

A Cooperative Structure-Redesigned-Based Bacterial Foraging Optimization with Guided and Stochastic Movements

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Abstract. The nested loop adopted in the original bacterial foraging optimization (BFO) is quite time-consuming and is the main reason for the complex computational process. Thus, in our previous work, an improved BFO with structure redesigned mechanism (SRBFO) is used to address this problem. Since the bacterial chemotaxis with stochastic direction in the original BFO has an adverse effect on the convergence rate, this paper proposes a new cooperative chemotactic movement strategy. In this cooperative strategy, some bacteria are selected to move toward a guided direction based on a predefined probability, while the other bacteria still swim to a stochastic direction as exhibited in the original BFO. By this strategy, all the bacteria alternatively use the guided movement and the stochastic movement to cooperatively balance global search and local search. The proposed improved algorithm is called Cooperative SRBFO (CSRBF0). A comparison of the CSRBF0 with other BFOs has been made to demonstrate the superiority of the proposed algorithm.

Keywords: Cooperative bacterial foraging optimization · Movement strategy · Structure-redesigned

1 Introduction

Inspired from natural phenomena or biological characteristics, lots of bio-inspired optimization algorithms have been developed in recent decades such as the Particle Swarm Optimization (PSO) [1], the Ant Colony Optimization (ACO) [2] and the Bacterial Foraging Optimization (BFO) [3]. Among these heuristic algorithms, the BFO is one of the most well-known nature-inspired algorithms which was presented by Passino [3] in 2002 by getting inspiration from the social foraging behavior of *E.coli* bacteria.

After its acceptance, BFO has attracted increasing attention of scholars and has been applied to diverse real life problems like vehicle routing problem [4], voltage collapse detection [5] and so on. Besides, the enhancement of BFO algorithm is also an important research field on BFO. Lately, more real world problems have been investigated by using new variations of BFO. For example, Awadallah [6] used five versions of BFO to extract parameters of photovoltaic modules from nameplate data. Yi et al. [7] proposed a process fault detection approach: extended bacterial foraging optimization

to optimize relative transformation matrix. The results proved the better accuracy of the proposed approach. Mohammadi et al. [8] developed an adaption scheme to enhance BFO's performance and used it to address optimizing the planning of passive power filters and distributed generations. We also have done numerous investigations on the improved BFOs. The adaptive chemotaxis step [9], the information communication mechanism [10, 11] and the redesigned algorithm structure [12] were proposed to incorporate into BFO to enhance the search capability. The primary experimental results proved the superiority of proposed algorithms.

In this paper, a new movement strategy with alternative guided and stochastic chemotactic movements is proposed to further keep the balance of exploration and exploitation. The movement of bacteria in the standard BFO is randomly determined, easily resulting in the low convergence speed. The combination of exploration using the stochastic movement method and exploitation using the guided movement method will facilitate bacteria to cooperatively find the global optima faster and more accurately. Besides, the aforementioned adaptive chemotaxis step and the redesigned algorithm structure are also used in our proposed algorithm. The proposed algorithm is named Cooperative SRBFO (CSRBF0).

The rest of the paper is organized as follows: the proposed cooperative structure-redesigned-Based bacterial foraging optimization is presented in Sect. 2. In Sect. 3, the original BFO and the proposed BFO have been applied to a series of benchmarks. Optimization results and analyses are also provided in Sect. 3, followed by conclusions in Sect. 4.

2 Cooperative Structure-Redesigned-Based BFO

2.1 A New Movement Strategy

The standard BFO consists of four primary steps, including chemotaxis, swarming, reproduction, and elimination & dispersal. These steps simulate the movement of an *E.coli* bacterium, the cell-to-cell signaling in the swarm and the death caused by sudden changes of the local environment.

In the standard BFO, the movements of bacteria in chemotaxis step are randomly decided. The lack of guided search may cause the problem of inefficient convergence rate. Moving toward to a stochastic direction will have some advantages, e.g. conserving high diversity, escaping from local minima. However, it may bring out some disadvantages, e.g. low convergence rate, low search accuracy. Inspired from the literature [13], we propose a new chemotactic movement strategy to address this issue.

