A Micro-Bacterial Foraging Algorithm for High-Dimensional Optimization

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Abstract - **Very recently bacterial foraging has emerged as a powerful technique for solving optimization problems. In this paper, we introduce a micro-bacterial foraging optimization algorithm, which evolves with a very small population compared to its classical version. In this modified bacterial foraging algorithm, the best bacterium is kept unaltered, whereas the other population members are reinitialized. This new small population μ-BFOA is tested over a number of numerical benchmark problems for high dimensions and we find this to outperform the normal bacterial foraging with a larger population as well as with a smaller population.**

1. INTRODUCTION

In 2002 Kevin M Passino, proposed bacterial foraging as a tool for distributed optimization and control. This bacterial foraging optimization algorithm (BFOA) [1-4] mimics the foraging strategy of *E. coli* bacteria (those living in our intestines) which try to maximize the energy intake per unit time. From the very early days it has drawn attention of researchers due to its effectiveness in the optimization domain. So as to improve its performance a large number of modifications have already been undertaken. In 2007 Kim *et al.* came up with BFOA-Genetic algorithm (GA) hybridization for better performance [5]. In the same year authors in [6] proposed BFOA-Particle Swarm Optimization (PSO) hybridization, BFOA-Differential Evolution (DE) hybridization [7] and an adaptive bacterial foraging optimization (ABFOA) [8] for function optimization. But this micro bacterial foraging optimization is modeled specially for handling higher-dimensional problems, where the cost of computation becomes a major bottle-neck.

We took inspirations from similar approaches undertaken in GA and PSO. Initially μ-GA [9] and μ-PSO [10] also proved their efficiency over normal GA and PSO mainly for higher dimensional problems. We have tried to extend this concept for BFOA. The new version BFOA deals with a very small population size compared to normal BFOA, thus reducing the computational cost. Best bacterium in the swarm is kept unaltered after completion of iteration and others are scattered to some random locations following certain rules. This is done to main diversity in the population to avoid premature convergence.

We have tested the efficacy of this algorithm over a test bed which contains 5 high dimensional numerical benchmarks and it performs better than two versions of normal bacterial foraging one with population thirty and another with population three, same as the μ - BFOA.

The rest of the paper is organized as follows. In Section 2, we briefly describe the bacterial foraging optimization algorithm. Section 3 introduces the modified version of bacterial foraging. Section 4 gives the computational results and illustrations. Finally the conclusion and future research scopes are enlisted in Section 5.

II. THE CLASSICAL BACTERIAL FORAGING OPTIMIZATION ALGORITHM

The bacterial foraging system consists of four principal mechanisms, namely chemotaxis, swarming, reproduction and elimination-dispersal [1]. A brief description of each of these processes along with the pseudo-code of the complete algorithm is described below.

i) **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 modes of operation for the entire lifetime. Suppose $\theta^i(j,k,l)$ represents i-th bacterium at j-th chemotactic, k-th reproductive and l-th

elimination-dispersal step. C(i) is the size of the step taken in the random direction specified by the tumble (run length unit). Then in computational chemotaxis the movement of the bacterium may be represented by

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

where Δ indicates a vector in the random direction whose elements lie in [-1, 1].

ii) **Swarming**: An interesting group behavior has been observed for several motile species of bacteria including *E.coli* and *S. typhimurium*, where stable spatio-temporal patterns (swarms) are formed in semisolid nutrient medium. A group of *E.coli* cells arrange themselves in a traveling ring by moving up the nutrient gradient when placed amidst a semisolid matrix with a single nutrient chemo-effecter. The cells when stimulated by a high level of *succinate*, release an attractant *aspertate*, which helps them to aggregate into groups and thus move as concentric patterns of swarms with high bacterial density. The cell-to-cell signaling in *E. coli* swarm may be represented by the following function.

$$J_{cc}(\theta, P(j,k,l)) = \sum_{i=1}^{S} J_{cc}(\theta, \theta^i(j,k,l))$$

$$= \sum_{i=1}^{S}[-d_{attractant}\exp(-w_{attractant}\sum_{m=1}^{p}(\theta_m - \theta_m^i)^2)]+$$

$$\sum_{i=1}^{S}[h_{repellant}\exp(-w_{repellant}\sum_{m=1}^{p}(\theta_m - \theta_m^i)^2)]$$

$$(2)$$

where $J_{cc}(\theta, P(j,k,l))$ is the objective function value to be added to the actual objective function (to be minimized) to present a time varying objective function, S is the total number of bacteria, p is the number of variables to be optimized, which are present in each bacterium and $\theta = [\theta_1, \theta_2, \ldots\ldots\ldots\ldots, \theta_p]^T$ is a point in the p-dimensional search domain. $d_{aatractant}, w_{attractant}, h_{repellant}, w_{repellant}$ are different coefficients that should be chosen properly.

