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A New Refined Bacterial Foraging Algorithm for Multi- Disciplinary and Multi-Objective Problems

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Summary

A novel bio-heuristic algorithm called Bacterial Foraging Algorithm (BFA) and improved version of BFA is proposed in the paper. The BFA is based on a metaphor of social interaction of E-coli bacteria the self adaptability of individuals in the group searching activities has attracted a great deal of interests in real word problems like high dimensional and complex problems. Although the basic BFA is applied to optimization of multi-disciplinary as well as multi-objective problems, the end results of this BFA algorithm so posses a poor performance in tracking of global positions. So, here the improved version of BFA algorithm is proposed in the paper with addressing all the issues. The proposed algorithm is called Refined Bacterial Foraging Algorithm (RBFA) and the RBFA is improved version of the basic BFA with search direction phenomenon, variation of step sizes in chemotaxis behavior and variation of position updating process. The search direction is process for improving speed of convergence and the variation of step sizes for correct identification step length. The point of updating process for finding best bacteria position, ability to bind or track other bacteria position. So, the Refined BFA (RBFA) is proposed and presented in this paper. The proposed algorithm performance was studied using several complex mathematical functions. The simulation result shows the performance of RBFA is superior or comparable to that of the other algorithms and is greatly in terms of speed of convergence, optimization quality, robustness and fast convergence ability.

Keywords: Bacterial Foraging Algorithm, Refined Bacterial Foraging Algorithm, Multi-objective optimization, Ant colony Optimization, Particle Swarm Optimization, Multi-model functions

Introduction

In recent years, bio-inspired and meta-heuristic algorithms are well known and give very much attention for solving complex optimization problems. Some of the well known bio-inspired computational intelligence algorithms are such as Particle Swarm Optimization (PSO), Ant Colony Optimization (ACO), Genetic Algorithm (GA), Artificial Bee's Algorithm, Bacterial Foraging Algorithm (BFA), etc. Among these BFA is gives much attention in complex optimization problems. In 2000, Kevin.M.Passino proposed idea of social behavior of bacteria for solving optimization problems [1], which was known as Bacterial Foraging Algorithms. Recently, the BFA has been successfully used in many practical applications. The BFA, which was inspired by the bacteria behavior of E coli bacteria searching for food, (in human intestines) attracts more and more attention and has been focus on solving global optimization of complex, numerical and real valued problems, where need of exact formulations and solutions [7] [14]. BFA has been applied many kind of real valued problems, such has optimal power system stabilizer [12], PID controller design [10], optimal power flow [15], transmission network expansion planning [14], constrained optimization [15], non-linear dynamic system [13] and RFID network planning [8].

The following methodology is to adopt best bacteria position via to obtain the solutions, way of searching the nutrients, evade noxious environments, communicating and moving circumstance, finally reaching of optimal solutions. But, the basic BFA fails in high dimensional problems, dynamic environments and multi-objective multi-disciplinary problems. So, the above mentioned all the real world problems [3] [5] [6] are in need of improved version of BFA [9] [12] [13]. In order to improve the Basic BFA, can analysis the following of chemotaxis behavior, search direction, step length and position updating process [1] [14].

The search dimension and search direction is very important phenomenon in all the optimization algorithms, initially the chemotaxis step starts with random and it is acceptable, it will helpful for searching the nutrients [11]. Finally, after the tumble step will concentrate more on run step but most of the BFA algorithms failed in this particular operation, so can able to address above requirements, the optimization problems can often be simplified to the search for an optimal solution. Here, the proposed RBFA is gives very much focus on towards the solution of chemotaxis behavior via search direction and search dimension. In the optimization algorithms, the random start gives solution but end result shows time consuming process. For this reason, the proposed RBFA gives high potential to chemotaxis behavior and proposed RBFA also introduced the position updating process and the follow up process of step length calculation. The best bacterium position is updated concurrently, because the claiming of more nutrient position is not very easy. The chemotaxis behavior is comprised of tumble–run process and it consists of tumble step followed by several run steps. In this Proposed RBFA, the search dimension is gives the address of tumble-run process and search direction gives the solution of chemotaxis steps, by the way of whether will continue the tumble process (searching for nutrient position) or run process (towards the nutrient position) and finally the position updating process carried out best bacteria position.