In addition to moving toward a stochastic direction (stochastic movement) for exploration, bacteria in the new movement strategy may swim to a guided direction for exploitation, including the global best (*gbest* movement) or a determined target (target movement). The target is determined randomly and could be any bacterium with different fitness value such as the global best or even the worst bacterium. In other words, bacteria in CSRBF0 can learn information from any other bacteria to decide the direction of movement instead of decide it stochastically. At each iteration, there are

three movement methods to choose for each bacterium to update the location and each bacterium chooses its own method according to the random index S :

$$S = \text{round}(\text{rand} \times SS) \quad (1)$$

where SS is the swarm size of bacteria and rand is a uniform distributed random number between 0 to 1. Thus the index S ranges from 0 to SS . If the index S of the i^{th} bacterium belongs to the range from 0 to T_{lo} which is the lower bound of target range, the bacterium moves toward a stochastic direction Δ that is the same as it was in standard BFO. Moving toward the global best will occur when S ranges from T_{up} which is the upper bound of target range to SS . The determined target is the moving direction when S belongs to the target range from T_{lo} to T_{up} .

On the other hand, as the value of the chemotactic step size is static, it's difficult to keep the balance of global search and local search. Inspired from this, we proposed an adaptive chemotaxis step for global optimization in [9]. In the beginning of evolution process, the step size is set to a maximum value C_{max} . When the number of iteration increases, the value of step size will be smaller until it reaches the minimum value C_{min} . The updating equations for each bacterium's direction and location are given as follows:

$$D(i) = \begin{cases} \theta^{GBest}(j, k, l) - \theta^i(j, k, l) & \text{if } S \in (T_{up}, SS) \\ \theta^S(j, k, l) - \theta^i(j, k, l) & \text{if } S \in (T_{lo}, T_{up}) \\ \Delta(i) / \sqrt{\Delta^T(i)\Delta(i)} & \text{if } S \in (0, T_{lo}) \end{cases} \quad (2)$$

$$C(i) = C_{min} + (MaxFEs - ChemIter) / MaxFEs \times (C_{max} - C_{min}) \quad (3)$$

$$\theta^i(j+1, k, l) = \theta^i(j, k, l) + C(i)D(i) \quad (4)$$

where $\theta^i(j, k, l)$ means the position of the i^{th} bacterium at the j^{th} chemotactic, k^{th} reproductive and l^{th} elimination and dispersal step. $C(i)$ is the chemotactic step size and $D(i)$ is the moving direction for the i^{th} bacterium. Δ represents a vector in the stochastic direction. $ChemIter$ is the iteration counter while $MaxFEs$ is the maximum number of iteration counters.

T_{lo} and T_{up} are calculated as $\text{round}(\alpha_1 \times SS)$ and $\text{round}(\alpha_2 \times SS)$ where α_1 and α_2 are used to control the ranges of stochastic movement, $gbest$ movement and target movement. If users set α_1 to 0.1 and α_2 to 0.8, it means that 10 % of bacterial swarm can be randomly selected as uniform bacteria that use stochastic movement strategy and 20 % of bacteria can be chosen as bacteria moving toward the global best bacterium. The remaining 70 % of bacterial population can move toward the target bacteria. Specifically, the smaller the value of α_1 , less exploration using stochastic movement and more exploitation using guided movement are considered. And the bigger the value of α_2 , more bacteria are guided to the location of global best and less

bacteria are guided to the target bacteria which means more exploitation considering best bacterium only and less exploitation considering any bacterium with different fitness value.

2.2 Redesign of Algorithm Structure

In the standard BFO, the chemotactic loop is nested inside the reproduction loop which is nested inside the elimination & dispersal loop once more. The complex structure of nested loop in standard BFO causes some problems, e.g., the standard BFO usually requests lots of time and memory consumption when handling problems with high dimension space. In order to address this issue, we proposed a Structure-Redesigned-Based Bacterial Foraging Optimization (SRBFO) in [12] for lower computational complexity and less memory consumption.

