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Computational Foraging in Bacterial Colony over Composition Environments

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The social foraging behavior of *E.coli* bacteria has been used to solve optimization problems. This work proposes a novel cooperative bacterial foraging algorithm (CBFA) for complex optimization problems. The proposed CBFA extend original bacterial foraging algorithm to adaptive and cooperative mode by combining bacterial chemotaxis, cell-to-cell communication, and an adaptive foraging mechanism. Then the performance analysis is given where the proposed algorithm is benchmarked against four state-of-the-art reference algorithms using a composition test function suites. Statistical analysis result highlights the significant performance improvement due to the beneficial combination and shows that the proposed algorithm outperforms the reference algorithms.

Key words: Bacterial Forging, Chemotaxis, Cooperative Foraging, Composition Function.

Recent studies of microorganisms have revealed diverse complex social behaviors, including cooperation in foraging, building, reproducing, dispersing and cell-to-cell communicating. In recent years, search and optimal foraging of bacteria have been used for solving optimization problems. A few models have been developed to mimic bacterial foraging behavior and have been applied for solving some practical engineering optimization problems (Passino, 2002; Badamchizadeh *et al*., 2010; Zhao *et al*., 2010). Among them, bacterial foraging algorithm (BFA) is a successful population-based optimization model that mimics the foraging behavior of *E. coli* bacteria. Until now, BFA has been applied to solve the engineering problems in optimal control, optimal power flow, color image enhancement, and machine learning domains (Chen *et al*., 2010). However, there are no cooperation or communication mechanisms in the original BFA model, and all bacterial individuals suffer premature convergence to the local optimum in the first generations when solving complex multimodal problems.

Quorum sensing, namely the cell-to-cell communication mechanism in bacterial colony, 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. 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).

Natural selection tends to eliminate animals with poor foraging strategies through methods for locating, handling, and ingesting food and favors the propagation of genes of those animals that have successful foraging strategies (Gendron and Staddon, 1983). In nature, living in groups allows individuals to allocate foraging effort between two different roles, namely the producer and the scrounger (Krakauera and Rodríguez-Gironés, 1995). The "producer" can be used to locate food patches independently, while the "scrounger" can be used to exploit the food

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discovered by other group members. Producer-scrounger models suggest equilibrium and flexibility in use between the two strategies in response to changes in environment, which alters the costs and benefits of producing and scrounging. It is essentially this idea that could be applied to complex optimization problems. The optimization problem search space could be modeled as a social foraging environment where groups of parameters adaptively updating for finding solutions to difficult engineering problems.

This paper extend the classical BFA algorithm to a novel cooperative bacterial foraging algorithm (CBFA) 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 CBFA, 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 CBFA on the novel hybrid benchmark called composition function (Liang *et al.*, 2005). The proposed algorithm is benchmarked against four state-of-the-art reference algorithms to show the merits of the beneficial combination of adaptive strategy and cell-to-cell communication mechanism.