In basic BFA, the bacterium attractants signal to other bacterium is not high cooperative to finding, which one is more nutrient areas or less nutrient areas. So, in the proposed RBFA introduce the attraction factor and velocity vector. The attraction factor is able converge the other bacteria to more nutrient position and velocity vector improves the speed of convergence and gives direction to global best according to the environments. The proposed algorithm provides addition care about repelling effects, because sometimes the repelling effect prevents the gathering of bacteria. Finally, the identification of step length calculation and the RBFA is introduced calculation based on search dimension and number of objectives.

The above mentioned all the modifications are carried out through proposed method and the end results shows improvement in, avoiding the local optima, improves the speed of convergence and reduces the computational time. For analysis and demonstrate the effectiveness of Proposed RBFA, The twenty five mathematical functions considered out of these nine mathematical functions results are given in subsequent section and dynamic variations also considered during the analysis. The proposed RBFA mainly focused on multi-disciplinary multi model and dynamics environments and the simulation results are compared with basic BFA [14], Modified BFA (MBFA) [15], Ant colony Optimization (ACO) [2] and Particle Swarm Optimization (PSO) [5].

The following sections gives a detail about basic BFA algorithm including chemotaxis behavior, swarming, cell to cell communications, reproduction and elimination-dispersal and followed by next section describes and detail about proposed RBFA algorithm. The computational procedure of RBFA algorithm is formulated in the fourth section and fifth section gives detail about validity analysis of proposed algorithm and discussion about complex mathematical functions, final section deals of conclusion of proposed work.

Bacterial Foraging Algorithms

The optimization in BFA comprises the following process: Chemotaxis, swarming, reproduction, elimination and dispersal. Chemotaxis is the activity that bacteria gathering to nutrient-rich areas spontaneously [1] [9]. A Cell-to-cell communication mechanism is established to simulate the biological behavior of bacteria swarming. Reproduction comes from the concept of natural selection and only the bacteria best adapted to their environment tend to survive and transmit their genetic characters to succeeding generations while those less adapted tend to be eliminated. Elimination – dispersal event selects parts of the bacteria to diminish and disperse into random position in the environment, which ensure the diversity of the species. [1] [7]

Chemotaxis

This is process achieved through swimming and tumbling by flagella. Depending upon the rotation of flagella in each bacterium decides it’s pattern, whether it should move in a predefined direction as swimming or altogether in different directions as tumbling in the entire lifetime. The entire lifetime bacteria are set to two mode operation; these modes enable the bacteria to move in the random directions. An E-coli bacterium can move in two different ways alternatively: tumble and run. A tumble is represented by a unit walk with random direction, a unit walk with the same direction as the previous step indicates a run. A chemotactic process is started by one step of tumble and followed by uncertain steps of run, depending on the variation of the environment.

In a tumble, the position of the i_{th} bacterium is updated as:

$$\theta^{i}(j+1,k,l) = \theta^{i}(j,k,l) + C(i)\angle\Phi(j) \tag{1}$$

Where θ^{I} (j,k,l) is the position of the i_{th} bacterium at the j_{th} chemotactic step of the k_{th} reproduction loop in the l_{th} elimination-dispersal event, C(i) is the size of the step taken in the random direction specified by the tumble,$\angle\Phi(j)$ is the angle of the direction which is randomly generated in the range of (0,2π).The fitness value of the i_{th} bacterium at $\theta^{i}(j,k,l)$ is represented by $j^{i}(j,k,l)$.If $\theta^{i}(j+1,k,l)$ the cost is better it means lower then at $\theta^{i}(j,k,l)$. Now the next step of step size of C(i) in this same direction will be taken and once again, if the step resulted in a position with the better cost the previous step means another step taken. This swim is continued as long as it continuous to reduce the cost and its depending upon maximum number of steps, Ns. The Nc is number of chemotaxis steps.

