

Computational Evolution of Social Behavior in Bacterial Colony Optimization Model

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Recent biological studies of bacterial colonies have revealed diverse complex social behaviors, including cooperation in foraging, building, dispersing and communicating. In order to provide the novel models of bacterial foraging behavior and new methods for distributed nongradient optimization, this paper proposed a computational simulation model of bacterial colony by combining chemotaxis, cell-to-cell communication, and a self-adaptive foraging strategy. The simulation results show that the proposed model of artificial bacterial colony exhibit the property identified by microorganisms that their foraging is social and adaptive in order to be able to climb noisy gradients in nutrients. This provides a connection between evolutionary forces in bacterial social foraging and distributed nongradient optimizational algorithm design for global optimization over noisy surfaces.

Key words: Bacterial Colony Forging, Chemotaxis, Global Optimization.

Nature serves as a rich source of concepts, principles, and mechanisms for designing artificial computational systems to solve complex engineering problems. In recent years, the computational models of chemotaxis (i.e. the bacterial foraging behavior) have attracted more and more attention, due to its research potential in engineering applications. A few models have been developed to mimic bacterial foraging behavior and have been applied for solving some practical problems (Passino, 2002; Badamchizadeh *et al.*, 2010; Zhao *et al.*, 2010). Among them, bacterial foraging optimization (BFO) is a successful population-based numerical optimization model that mimics the foraging behavior of *E. coli* bacteria. Until now, BFO has been applied to some

engineering problems, such as optimal control, optimal power flow, color image enhancement, and machine learning (Chen *et al.*, 2010).

Through natural selection, some predatory animals have developed a self-adaptive foraging strategy called area concentrated search (ACS, also called area-restricted search), by which a predator is able to respond to variations in prey distributions by varying its searching efforts: following an encounter with food resource, a forager searches intensively in a more circumscribed region, while a failure to encounter a resource leads to a more extensive, less circumspect mode of search. That is, ACS assumes that regions dense with preys should be exploited slowly, to maximize the chances of encounter, and less dense regions explored rapidly, to minimize the time spent searching in unprofitable areas (Gendron and Staddon, 1983). ACS in a continuous patchy environment thereby ensures that foraging behaviors will, to some extent, match the

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distribution of resource, and may be viewed as a simple form of optimal habitat selection (Krakauer and Rodríguez-Gironés, 1995). The ACS behavior is regarded as an efficiently adaptive search strategy, which is employed by many search-intensive predators, such as birds, lizards, insects and even some microorganisms.

As a new branch of microbiology, quorum sensing was discovered by Miller and Bassler (Miller and Bassler, 2001). Generally, it is a process that allows bacteria to search for similar cells in their close surroundings using secreted chemical signaling molecules called autoinducers. This is also called “cell-to-cell communication”. Recent studies of microorganisms have revealed that bacteria could function as groups and the individuals within the group could respond to and benefit from the group as a whole. That is, through cell-to-cell communication, bacteria can glean information from the environment and from other organisms, interpret such information into common knowledge and learn from past experience (Jacob *et al.*, 2004). For this reason, bacterial colonies display diverse complex social behaviors, including cooperation in foraging, building, reproducing, purposeful alteration of colony structure and decision-making. In such a perspective, the bacterial colony behaves much like a multicellular organism or a social community.

This paper aims to demonstrate convincingly that the self-adaptive and communication approaches are both effective strategies and can be utilized to help scaling up the performance of bacterial foraging. That is, this paper extend the classical BFO model to a novel bacterial colony foraging (BCF) simulation model by applying two enhanced manipulated steps, namely a cell-to-cell communication (i.e. the quorum sensing) and a self-adaptive foraging strategy (i.e. the ACS). In the proposed BCF model, each artificial bacterium can climb the nutrient gradient based on not only its own experience but also the knowledge of the others; also, each bacterium can strike a balance between the exploration and the exploitation of the search space during its evolution, by adaptively tuning the magnitude of its chemotactic step size.

In the experiment, we validate the models and show that the principle of climbing noisy gradients introduced in this paper.