Table 1. The pseudo-code of BFO

```

Initialize parameters and the location of bacteria
For ( $l = 1: N_{ed}$ ):
  For ( $k = 1: N_{re}$ ):
    For ( $j = 1: N_c$ ): chemotactic loop
      Tumble;
      Swimming;
      Update position and fitness
    End
  reproduction loop
End
elimination&dispersal loop
End

```

Table 2. The pseudo-code of SRBFOs

```

Initialize parameters and the location of bacteria
While  $ChemIter \leq MaxFEs$ 
  Tumble;
  Swimming;
  Update position (using equations (2)- (4) in CSRBFO) and fitness;
   $ChemIter = ChemIter + 1$ ;
  If Mod ( $ChemIter, Fre$ )=0
    Reproduction step;
  End
  If Mod ( $ChemIter, Fed$ )=0
    Elimination&dispersal event;
  End
End

```

As the reproduction and elimination & dispersal steps take place after the chemotactic behavior is finished, iteration counters can be used to take the place of the nested loop. When a number of iterations have been completed, the reproduction and elimination & dispersal event can be triggered by the iteration counter $ChemIter$. For instance, when the total number of bacteria $SS = 10$, the number of chemotactic steps

$N_c = 10$, the number of reproduction steps $N_{re} = 4$ and the number of elimination & dispersal events $N_{ed} = 3$, the maximum number of iteration counters in total $MaxFEs$ can be calculated as:

$$MaxFEs = SS \times N_c \times N_{re} \times N_{ed} \quad (5)$$

to get the value of $MaxFEs$ 1200. The counter for N_{re} can be replaced by an event every 240 iterations (Fre), and the counter for N_{ed} also can be replaced by an event every 300 iterations (Fed). The pseudo-codes of BFO and SRBFO/CSRBFO are presented in Tables 1 and 2.

3 Experiments and Analyses

3.1 Benchmark Functions and Experimental Parameters

To demonstrate the superiority of the proposed algorithm CSRBFO, CSRBFO is used to optimize eight well-known benchmark functions that are shown in Table 3, including Sphere, Quartic, SumPowers, Rosenbrock, Ackley, Griewank, Rastrigin and Schwefel2.22. These selected benchmark functions are classified as two categories: unimodal and multimodal functions. The unimodal functions (Sphere, Quartic, SumPowers, Rosenbrock) have a single optimal solution. On the contrary, the multimodal functions (Ackley, Griewank, Rastrigin and Schwefel2.22) have two or more local optima, resulting in the high possibility of being trapped into local optima and the difficulty in searching global optima.

As the proposed algorithm is a variant of the standard BFO, we compared the proposed algorithm with the standard BFO [3] and the structure-redesigned-based BFO (SRBFO) [12]. The three competitive algorithms are set to have similar experimental settings. For example, for each benchmark functions these algorithms are conducted independently for approximately 15 times with the search space dimension 30. The swimming length N_s is 10 and the probability of elimination & dispersal P_{ed} is set to 0.2. More parameters setting of BFO, SRBFO and CSRBFO are presented as follows:

- In BFO, SRBFO and CSRBFO, $MaxFEs = 80000$,
- In BFO, $N_c = 100$; $N_{re} = 4$; $N_{ed} = 2$; $C = 0.15$,
- In SRBFO and CSRBFO, $F_{re} = 16000$; $F_{ed} = 26667$,
- IN CSRBFO, $C_{max} = 0.15$; $C_{min} = 0.01$; $\alpha_1 = 0.2$; $\alpha_2 = 0.8$

3.2 Experimental Results and Analyses

MATLAB R2011a is used for coding these optimization algorithms. BFO, SRBFO and CSRBFO are executed to get optimal numerical results for four unimodal functions and four multimodal functions. The mean and the standard deviation of optimal solutions obtained in 20 run times are presented in Table 4. The computational time used by the

three algorithms is also given in Table 4. The best of all the numerical values obtained by the three competitive algorithms are emphasized by using a bold type. Figures 1, 2, 3, 4, 5, 6, 7 and 8 are convergence graphs of the average values obtained by all the competitive algorithms for the eight test functions.

From these Table and Figs we can conclude the following findings:

- CSRBFO algorithm gets the optimal solutions among the three competitive algorithms for all the 8 algorithms. It means that CSRBFO outperforms other two algorithms in terms of the search accuracy no matter the categories of the functions.
- CSRBFO algorithm acquires far better standard deviation values than BFO and SRBFO in these all cases. It means that the search stability of CSRBFO is usually better as compared to BFO and SRBFO.
- In terms of the computational time, CSRBFO uses the least time on SumPowers and Griewank and SRBFO have the best performance when dealing with the other 6 functions. Both the performance of CSRBFO and SRBFO is much better than that of BFO, which means the redesign of algorithm structure is effective in reducing computational time.
- Although SRBFO successfully lower the computational complexity and consumed time, SRBFO cannot always get better optima than BFO can get. This problem can be successfully solved by CSRBFO which maintains the low computational complexity of SRBFO but possesses a much better search accuracy.