Swarming

During the process, the E-coli bacterium produces attraction convergence characteristics and has to desire when anyone bacteria reaches the best position or location, it should attract other bacteria. So, that they converge in that location and this will happen by generation of attraction signal and also in the meantime, each bacterium releases repellent to warn other bacteria to keep a safe distance from. The E-coli bacterium has own in is, a specific sensing, cell to cell signalling, actuation and decision-making mechanism and because of these properties is lead to provide global search . BFA simulates this social behavior by representing the cell to cell signaling

$$j_{\alpha}\left(\theta^{i}(j,k,l),\theta(j,k,l)\right) = \Sigma_{i=1}^{s} j_{cc}^{i}\left(\theta,\theta^{i}(j,k,l)\right)$$
$$= \Sigma_{i=1}^{s}\left[-d_{attract}\exp\left(-w_{attract}\Sigma_{m=1}^{p}\left(\theta_{m}-\theta_{m}^{i}\right)^{2}\right)\right]$$
$$+\Sigma_{i=1}^{s}\left[h_{repellant}\exp\left(-w_{repellant}\Sigma_{m=1}^{p}\left(\theta_{m}-\theta_{m}^{i}\right)^{2}\right)\right] \tag{2}$$

Where

$d_{attract}$	Depth of the attractant effect
$\omega_{attract}$	Measure of the width of the attractant
$h_{repellant}=d_{attract}$	Height of the repellent effect
$\omega_{repellant}$	Measure of the width of the repellent

P	Number of parameters to be optimized
S	Number of bacteria

Where $\theta^i=[\theta_1,\theta_2,\ldots\ldots, \theta_p]T$ is a point optimization domain and it's the location of the i_{th} bacterium on the P-dimensional optimization domain,$\theta^i{}_m$ is the m_{th} component of i_{th} bacterium position, $\theta=\{\theta^i li=1,2,\ldots,S\}$ represents the position of each member in the population of the S bacteria, $\theta^i{}_m$ is the m_{th} component of θ^I, $\theta^i{}_m$ is the m_{th} component of position θ^t for the t_{th} bacterium, $d_{attract}$ is a quantification of how much attractant is released,

$\omega_{attract}$ is a measure of the diffusion rate of the chemical signal, $h_{repellant}$ and $\omega_{repellant}$ are the magnitude and width of the repelling effect respectively, $J^i{}_{cc}(\theta,\theta^i(j,k,l))$ indicates the signals released by the i_{th} bacterium and $J_{cc}(\theta^i, \theta)$ is time-varying function. $J_{cc}(\theta^i,\theta)$ represents the combined attraction and repelling effects received by the i_{th} bacterium.

Reproduction

After Nc chemotactic steps, a reproduction step is taken. Assume that, N_{re} is the number of reproduction steps is taken. The final population of bacteria undergoes the reproduction process and here, the least healthy bacteria die and other healthiest bacteria split into two at the same location. All the bacteria are sorted according to their fitness S_r (S_r=S/2, for convenience S is assumed to be a positive even integer) and the step fitness during the life and fitness values for the i_{th} bacterium in the chemotactic loop are accumulated and calculated by:

$$\sum_{j=1}^{Nc} Ji(j,k,l)$$

$$j_H^i = \sum_{j=1}^{Nc+1} Ji(j,k,l) \tag{3}$$

Where $j^i{}_H$ represents the health of the i_{th} bacterium.

For simplification the number of the bacteria keeps constant in each chemotaxis process. The characters including location and step length of the mother bacterium all reproduced to the children bacteria. Through this selection process the remaining S_r unhealthier bacteria are eliminated and discarded.

Elimination-Dispersal

The process of chemotaxis and reproduction are not enough for finding global solutions and to improving process of global search ability, the elimination-dispersal event introduced after N_{re} steps of reproduction. This elimination-dispersal event helps the bacterium avoid being trapped into local optima and dispersal events may place bacteria near global solutions and also the behavior of bacteria seeks out in favorable environments. The bacteria are eliminated and dispersed to random positions in the optimization domain according to the probability, p_{ed} and the number of the event is denoted as N_{ed}.