iii) **Reproduction:** The least healthy bacteria eventually die while each of the healthier bacteria (those yielding lower value of the objective function) asexually split into two bacteria, which are then placed in the same location. This keeps the swarm size constant.

iv) **Elimination and Dispersal**: Gradual or sudden changes in the local environment where a bacterium population lives may occur due to various reasons e.g. a significant local rise of temperature may kill a group of bacteria that are currently in a region with a high concentration of nutrient gradients. Events can take place in such a fashion that all the bacteria in a region are killed or a group is dispersed into a new location. To simulate this phenomenon in BFOA some bacteria are liquidated at random with a very small probability while the new replacements are randomly initialized over the search space.

III. THE MICRO - BFOA

A three bacteria population evolves through iterations in this proposed modification. We have used chemotactic operator for updating position of individual bacterium. In this algorithm the population size is very small. So, reproduction is not carried out to avoid saturation and premature convergence. Elimination dispersion step of original algorithm is adopted without any modification. After one complete chemotaxis loop, bacteria in population move to some new foraging locations. At this point, the population may be ranked according to objective function values. The best bacterium (rank 1) of the population retains its position. The second best bacterium (rank 2) is moved to a position very close to the best one. Worst bacterium (rank 3) is initialized at a random position. Fig.1 depicts a three bacteria system scattered over a single dimensional objective function landscape and steps undertaken after chemotaxis are shown. After each complete chemotaxis operation best bacterium contains most valuable information about the fitness landscape. So, by retaining its position we conserve the best discovered location. Now, second best bacterium is liquidated to a position close to the best bacterium in order to facilitate local search during next chemotactic loop execution. The worst bacterium is utilized in maintaining population diversity and avoiding premature convergence. Figure 2 provides a flow-chart for the algorithm.
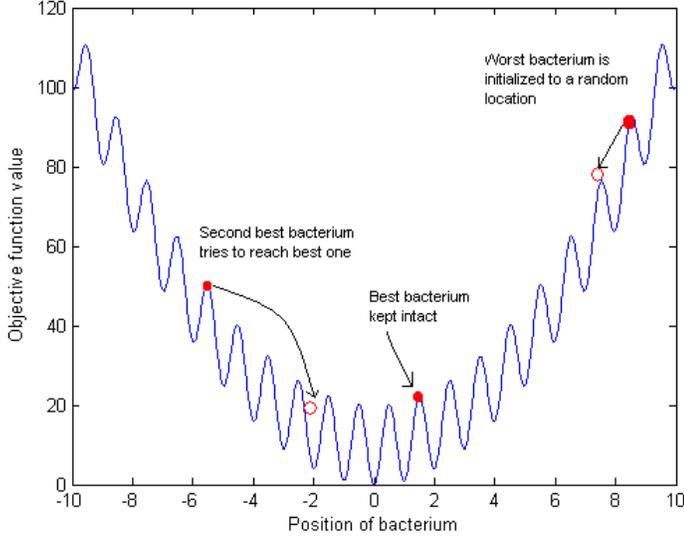
FIGURE 1: A SIMPLIFIED SCHEMATIC DIAGRAM FOR THREE BACTERIA MICRO SYSTEM OPTIMIZING SINGLE DIMENSIONAL OBJECTIVE FUNCTION.

IV. ANALYTICAL BASIS OF MICRO-BF

Two main driving forces of the algorithm are exploration of entire functional landscape by worst bacterium and local search around best discovered location on fitness landscape. Let us denote bacteria triplet as $\vec{\theta}_{best}$, $\vec{\theta}_{medium}$, $\vec{\theta}_{worst}$ according to their objective function value.

Theorem: Probability that $\vec{\theta}_{worst}$ will fall within the hypercube including $\vec{\theta}_{best}$ and $\vec{\theta}_{medium}$ decays exponentially with problem dimension.