Table 3. The details of benchmark functions

Function name	Formula	Search range
Sphere	$f(x) = \sum_{i=1}^n x_i^2$	$[-100,100]^n$
Quartic	$f(x) = \sum_{i=1}^n ix_i^4$	$[-1.28,1.28]^n$
SumPowers	$f(x) = \sum_{i=1}^n x_i ^{i+1}$	$[-10,10]^n$
Rosenbrock	$f(x) = \sum_{i=1}^n 100 \times (x_{i+1} - x_i^2)^2 + (1 - x_i)^2$	$[-100,100]^n$
Ackley	$f(x) = -20 \exp(-0.2 \times \sqrt{\frac{1}{30} \sum_{i=1}^n x_i^2}) - \exp(\frac{1}{30} \sum_{i=1}^n \cos 2\pi x_i) + 20 + e$	$[-32.32]^n$
Griewank	$f(x) = \frac{1}{4000} \sum_{i=1}^n x_i^2 - \prod_{i=1}^n \cos(\frac{x_i}{\sqrt{i}}) + 1$	$[-600,600]^n$
Rastrigrin	$f(x) = \sum_{i=1}^n (x_i^2 - 10 \cos(2\pi x_i) + 10)^2$	$[-5.12,5.12]^n$
Schwefel2.22	$f(x) = \sum_{i=1}^n x_i + \prod_{i=1}^n x_i $	$[-10,10]^n$

Table 4. Optimal results of benchmark functions obtained by algorithms

Algorithm		Sphere	Quartic
BFO	mean	2.161233e+004	1.830501e+006
	SD	4.121535e+003	8.000643e+005
	time	1.688580e+002	2.740903e+002
SRBFO	mean	3.455068e+002	1.687083e+005
	SD	1.554593e+002	7.721484e+004
	time	9.940292e+000	1.140782e+002
CSRBFO	mean	5.00E-04	1.51E-05
	SD	1.20E-04	7.83E-06
	time	2.707242e+001	1.253987e+002
		SumPowers	Rosenbrock
BFO	mean	1.536610e+002	9.362519e+006
	SD	2.064995e+002	4.326234e+006
	time	1.659585e+002	1.791519e+002
SRBFO	SD	2.064995e+002	4.326234e+006
	time	1.659585e+002	1.791519e+002
	mean	1.776366e+006	9.857264e+003
CSRBFO	mean	5.61E-06	3.903938e+001
	SD	4.34E-06	2.387991e+001
	time	1.141269e+002	3.990767e+001
		Ackley	Griewank
BFO	mean	1.964264e+001	4.756842e+002
	SD	1.54E-01	7.031533e+001
	time	9.490752e+001	2.864881e+002
SRBFO	mean	1.977602e+001	3.895342e+002
	SD	2.25E-01	4.157214e+001
	time	2.030747e+001	1.187595e+002
CSRBFO	mean	7.648295e+000	2.340888e+000
	SD	1.201768e+000	1.079698e+000
	time	4.284316e+001	1.163687e+002
		Rastrigrin	Schwefel2.22
BFO	mean	2.243968e+002	8.458650e+001
	SD	1.033303e+001	1.040385e+001
	time	8.805903e+001	9.168354e+001
SRBFO	mean	3.563115e+002	9.530744e+001
	SD	2.002577e+001	8.057249e+000
	time	1.474507e+001	1.555536e+001
CSRBFO	mean	1.134836e+001	2.879101e+000
	SD	4.094528e+000	1.209057e+000
	time	3.074022e+001	3.427830e+001