Refined Bacterial Foraging Algorithm

The survival of species in any natural evolutionary process depends upon their fitness criteria, which relies upon their food searching and motile behavior. The law of evolution supports those species who have better food searching ability and either eliminates or reshapes those with poor search ability. The genes of those species who are stronger are propagated in the evolution chain since they posses ability to reproduce even better species in future generations. So a clear understanding and modeling of foraging behavior in any of the evolutionary species, leads to attempts better solution for any optimization. So, this is way here proposed the new algorithm.

The basic foraging algorithm consists of four steps are Chemotaxis, swarming, reproduction, elimination and dispersal [1]. Chemotaxis is the activity that bacteria gathering to nutrient-rich areas spontaneously. A cell-to-cell communication mechanism is established to simulate the biological behavior of bacteria swarming. Reproduction comes from the concept of natural selection and only the bacteria best adapted to their environment tend to survive and transmit their genetic characters to succeeding generations while those less adapted tend to be eliminated. Elimination – dispersal event selects parts of the bacteria to diminish and disperse into random position in the environment. The proposed method based on foraging behavior of bacteria and some modifications is made through from basic foraging algorithm. The modified algorithm named as Refined Bacterial Foraging Algorithm (RBFA) and RBFA is proposed in this paper. The performance of basic foraging algorithms is well suitable in single objective problems and static environments and step length of the basic BFA is a constant parameter which may guarantee good searching results for small optimization problems. However it is applied to multiple objectives, dynamic environments and high dimensional problems it's gives poor performance and convergence characteristics also not good and many times it trapped into local optima solutions. The process of search direction and step length is important in multiple objectives and dynamic environments. The proposed approach made some modification in step length; Chemotaxis behavior and adding velocity vector for improve speed of convergence and attaining global solution and also suitable diversity for global search and its improves speed of convergence.

Search Direction and Chemotaxis Process

The Chemotaxis behavior is modelled by a tumble-run process that consists of a tumble step and several run steps. The tumble run process follows gradient searching principles, which means the bacteria's position is updated in the run steps by the gradient information provided by the tumble step. In each bacteria step size, unit length, dimension and random direction coordination are much important, a search direction W_{id} (j) and a step length L_{id} (j) are calculated separately for each bacteria i, on each dimension d for each time step or tumble-run process or iteration j, W_{id} (j) =1 means the i-th bacteria goes towards the positive direction of the coordinate axis on the dimension d, its indicates the follow tumble process and consecutive run process. W_{id} (j) = -1 means the bacteria goes towards the negative direction, its follow again tumble process and W_{id} (j) =0 means the bacteria stays at the current position; it means the bacteria reaches more nutrient position.

When any one of bacteria finds best position, it should attract other bacteria so that they converge in that location. The Figure.1 and Figure.2 shows the difference of random direction and after the search dimension estimation, there is enough change in tumble-run process. In this search direction estimation leads to finding the distance of best bacteria from rest of others and the process convergence time minimized. While the distance known, it's easy to attain the swarming process for new Chemotaxis stage. The current position i_{th} the bacterium, in d dimensional search space and j_{th} tumble-run process is updated

$$X_{id}(j+1) = X_{id}(j) + L_{id}(j) W_{id}(j) \tag{4}$$

Once the direction and angle is decided by the tumble step, to reach the position it takes several steps (until the position of worst). The rotation angle Φ is related to the number of the dimensions, the number dimensions desired by objectives.

$$\phi = \frac{\pi}{round\sqrt{d+1}} \tag{5}$$

Where, d- search dimension and π is the number of dimensions.

