by Bao Pang et al. in 2018[27]. The formula of the adaptive step-size is as follows:

$$C'(i) = \frac{\alpha}{t(i)}|s| \tag{4}$$

where α is a parameter for controlling the strength of change in step-size, t(i) is the number of chemotaxis the *i* bacterium has gone through. As bacterium experiences more chemotaxis, the step size will dwindle as t(i) gets larger, and hence bacteria can become more concentrated on exploiting the current position. *s* is calculated by:

$$s = \frac{u}{|v|^{\frac{1}{\beta}}} \tag{5}$$

in which β is a random number between 0.3 and 1.99. u and v are two normal random variables with means equal to zero and with variances set as σ_u and σ_v respectively. σ_u and σ_v is calculated as follows:

$$\sigma_u = \frac{\Gamma(1+\beta)sin(\frac{\pi\beta}{2})}{\Gamma[\frac{(1+\beta)}{2}]2^{\frac{\beta-1}{2}}\beta}$$
(6)

$$\sigma_v = 1 \tag{7}$$

B. Novel Step Evolution Strategy

In the original BFO algorithm, chemotaxis step length is set fixed for each bacterium. Fixed step size saps bacterium's strength to exploit, resulting in a greater possibility of falling into local optima. To address the limitation, the other step-size evolution strategy is applied here. After bacteria and their step sizes are ranked and reproduced, step lengths of bacteria will be updated by the following equation:

$$C'(i,k+1) = C(i,k+1)\boldsymbol{b}$$
 (8)

$$C(i,k+1) = [C''(i,k+1) - C(i,k+1)] \cdot (1 - \frac{1}{lk+1})$$
(9)

where **b** denotes a $p \times 1$ vector, p is the dimension of bacteria.

This novel step-size evolution strategy is introduced to make bacteria move adaptively and efficiently. As moving step sizes significantly decide the ability of bacteria to search glocal optimum, careful moving can dramatically improve the odds of finding the global optimum. The novel step length evolution strategy allows bacteria to move with longer step sizes in the beginning, and make them budge at later stage. Combined with Levy-flight step length strategy, the adaptive moving strategy efficiently mitigates the problem of trapping into local optima.

C. Conjugation Strategy

Conjugation strategy proposed in BFO-CC algorithm by Cuicui Yang et al. in 2016[26] is a novel strategy that simulates the process of transferring genetic material among creatures. The proposed BFO-CC algorithm introduces conjugation mechanism to bacteria, constructing a message exchange mechanism by which diversity of bacteria can be improved. By this way, conjugation strategy enhances bacteria's capability of searching for glocal best. In BFO-CC algorithm, each bacterium chooses another bacterium θ^{i} and a conjugation point *pt* randomly. The formula for conjugation mechanism is given as follows:

$$\theta_{new}^i = \theta^i(j,k,l) + \boldsymbol{a} \cdot [\theta^{i'}(j,k,l) - \theta^i(j,k,l)]$$
(10)

where a is a p-dimension random vector in which the values of the components pt to pt+L-1 are random numbers uniformly distributed from 0 to 1, with the rest of components being 0. Lindicates the length of exchange of dimensions. By taking the conjugation strategy, the bacterium is mutated to learn from other bacteria, whereby avoid premature convergence.

D. Process of The Improved BFO Algorithm

Pseudocode for the improved BFO algorithm is shown in algorithm 1.

IV. EXPERIMENTS AND ANALYSIS

To prove the efficiency of the proposed CNS-BFO algorithm, it is compared with other sorts of heuristic algorithms: GA[7] and PSO[4]. Besides, as a variant of BFO algorithm, CNS-BFO is compared with standard BFO[5] and several popular BFO variants: BFO-LDC[29], BFO-NDC[29], and BCO[32] algorithms. To make the comparison fair, algorithms are assigned with the same initialization positions and recommended parameters are adopted for comparison algorithms. The population sizes for all BFO algorithms are set to 50. The total number of FEs is set to 10,000 for 15-D functions. All the algorithms are tested for ten times in all the benchmark functions. Parameters of BFO algorithms are set as follows: $N_c = 1,000$, $N_{re} = 10$, $N_{ed} = 2$, $P_{ed} = 0.25$, $Sr = \frac{S}{2}$, n = 30, s = 2, and g = 2. For CNS-BFO algorithm, additional parameters are set as follows: $\alpha = 1,000, \beta = 1.5,$ $p_{con}=0.2, N_n=30, L=2$. To demonstrate the effectiveness of CNS-BFO, 8 popular benchmark functions are employed to test its performance. Benchmark functions include one basic unimodal function(f_1), 6 basic multimodal function($f_2 - f_7$), and 1 2D multimodal function(f_8). Benchmark functions used in evaluating algorithms are shown in Table.I. The test results are demonstrated in Fig.1 and Table.II. Note that the best results have been marked with boldface. Also, the standard deviations of the best value in each run are bracketed.