Table 1. The dynamic self-adaptive strategy

1.	FOR (each bacterium i) IN PARALLEL
2.	IF (<i>Criterion-1</i>) then //exploitation
3.	$C_j(t+1) = C_j(t) / \lambda$;
4.	$\varepsilon_i(t+1) = \varepsilon_i(t) / \lambda$;
5.	ELSE IF (<i>Criterion-2</i>) then //exploration
6.	$C_j(t+1) = C_j^{initial}$;
7.	$\varepsilon_i(t+1) = \varepsilon_i^{initial}$;
8.	ELSE
9.	$C_j(t+1) = C_j(t)$;
10.	$\varepsilon_i(t+1) = \varepsilon_i(t)$;
11.	END IF
12.	END FOR IN PARALLEL

Bacterial colony foraging model

In the proposed BCF model, the most important contributions are: (1) to define the bacterial self-adaptive foraging strategy that dynamically balances the exploration and exploitation behaviors during the foraging process of each bacterium; (2) to define the bacterial cell-to-cell communication mechanism that enables the information sharing among bacterial colony. This work extends the classical BFO to a self-adaptive and cooperative foraging model by constructing the following processes:

Self-adaptation

A central problem for the natural predators in the foraging process is how to balance two conflicting alternatives: the exploitation (i.e., to search thoroughly in promising areas) and the exploration (i.e., to move to distant areas potentially better than the actual one).

According to the ACS strategy, each bacterium in the colony has to permanently maintain an appropriate balance between “Exploration” and “Exploitation” states by varying its own run-length unit adaptively. The criteria that determine the adjustment of individual run-length unit and the entrance into one of the states are defined as following:

Criterion-1

if the bacterium discovers a promising domain, the run-length unit of this bacterium is

adapted to a smaller one. Here “discovers a promising domain” means this bacterium registers a fitness improvement beyond a certain precision from the last generation to the current. Following Criterion-1, the bacterium’s behavior will self-adapt into the Exploitation state.

Criterion-2

if the bacterium’s current fitness is unchanged for a number K_u (user-defined) of consecutive generations, then augment this bacterium’s run-length unit and this bacterium enters the Exploration state. This situation means that the bacterium searches on an un-promising domain or the domain where this bacterium focuses its search has nothing new to offer.

This self-adaptive strategy is given in pseudocode in Table 1. Where t is the current generation number, $C_i(t)$ is the current run-length unit of the i th bacterium, $\epsilon_i(t)$ is the required precision in the current generation of the i th bacterium, l is the run-length unit decreasing parameter that is a user-defined constant,

$C_i^{initial}$ and $\epsilon_i^{initial}$ are the initialized run-length unit and the precision goal respectively.

Cell-to-cell Communication

In the light of the analogy between bacterial quorum sensing and swarming pattern of bird flocking and fish schooling, a novel principle of cell-to-cell communication for bacterial foraging model is introduced.

In BCF model, when a bacterial turns, its choice of a new direction should not be governed by a probability distribution, while be dominated by the information combination of itself and its colony members. Accordingly, we introduce an additional direction component D_i to each bacterium. Then in the BCF model, at the t th iteration the direction is computed as:

$$D_i(t) = kD_i(t-1) + \phi_1 R_1 \|X_{p_i} - X_i(t-1)\| + \phi_2 R_2 \|X_{s_i} - X_i(t-1)\| \quad \dots(1)$$

where k is the weight for the previous direction of the i th bacterium, which represents how the bacterium trusts its own status at present location, X_{p_i} is the best position where this

bacterium had been, X_{s_i} is the overall global best position ever achieved by the bacterial colony, $\|X_{p_i} - X_i(t-1)\|$ and $\|X_{s_i} - X_i(t-1)\|$ are both unit vectors for indicating the directions only, ϕ_1 and ϕ_2 are the learning rates that control the influence levels of cognitive and social components to make different swimming directions, R_1 and R_2 are random numbers uniformly distributed in $[0, 1]$.

In this context, each bacterium adjusts its tumble angle according to the personal historical experience and the bacterial colony social knowledge. This cell-to-cell communication based cooperation may provide bacteria with more accurate information about the search because it is the whole colony that engaged in searching the solution space not just the single bacterium.