Position updating Process

In this process the step size calculation are initiated with help of position updating process. The basic methodology is adopted in BFA, In order to meet these criteria. The E-coli cells provides attraction signal to each other, so that they swarm or swim together and towards to the best location and swarming pattern based on cell-to-cell communication. But in this process shows slow converge only and in order to improve this process, the velocity factor added with other bacteria so as to reach best bacteria position and this velocity vector added according to other bacteria position. The Figure.3 and Figure.4 shows strength of RBFA algorithm with help of velocity factor and attraction factor leads to converge the bacteria in global position. The position updating process mainly focus on best bacteria and each dimension is given by

$$X_{id}(j) = \alpha\left(X_{id\ best} - X_{id}\right) \tag{6}$$

Where α is a factor to desire the strength of the bacterium's attraction factor for improving the strength of the bacterium's attraction towards to the best position and for faster convergence., X_{best} indicates the position of current best global solution updated after each function evaluation, and Xi is the position of the i_{th} bacterium at the j_{th} iteration after the tumble run process.

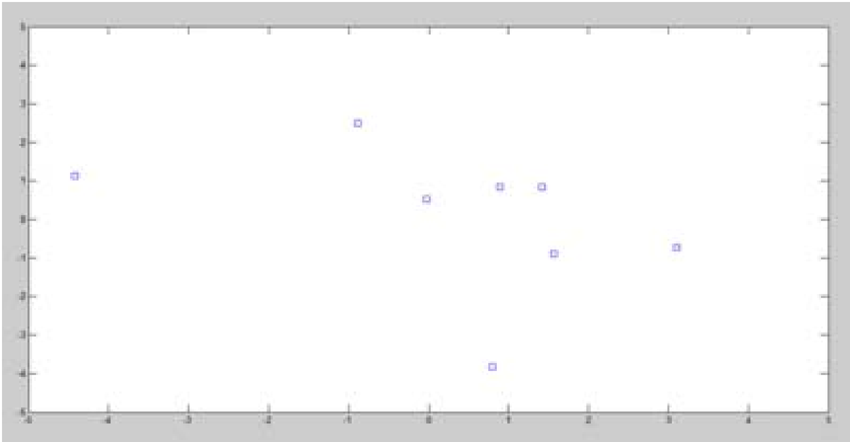

Figure 1: Initial search with random directions

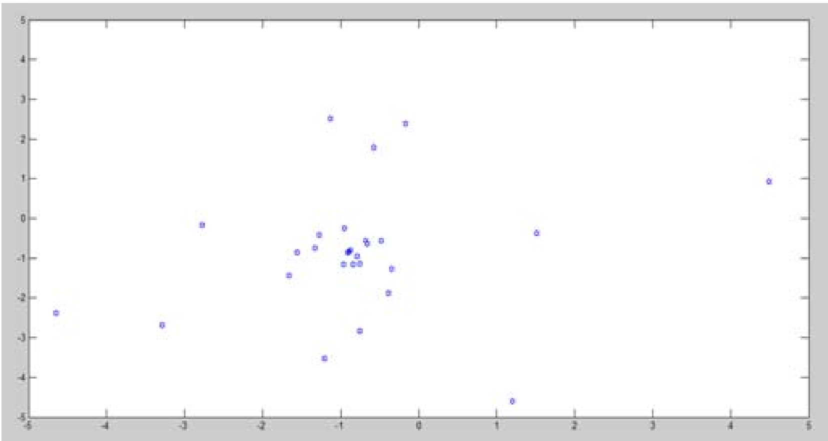

Figure 2: Modification of Chemotaxis behavior in run process with help of Search direction and search dimension