Table 1. The dynamic adaptive strategy

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IF (t mod n = 0) then
    IF ( $f_{best} < E(f)$ ) then
        $C(t+1) = C(t-n) / \alpha$ ;
        $E(t+1) = E(f) / \beta$ ;
    ELSE
        $C(t+1) = C(t-n)$ ;
        $E(t+1) = E(t-n)$ ;
    END IF
ELSE
    $C(t+1) = C(f)$ ;
    $E(t+1) = E(f)$ ;
END IF
```

Cooperative bacterial foraging algorithm

This work extends the classical BFA to an adaptive and cooperative foraging model by constructing the following processes:

Adaptation

As indicated in the previous study, the bacterium with a small run-length unit has the exploring ability while the bacterium with a relatively large run-length unit has the exploiting skill. This inspired us to divide the foraging procedure of artificial bacteria colony into multiple Explore/Exploit phases, each characterized by the different value of run-length unit and occupies a portion of generations. This approach produces two classes of bacterial individuals – producers and scroungers – depending on the particular run-length unit that they used. The bacterial producer explores the search space and has the responsibility to find the promising domains and to leave the local optima that have visited, while the bacterial scrounger focuses on the precision of the found solutions, i.e. the bacteria perform exploitation of the neighborhood of the best-so-far solutions found by the producers. This strategy encompasses the following features:

In the initial phase, the bacteria colony searches the whole space of the problem with a large run-length unit – C_{initial} (Here, the same run-length unit is used for all bacteria in the colony), which permits all the bacterial individuals (i.e. the producers) to explore the whole space efficiently and avoid being trapped in local optima. Each bacterial producer records all its visited points and the point with the highest fitness value is considered as potential solution candidate, which are supplied as an input to the next phase. When entering into the next phase, the bacteria colony is reinitialized with a relatively smaller run-length unit from the potential