Proof: At any instant of time in a particular dimension p, $\max\left\|\vec{\theta}_{best}(p) - \vec{\theta}_{medium}(p)\right\| = \varepsilon$

Let us assume dimensionality of the optimization problem be N. Hence maximum volume of the hypercube including $\vec{\theta}_{best}$, and $\vec{\theta}_{medium}$ is ε^N.

Total volume of the hyperspace including entire search space is $(\max - \min)^N = Range^N$.

Let, $P_{saturation}$ = Probability that $\vec{\theta}_{worst}$ will fall within the hypercube including $\vec{\theta}_{best}$ and $\vec{\theta}_{medium}$.

$\therefore P_{saturation}$ = Ratio of volume of two hyperspaces

$$= \frac{\varepsilon^N}{Range^N} = \left(\frac{\varepsilon}{Range}\right)^N$$

Now, we have taken $\varepsilon = 0.06 \times range$

$\therefore P_{saturation} = 0.06^N$

$\therefore P_{saturation} \to 0$ as N becomes very large.

Explanation:

$P_{saturation}$ denotes the probability that $\vec{\theta}_{worst}$ will fall within the hypercube including $\vec{\theta}_{best}$ and $\vec{\theta}_{medium}$. In this case population diversity decreases and there is a chance for premature convergence. But probability of its occurrence is very small. In most of the time population diversity is maintained. So, the global search is almost never hampered.
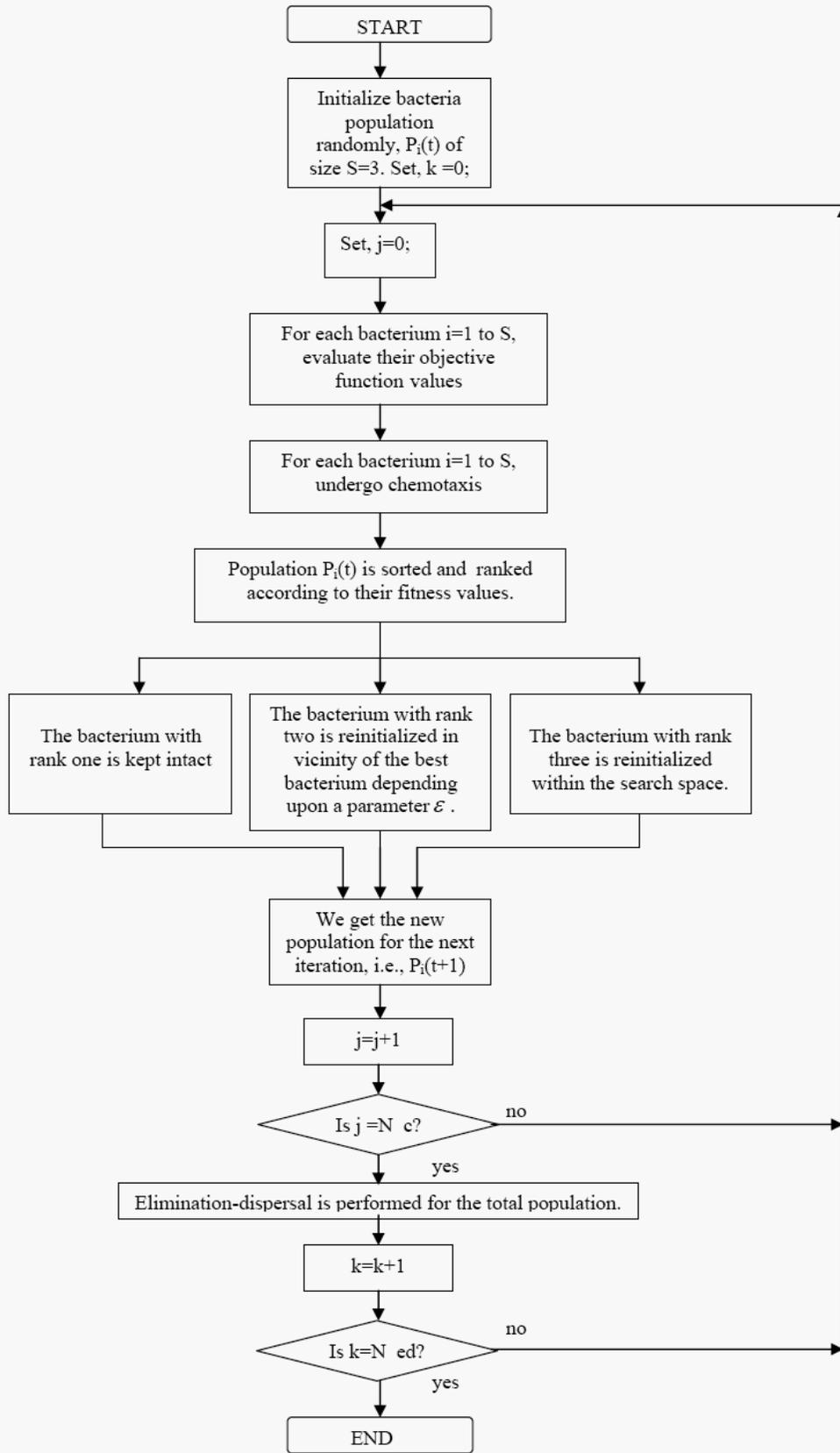
FIGURE 2: FLOW-CHART OF MICRO-BFOA.