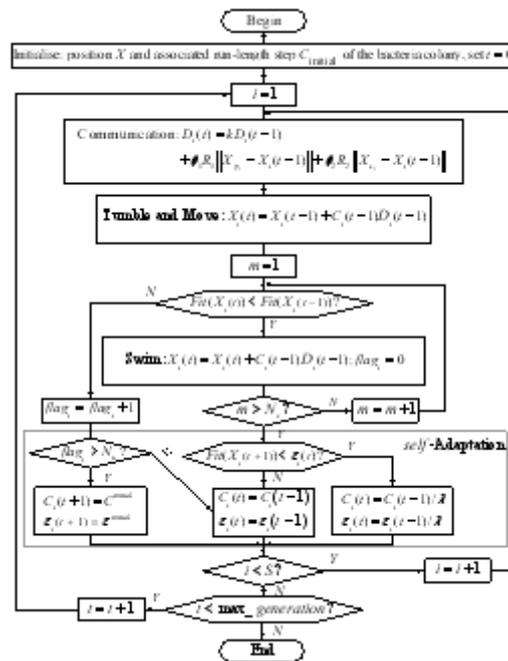


Fig. 1. Flowchart of the BCF Model

Enhanced Chemotaxis

Then in each chemotactic step, the self-adaptive chemotactic step-size C_i controls the swim amplitude taken by the i th bacterium towards a desired direction, which is specified by the cell-to-cell communication based tumble direction D_i :

$$X_i(t) = X_i(t-1) + C_i(t-1)D_i(t-1) \quad \dots(2)$$

The flowchart of the BCF model is illustrated in Fig. 1, where S is the colony size, t is the chemotactic generation counter from 1 to max-generation, i is the bacterium's ID counter from 1 to S , X_i is the position of the i^{th} bacterium, N_s is the maximum number of steps for a single activity of swim, flag_i is the number of generations that the i^{th} bacterium has not improved its own fitness.

Simulation results

In order to analyze the self-adaptive and group foraging behaviors of the BCF model, the evolution dynamics of the single artificial bacterium and the bacterial colony are both simulated in this section.

In the first simulation, we demonstrate the self-adaptive foraging behaviors of a single bacterium on 2-D Sphere, Rosenbrock, Rastrigrin and griewank functions, which are formulated in Table 2 and illustrated in Fig. 2(a)~(d) respectively. the initialized run-length unit C^{initial} was set to be 1% of the search space, the initial precision goal $e^{\text{initial}}=100$, the generation limit for jumping out of local optima $K_u=20$, and after performing a series of hand-tuning experiments, the run-length unit decreasing parameter $\lambda=10$, the population size $S=1$, and the evolution process proceeds 1000 chemotactic steps.

Fig. 3(a) illustrates the bacterial trajectories in the 2-D unimodal Sphere function, which start at point $(-5,-5)$. As we can see, the proposed self-adaptive strategy is important because it permits the bacteria to refine its foraging behaviors adaptively. At the beginning of the

simulation, the bacterium starts exploring the search space. In that manner, the bacterium does not waste much time before finding the promising region that contains the global optimum, because the large run-length unit encourages long-range search. On the other hand, by self-adapting the parameters, the bacterium slows down (i.e. the bacterium enter the exploitation state) near the optimum in order to pursue the more and more precise solutions. Fig. 3(c) illustrates the bacterial trajectories (start at point $(-4,-4)$) in the contour plotted 2-D multimodal Rastrigrin function. We can observe that the bacterium is switching between exploitation and exploration states by self-adapting its run-length unit. Whenever the bacterium encounters a fitness improvement, this forager starts searching intensively in this promising region. Whereas, whenever it is highly probable that the good solutions lying in this region have been found by this bacterium, it moves away from this region and starts to explore the other regions of the search space until another better region is discovered. Finally, we can observe that the bacterium find the domain that contains the global optimum. The similar self-adaptive pattern can be noticed in Fig. 3(b) and (d), which plotted the bacterial foraging trajectories on Rosenbrock and Griewank function respectively. Clearly, this result captures the important aspects of the ACS mechanism that takes place in nature.