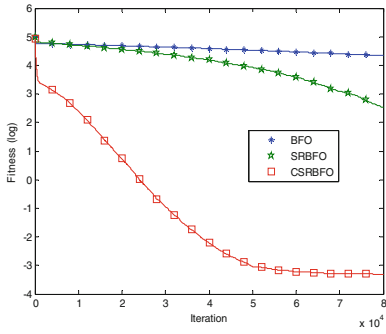


Fig. 1. Sphere function

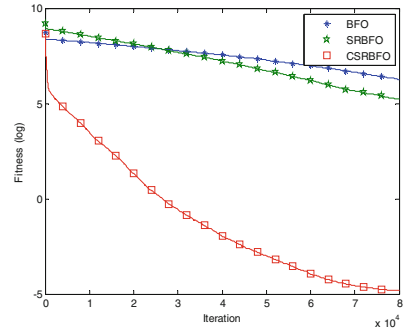


Fig. 2. Quartic function

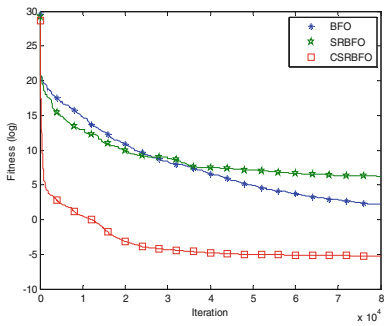


Fig. 3. SumPower function

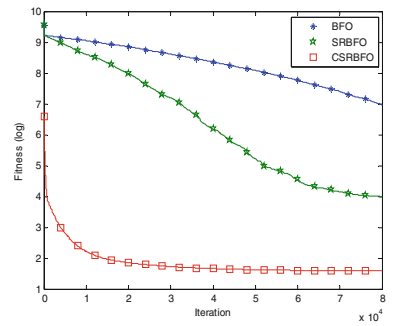


Fig. 4. Rosenbrock function

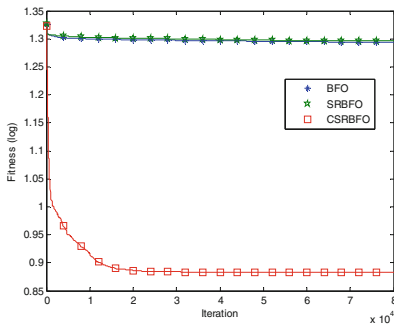


Fig. 5. Ackley function

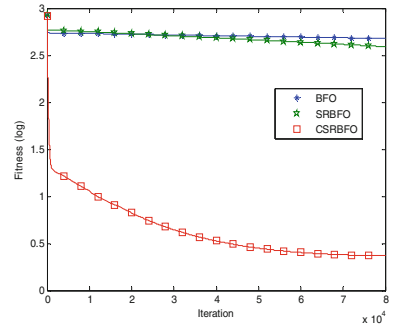


Fig. 6. Griewank function

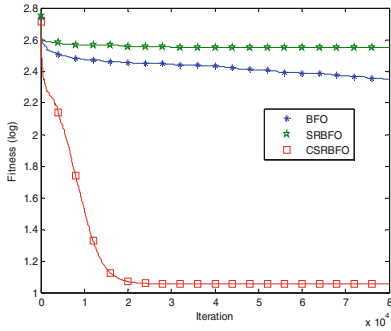


Fig. 7. Rastrigin function

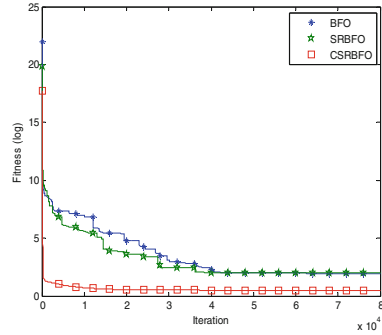


Fig. 8. Schwefel2.22 function

4 Conclusions

By incorporating cooperative movement strategy, adaptive chemotaxis step and redesigned algorithm structure into original BFO, this paper proposes a Cooperative Structure-Redesigned-Based Bacterial Foraging Optimization. In order to simplify the structure of proposed CSRBFO algorithm, the nested loop adopted in original BFO is replaced with a single loop used in SRBFO [12]. The reproduction step and elimination & dispersal event are triggered by the iteration counter. In other words, the reproduction and elimination & dispersal events will be triggered when the iteration counter reaches a predefined value. The computational time is reduced significantly because of the simplified algorithm structure.

A new chemotactic movement strategy is proposed in this paper to speed up convergence rate and enhance search accuracy. Instead of the stochastic chemotactic movement in aforementioned BFO, bacterial moving directions in CSRBFO are decided by obtaining information from the global best bacterium or any other bacteria with different fitness value. In the new movement strategy, a random index is designed to decide whether stochastic movement or guided movement is used. In addition to moving toward a stochastic direction, bacteria can be guided to the global best or a determined target. By using these three movement methods, a right balance of exploration and exploitation is expected to be obtained.

The proposed algorithm is used to optimize several functions. Experimental results obtained by CSRFO are compared with that of BFO and SRBFO, illustrating its superior performance in terms of the search accuracy & stability and the computational time.

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