candidates found in the previous phase. That is, the bacterial scroungers join resources uncovered by the producers. Then they start exploiting the neighborhood of these current best positions until the needed criteria (the feedback from the search process) for switching to the next phase is reached. That is, in each phase (except the initial phase), the newly initialized bacterial scroungers will join the resources uncovered by others in the forgoing phase and then exploit them for more precise solutions.

This dynamic adaptive strategy is given

in pseudocode in Table. 1. Where *t* is the current generation number, f_{best} is the best fitness value among all the bacteria in the colony, $\varepsilon(t)$ is the required precision in the current generation and *n*, α and β are user-defined constants. Using this strategy, changes in the parameter values of *C* are now based on feedback from the search, and the adaptation happens every *n* generations. Here, in order to perform fine-tuning exploitation of the global optimum, the run-length unit *C*(*t*) adaptively decreases form phase to phase.

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 tth iteration the direction is computed as:

$$D_i(t) = kD_i(t-1) + \phi_1 R_1 \left\| X_{p_i} - X_i(t-1) \right\| + \phi_2 R_2 \left\| X_{s_i} - X_i(t-1) \right\| \qquad ...(1)$$

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

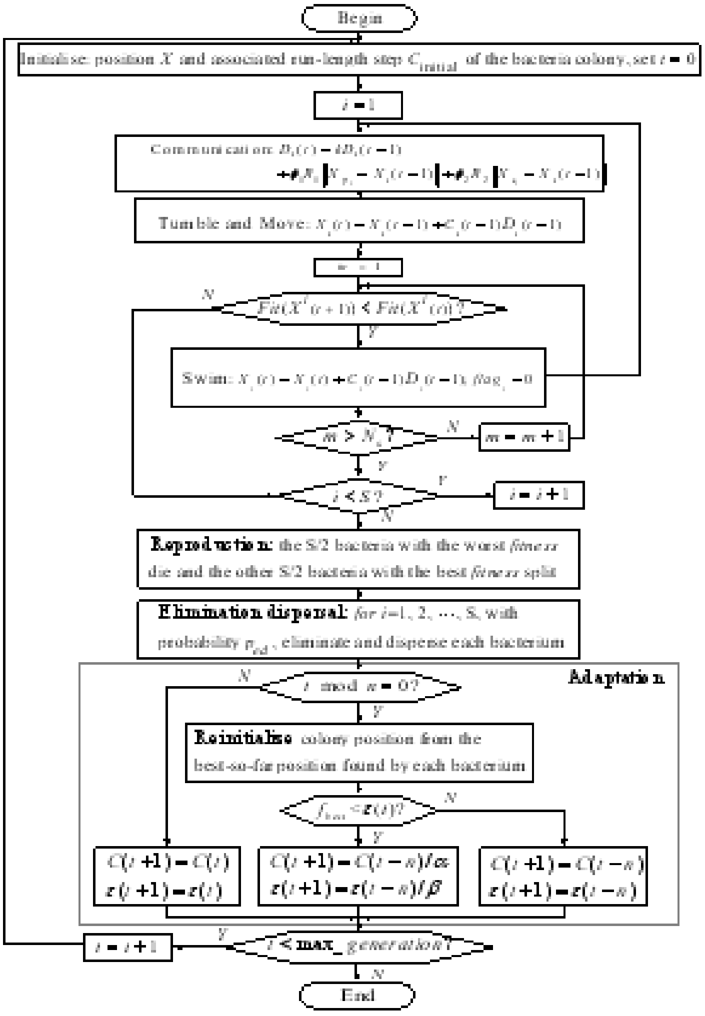


Fig. 1. Flowchart of the CBFA

bacterium had been, X_{g_i} is the overall global best position ever achieved by the bacterial colony, $\|X_{p_i} - X_i(t-1)\|$ and $\|X_{g_i} - X_i(t-1)\|$ 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.

Enhanced Chemotaxis

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

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

The flowchart of the CBFA 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 ith bacterium, N_s is the maximum number of steps for a single activity of swim, flag$_i$ is the number of generations that the ith bacterium has not improved its own fitness.

Simulation results