In the second simulation, the evolution of the bacterial colony was simulated on 2-D Sphere, Rosenbrock, Rastrigrin and griewank

Table 2. Benchmarks

Name	Function	Limits
Sphere	$f_1(x) = \sum_{i=1}^D x_i^2$	$x_i \in [-5.12, 5.12]^D$
Rosenbrock	$f_2(x) = \sum_{i=1}^D 100 \times (x_{i+1} - x_i^2)^2 + (1 - x_i)^2$	$x_i \in [-2.048, 2.048]^D$
Rastrigrin	$x_i \in [-2.048, 2.048]^D$	$x_i \in [-5.12, 5.12]^D$
Griewank	$f_4(x) = \frac{1}{4000} \sum_{i=1}^D x_i^2 - \prod_{i=1}^D \cos\left(\frac{x_i}{\sqrt{i}}\right) + 1$	$x_i \in [-600, 600]^D$

function respectively. In each case, the bacteria colony is distributed randomly over the nutrient map defined by each function, and the evolution process proceeds 1000 chemotactic steps, and the other parameters were the same as in the bacterial

colony foraging simulation, except $S = 6$.

The motion trajectories of the bacterial colony with cell-to-cell communications are shown in Fig. 4, in which the search space that defines by

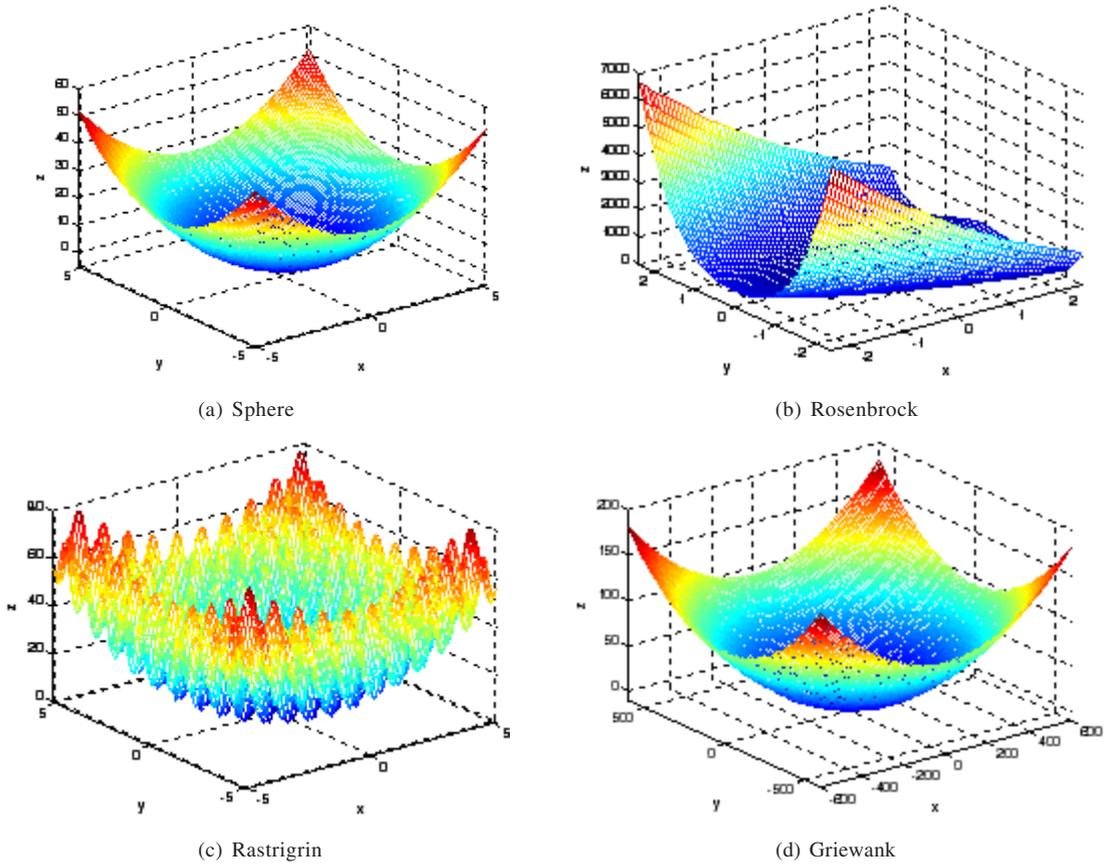
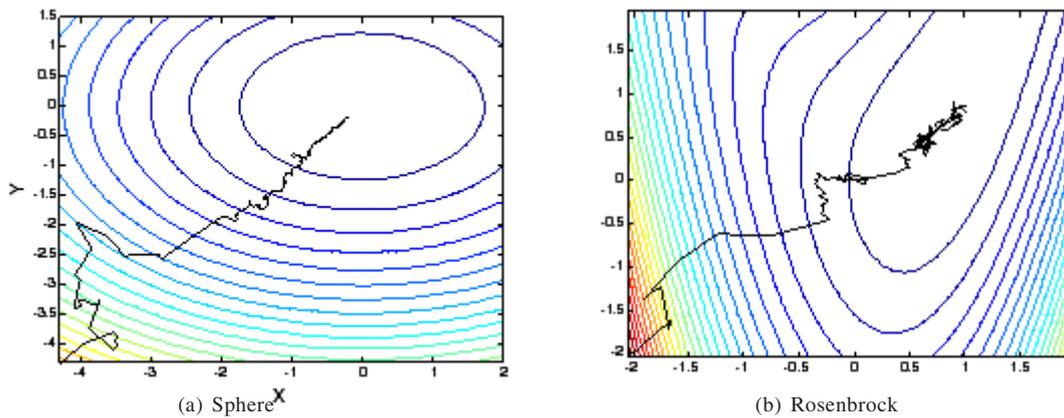