TABLE 1: DESCRIPTION OF BENCHMARK FUNCTIONS USED

Function	Mathematical Representation	Range of search	Theoretical Optima
Ackley (f_1)	$f_1(\vec{X}) = -20\exp\left(-0.2\sqrt{\frac{1}{500}\sum_{i=1}^{500} x_i^2}\right) -$ $\exp\left(\frac{1}{500}\sum_{i=1}^{500}\cos 2\pi x_i\right) + 20 + e$	$(-2, 2)^{500}$	$f_1(\vec{0}) = 0$
Griewank (f_2)	$f_2(\vec{x}) = \frac{1}{4000}\sum_{i=1}^{500} x_i^2 - \prod_{i=1}^{500}\cos(\frac{x_i}{\sqrt{i}}) + 1$	$(-10, 10)^{500}$	$f_2(\vec{0}) = 0$
Rastrigin (f_3)	$f_3(\vec{x}) = \sum_{i=1}^{500}[x_i^2 - 10\cos(2\pi x_i) + 10]$	$(-2, 2)^{500}$	$f_3(\vec{0}) = 0$
Rosenbrock (f_4)	$f_4(\vec{x}) = \sum_{i=1}^{500-1}[100(x_{i+1} - x_i^2)^2 + (x_i - 1)^2]$	$(-2, 2)^{500}$	$f_4(\vec{1}) = 0$
Schwefel (f_5)	$f_5(\vec{X}) = -\sum_{i=1}^{500} x_i \sin\left(\sqrt{|x_i|}\right)$	$(-500, 500)^{500}$	$f(\overrightarrow{416.99}) = -416.99\times 500$

TABLE 2: PARAMETRIC SET-UP FOR μ-BF

| Parameters	Parameter Values
S (Population size)	3
N_c (Chemotactic loop counter)	50
N_ed (elimination dispersal counter)	20
p_ed (elimination dispersal probability)	0.25
ε (distance parameter)	$0.06\times range$
$C(i), i = 1,.....,S.$ (Step size)	$0.2\times range$

V. EXPERIMENTAL RESULTS

To test the efficiency of the proposed micro bacterial foraging the following five numerical benchmark test functions have been chosen and are described in Table 1. The dimension for all test problems have been taken to be 500.The parameters taken for the μ BFOA algorithm is given in Table.2. In Table 2 *range* signifies difference between maximum and minimum value of the variable. The parameter ε is the maximum separation introduced at a particular dimension between bacterium of rank 1 and

2 after chemotaxis. Step-size and ε are scaled so that bacterium can have access to all parts of fitness landscape. We have compared the proposed algorithm with normal bacterial foraging with population size 30 and 3.For all these algorithms the maximum cut-off function evaluations is set to be 5000.We take results for 50 independent runs and report the minimum ,mean and standard deviation of the final objective function values for the three competitive algorithms. Performance is illustrated in Figure 3.