The test suite contains four composition functions (Cf_1 – Cf_4), each of which is composed by 10 basic functions of 10 dimensions:

$$Cf_{1-4}(x) = \sum_{i=1}^{n}\{w_i * [f_i'((x - o_i + o_{iold})/\lambda_i * M_i) + bias_i]\} + f\_bias \quad ...(3)$$

where

n: the number of basic function.

$w_{i:}$ weight value for each $f_i(x)$.

$f_i(x)$: i^{th} basic function used to construct the composition function.

o_i: new shifted optimum position for each $f_i(x)$.

o_{iold}: old optimum position for each $f_i(x)$.

»$_i$: used to stretch or compress the function.

M_i: orthogonal rotation matrix for each $f_i(x)$.

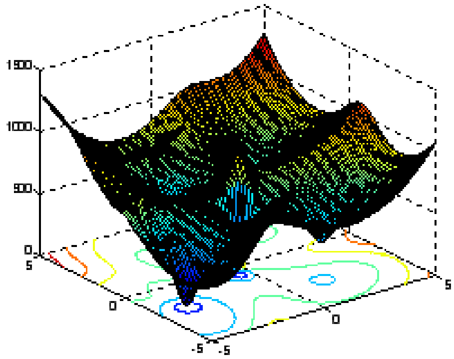
$bias_i$: define which optimum is global optimum.

The basic function set that constructs composition functions is given by the Sphere, Rastrigin, Weierstrass, Griewank, and Acley functions, which have been formulated in Table 2. The search range for all the composed functions is $[-5, 5]^D$. The detailed description of the method for constructing these composite functions can be referred to[17].

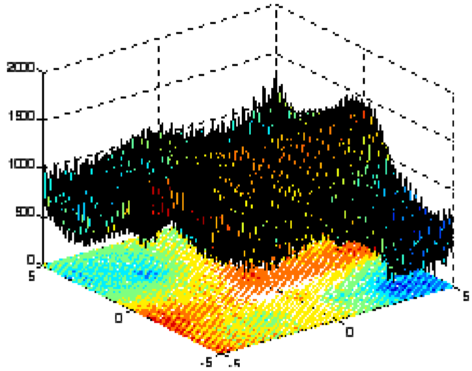
In general the multimodal composite function Cf_1 (Fig. 2a) was constructed using 10 unimodal Sphere functions, this resulting function

Table 2. Performance of all algorithms on composition test suite. In bold are the best results

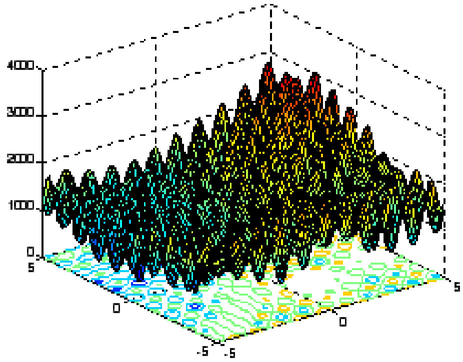
Functions		CBFA	BFA	PSO	GA
Cf_1	Best	3.89e-23	385.3748	0.0479	218.1051
	Worst	154.5088	749.5304	400	473.9154
	Mean	80.0451	543.6946	170.0000	340.0539
	Std	51.48185	121.0532	115.9502	182.6628
Cf_2	Best	4.41875	305.4715	13.6612	237.7604
	Worst	163.3168	981.2563	412.2278	654.8377
	Mean	87.0864	704.4957	206.1286	503.5424
	Std	49.6802	177.0293	121.0506	131.9398
Cf_3	Best	4.1393	614.8877	188.0639	545.0193
	Worst	203.7025	1.1640e+003	409.3549	973.2386
	Mean	85.813	911.7979	249.5267	775.7547
	Std	66.75095	184.0234	71.9234	154.0171
Cf_4	Best	147.3339	606.2175	298.3002	602.1163
	Worst	304.2291	1.4776e+003	721.5762	1.0681e+003
	Mean	187.9278	1.0816e+003	464.4095	848.6733
	Std	48.63005	269.5876	164.5941	151.5677



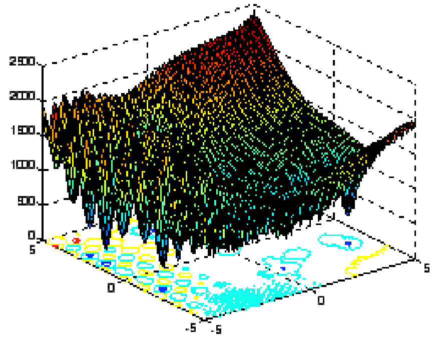
(a) Cf_1



(b) Cf_2

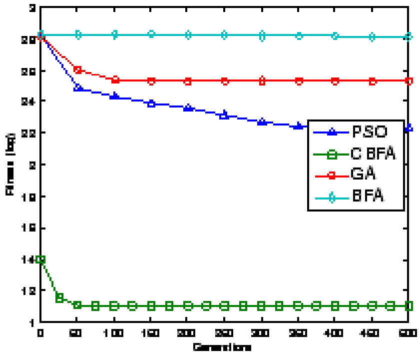


(c) Cf_3