Fig. 2. Nutrient landscape



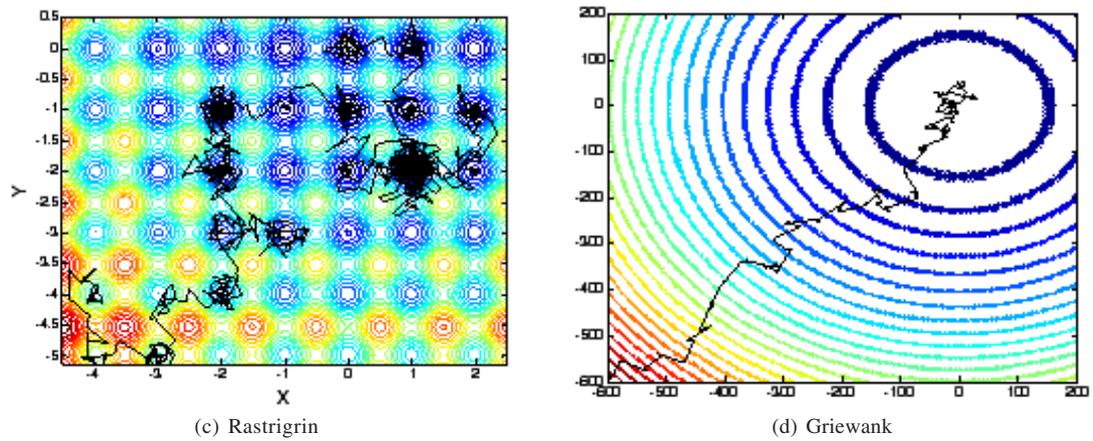


Fig. 3. Self-adaptive foraging trajectories of single bacterium on nutrient landscapes