Algorithm 1 Pseudocode of CNS-BFO Algorithm

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1:	Initialize parameters $d, S, N_s, N_c, N_{re}, N_{ed}, N_n, Sr, p_{ed}$,
	$p_{con}, \alpha, \beta, \delta_v, \delta_u, u, v, e, L$
2:	for $l = 1, 2,, N_{ed}$ do
3:	for $k = 1, 2,, N_{re}$ do
4:	for $j = 1, 2,, N_c$ do
5:	for $i = 1, 2,, S$ do
6:	Set $t = j + (k - 1)N_c + (l - 1) \cdot rand(p, 1)$
7:	Compute fitness function J^i
8:	Set $J_{last} = J^i$
9:	Tumble with Levy-Flight step size computed by
	equation (4)
10:	Move. Compute J^i
11:	Swim:
12:	while $m < N_s$ do
13:	if J^i is smaller than J_{last} then
14:	Update θ^i
15:	else
16:	Stop
17:	end if
18:	end while
19:	Conjugate:
20:	Select a bacterium randomly
21:	if $rand < p_{con}$ then
22:	Choose a conjugation point pt , in which $1 \leq \frac{1}{2}$
	$pt \le pt - L + 1$
23:	Compute θ_{new} using equation (10)
24:	if $J^i < J_{last}$ then
25:	$ heta^i= heta_{new}$
26:	end if
27:	end if
28:	end for
29:	end for
30:	Compute the health status J^i for the <i>i</i> -th bacterium
31:	Sort bacteria by health status for $i = 1$ to Sr do
32:	for $j = 1$ to Sr do
33: 34:	split for $e = 1$ to N_n do
34: 35:	Update $C_{i,k+1}$ using equation (8) and (9)
36:	end for
30. 37:	end for
38:	end for
39:	for $m = 1, 2,, S$ do
40:	Eliminate each bacterium if $rand < p_{ed}$
40. 41:	end for
42:	end for

According to the test graphs, it is noticeable that the proposed CNS-BFO algorithm tremendously outperforms other algorithms on nearly all the benchmark functions. In the all test functions, CNS-BFO algorithm seeks out optimal global considerably faster than all the other algorithms. Moreover, global optima found by CNS-BFO algorithm is significantly better than other comparison algorithms. In the last test function, the performance of CNS-BFO algorithm is as good as that of PSO algorithm. Overall, CNS-BFO algorithm effectively mitigates the problem of premature convergence, whereby dramatically improves the efficiency of BFO algorithm.

TABLE	I:	Benchmark	Functions
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Function	Name	n	SD	f_{opt}
f_1	Sphere	15	$[-100, 100]^n$	0
f_2	Rastrigin	15	$[-5.12, 5.12]^n$	0
f_3	NCRastrigin	15	$[-5.12, 5.13]^n$	0
f_4	Schwefel 1.2	15	$[-100, 100]^n$	0
f_5	Schwefel 2.22	15	$[-500, 500]^n$	0
f_6	Ackley	15	$[-32.768, 32.768]^n$	0
f_7	Griewank	15	$[-600, 600]^n$	0
f_8	Brain2D	2	$[-500, 500]^n$	0.397887

V. CONCLUSION

Conjugated Novel Step-size BFO algorithm(CNS-BFO) is proposed to improve the performance of BFO algorithm. Improvements lie in the way of constructing a novel step evolution strategy and incorporating both Lévy flight stepsize strategy and conjugation strategy. By modifying the moving strategy and introducing a learning mechanism, CNS-BFO strikes a balance between exploitation and exploration, whereby efficaciously improves the limitation of premature convergence in BFO algorithms. Benchmark functions tests are implemented to compare the performance of the CNS-BFO algorithm with those of other algorithms. The experimental results indicate that the proposed CNS-BFO algorithm significantly enhances the performance of BFO algorithm in both avoiding premature convergence and accelerating convergence. As a result, the proposed CNS-BFO algorithm will contribute to the perfection of the bacterial foraging optimization algorithm and even other metaheuristic algorithms.

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Fig. 1: The Test Graphs on Benchmark Functions.

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No.	GA	PSO	BFO	BFO-LDC	BFO-NDC	BCO	CNS-BFO
f_1	7.00E-02	2.24E-02	8.72E-02	7.98E+02	6.11E-01	7.63E-02	(2.34E-48)
	(2.24E-02)	(5.29E-02)	(1.58E-02)	(1.23E+02)	(1.17E-01)	(9.00E-03)	(7.27E-48)
f_2	4.50E+01	3.17E+01	4.23E+01	2.82E+01	1.12E+02	2.49E+01	0.00E+00
	(3.36E+00)	(1.18E+01)	(3.55E+00)	(3.47E+00)	(1.67E+01)	(2.53E+00)	(0.00E+00)
f_3	4.18E+01	3.19E+01	4.27E+01	3.76E+01	9.56E+01	1.28E+01	0.00E+00
	(6.65E+00)	(8.82E+00)	(9.17E+00)	(1.27E+01)	(1.31E+01)	(2.72E+00)	(0.00E+00)
f_4	4.88E-01	7.37E+02	5.16E-01	4.94E+03	4.90E+00	3.38E-01	8.62E-26
	(1.08E-01)	(2.33E+03)	(9.23E-02)	(2.32E+02)	(9.59E-01)	(5.65E-02)	(2.55E-25)
f_5	3.08E+22	7.62E+22	7.06E+21	5.96E+22	7.92E+19	7.16E+20	3.14E-27
	(5.71E+22)	(1.24E+23)	(7.64E+21)	(8.36E+2)2	(1.17E+20)	(2.26E+21)	(6.50E-27)
f_6	1.74E+01	3.13E+00	1.75E+01	1.85E+01	2.75E+00	6.81E-01	4.09E-15
	(5.23E-01)	(8.01E-01)	(4.51E-01)	(3.06E-01)	(2.08E-01)	(7.94E-02)	(1.12E-15)
f_7	9.20E+01	6.72E+01	9.12E+01	2.09E+02	8.08E-02	5.18E+01	0.00E+00
	(1.46E+00)	(9.60E+00)	(1.98E+00)	(9.14E-01)	(1.87E-02)	(7.06E+00)	(0.00E+00)
f_8	3.98E-01						
	(6.24E-07)	(0.00E+00)	(4.67E-07)	(6.46E-07)	(1.35E-05)	(1.38E-06)	(0.00E+00)

TABLE II: Mean Values and Standard Deviation of the Eight Algorithms on Benchmark Function $f_1 - f_8$

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