| Name of function	Statistical Measurements	Micro Bacterial Foraging (pop=3)	Bacterial Foraging(pop=30)	Bacterial Foraging(pop=3)
Ackley	Minimum	**3.5924**	4.4981	4.0712
	Mean	**3.8175**	4.6555	4.3383
	Std. dev.	0.1128	**0.0583**	0.1549
Griewank	Minimum	**2.5401**	3.5872	3.6338
	Mean	**2.7074**	3.7690	3.7693
	Std. dev.	**0.0394**	0.0426	0.0459
Rastrigin	Minimum	**2151.2082**	3077.7121	2892.6204
	Mean	**2285.0032**	3052.8201	3102.7995
	Std. dev.	36.5299	**27.6755**	56.7978
Rosenbrock	Minimum	**45748.2570**	62805.2019	67669.1890
	Mean	**49035.5738**	66463.91399	71454.2668
	Std. dev.	1745.5252	**777.7251**	884.7100
Schwefel	Minimum	-96558.5871	**-98661.0729**	-97528.9802
	Mean	-93079.6066	**-93905.7658**	-92945.7018
	Std. dev.	2067.9320	**1904.1674**	1905.7137
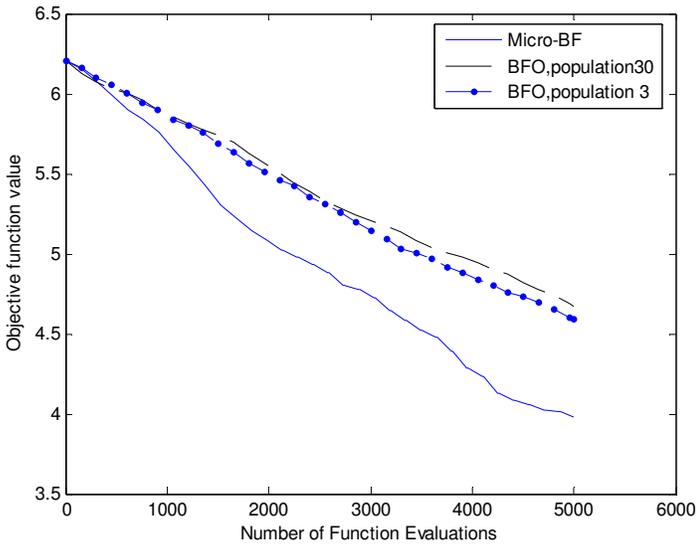
(a)
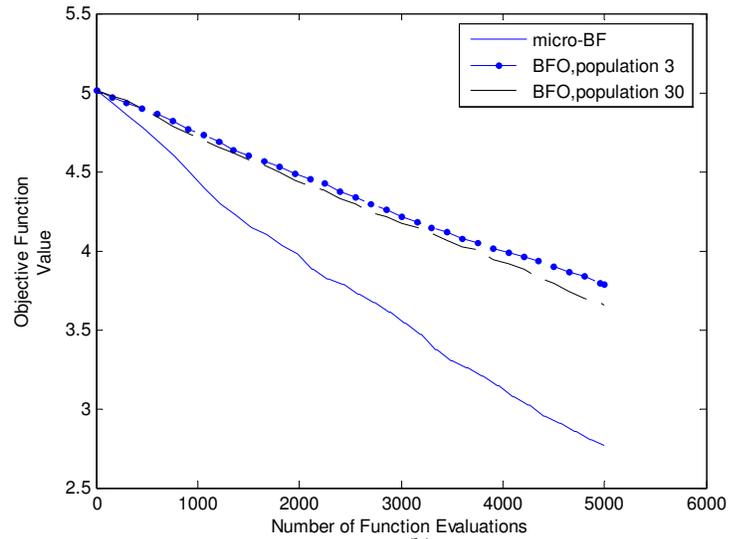
(b)
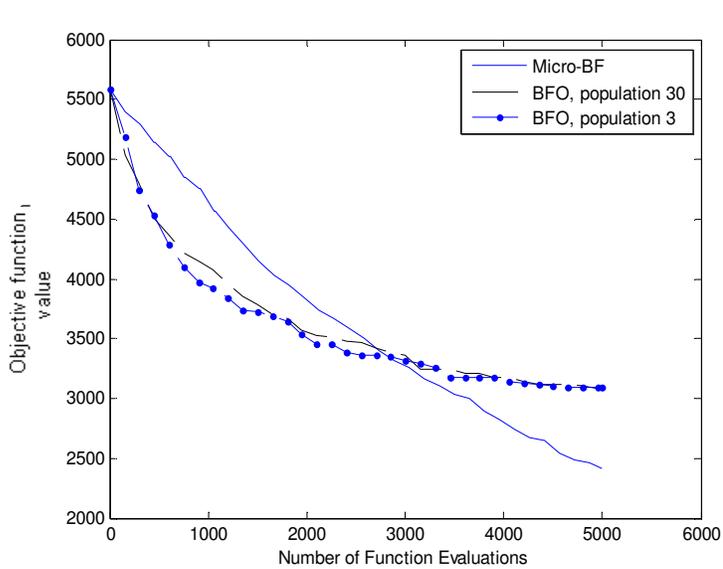
(c)
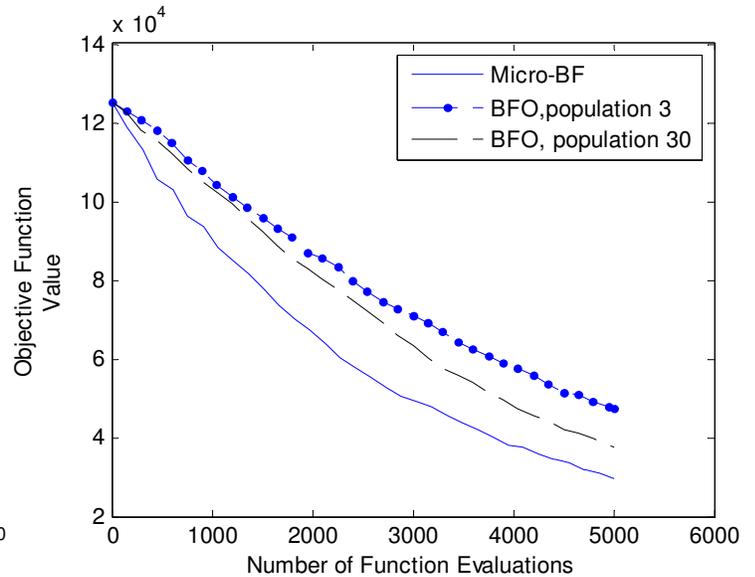
(d)
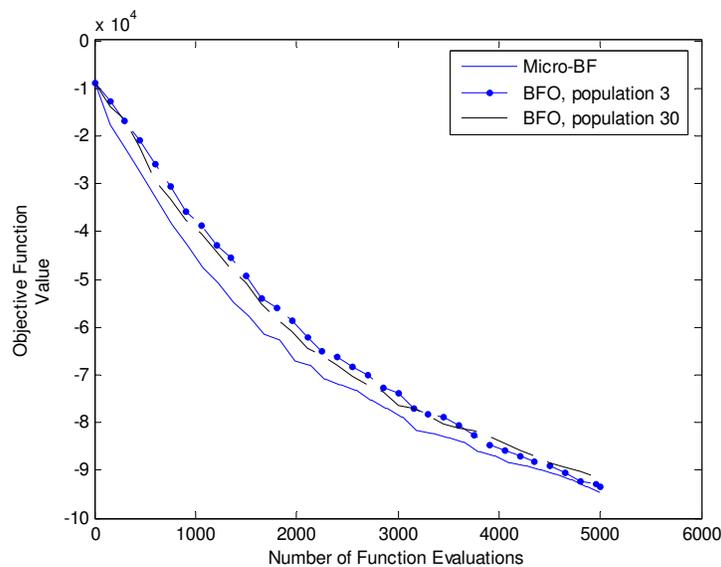
(e)

FIGURE 3: A COMPARATIVE STUDY OF MICRO-BF WITH CLASSICAL BFO OVER VARIOUS FUNCTIONS FOR DIMENSION=500. ACKLEY FUNCTION, (B) GRIEWANGK FUNCTION, (C) RASTRIGIN FUNCTION, (D) ROSENBROCK FUNCTION, AND (E) SCHWEFEL FUNCTION.

VI. CONCLUSIONS

This paper presents a new version of bacterial foraging optimization which evolves with a very small population of size three and designed specially for tackling higher - dimensional problems. The major advantage of this algorithm lies in the reduction of computational cost and computational time. The newly developed algorithm is highly suitable for real time computing. Performance of the proposed algorithm is tested on a test bed of five benchmark functions where it performed well enough compared to the normal bacterial foraging with population size thirty and with population size three. Further research work may focus on developing some new algorithms related to bacterial foraging to decrease the computational cost and time during global optimization. Also some modifications of the normal bacterial foraging

optimization can be undertaken to enhance the performance of the said algorithm near global optima.

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