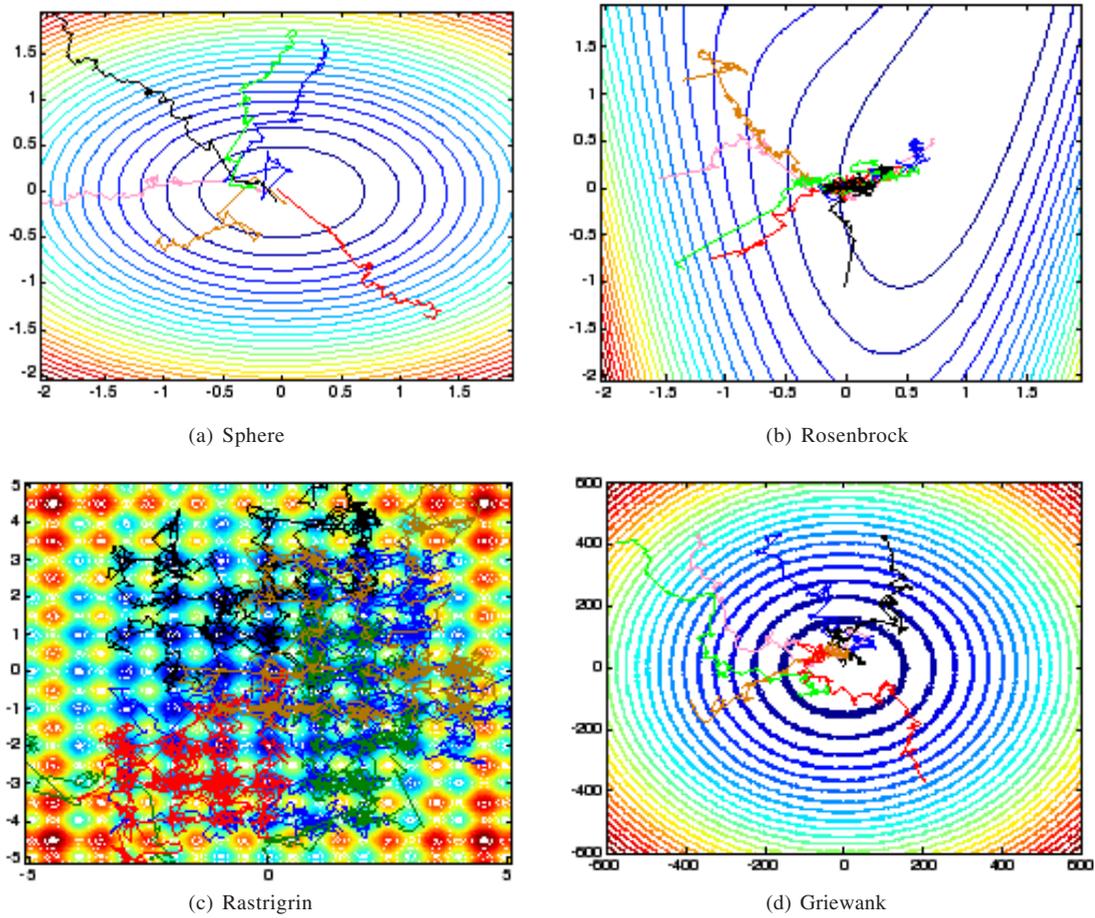


Fig. 4. Cooperative foraging trajectories of bacterial colony on nutrient landscapes

the four functions are contour plotted. In Fig. 4(b), we can observe that with the new cell-to-cell communication mechanism, all the bacteria have found the long and narrow valley of the Rosenbrock function (which contains the global optimum) and move around it in the end of the foraging phase. We found a similar pattern in Fig. 4(c), where the bacteria colony pursue the valleys and avoid the peaks of the multimodal Rastrigrin function. In the first phase the bacterial colony explore many regions of the nutrient map. According to the information transferred by the bacteria in the better positions, the other bacteria join these food sources and then find a good deal of local optima, including the global optimum. The similar group foraging pattern can be also found in Fig. 4(a) and (d), which also plotted the foraging trajectories of bacterial colony on Sphere and Griewank function.

CONCLUSION

The main conclusions that can be drawn from this study include:

- (i) A continuous optimization model is appropriate for bacterial colony foraging.
- (ii) The model of social bacterial colony foraging is also distributed nongradient optimization method and that has the potential to be useful in practical optimization problems.

There are a wide variety of fruitful researches directions in the future work. There are ways to improve the models (e.g., modeling more dynamics of the lifecycle of bacterial colony). Moreover, it remains to be seen how practically useful the optimization algorithms are for engineering optimization problems, which depend on the theoretical properties of the algorithm, theoretical and empirical comparisons to other methods, and extensive evaluation on many benchmark problems and real-world problems.

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