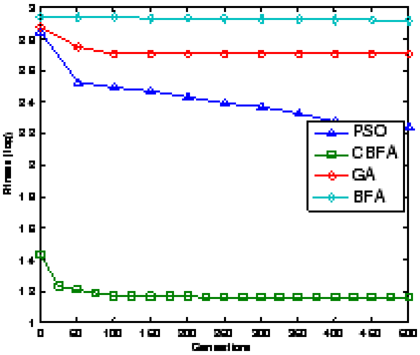


(d) Cf_4

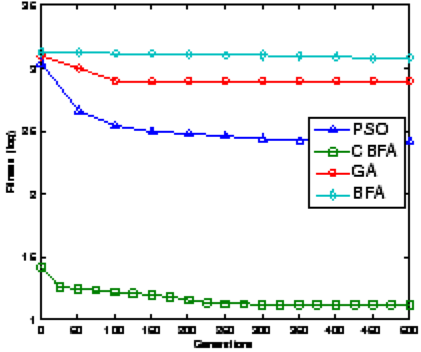
Fig. 2. Composition landscape



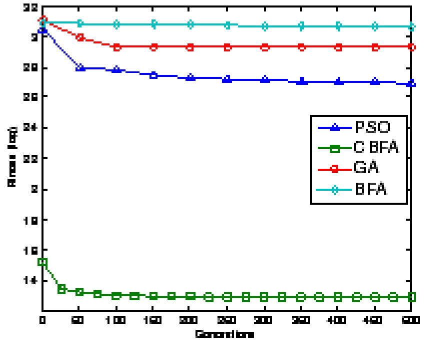
(a) Cf_1



(b) Cf_2

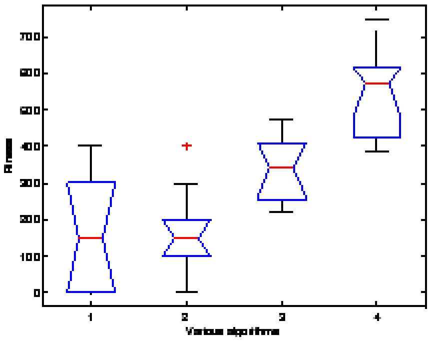


(c) Cf_3

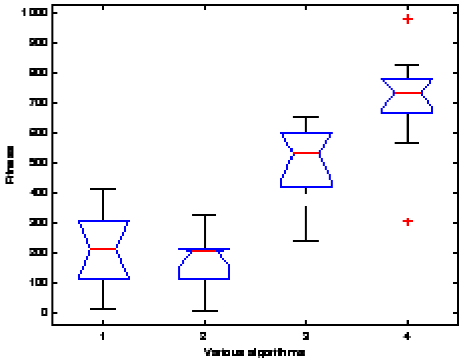


(d) Cf_4

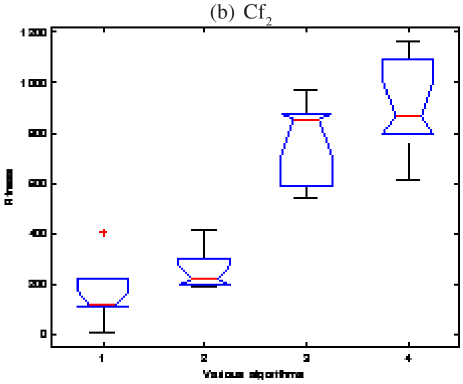
Fig. 3. Fitness convergence on composition nutrient landscapes



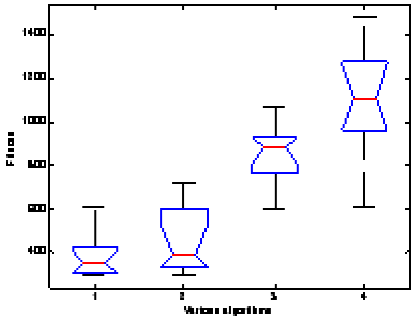
(a) Cf$_1$



(b) Cf$_2$



(c) Cf$_3$



(d) Cf$_4$

Fig. 4. ANOVA test on composition functions. 1, 2, 3, 4 is the algorithm index of CBFA, PSO, GA, BFA, respectively

has one global optimum and nine local optima. Cf_2 (Fig. 2b), and Cf_3 (Fig. 2c) were constructed using 10 Griewank and Rastrigin functions, respectively. Since they have more complex multimodal functions, localizing their local optima becomes more complex. Cf_4 is called hybrid function because it is constructed with different basic functions. That is, Cf_4 (Fig. 2d) is composed by the Acley function (f_1–f_2), Rastrigin function (f_3–f_4), Weierstrass function (f_5–f_6), Griewank function (f_7–f_8), Sphere function (f_9–f_{10}). For these composite functions the global optima are very difficult to reach even when the global optima areas have been found.

To fully evaluate the performance of the proposed CBFA, three successful optimization algorithms were used for comparison (Chen *et al.*, 2010):

- Canonical particle swarm optimization with constriction factor (PSO);
- Classical bacterial foraging algorithm (BFA);
- Standard genetic algorithm (GA).

The optimization results, the convergence characteristics, and the box plots of the ANOVA test of the 30 runs are presented in Table 2, Fig. 2, 3 and 4 respectively. From these results, we can observe that the CBFA algorithm surpasses all other algorithms on all composition fnctions.

CONCLUSION

The main conclusions

(i) An adaptive and cooperative optimization model is appropriate for bacterial foraging algorithm.

(ii) The model of proposed CBFA has the potential to be useful in many benchmark problems and real-world problems.

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