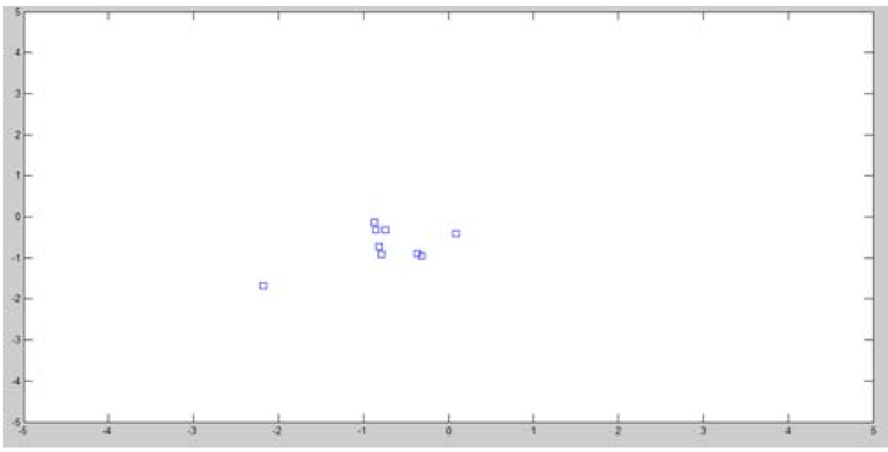

Figure 3: Reaching more Nutrient (best) position

If a anyone bacteria reaches better position in order to direct the other bacteria to best position, the attraction signal is not enough to reach the best position. Therefore, in order to attract other bacteria and also obtain the bacteria position by using equation

$$X_{id}(j+1) = \alpha \left(X_{id\,best} - X_{id}\right) + V_j \tag{7}$$

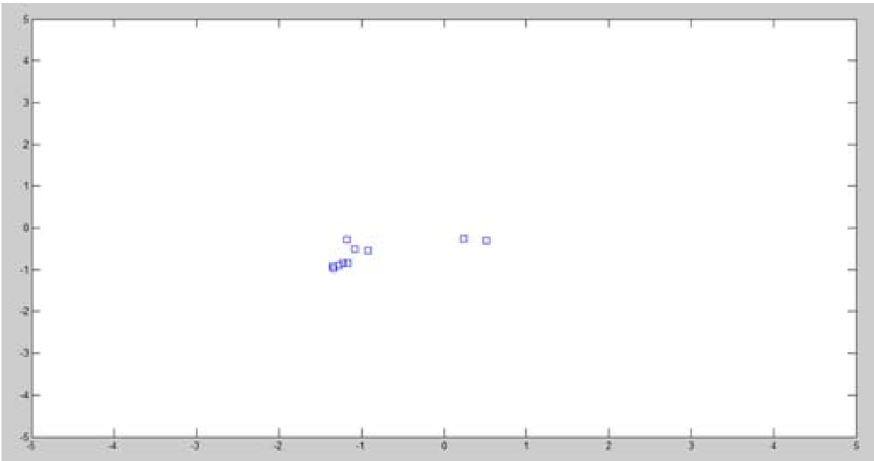

Figure 4: Communicating to other bacteria

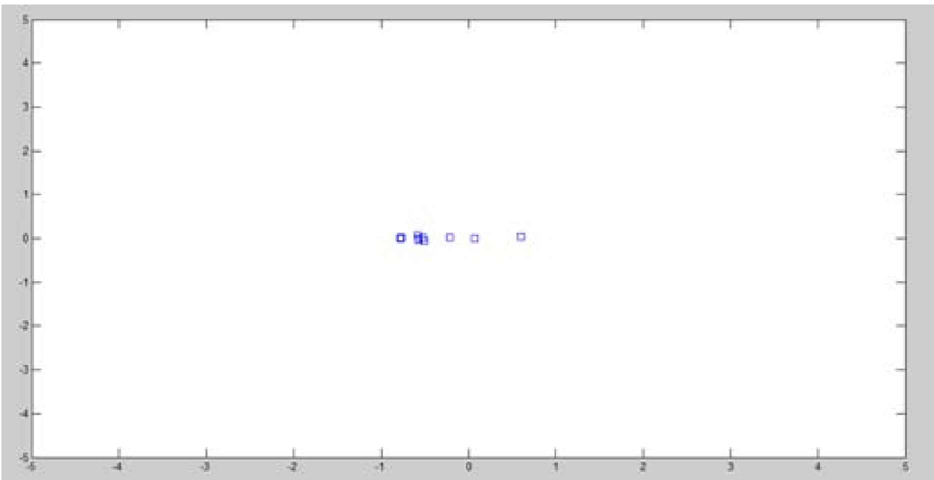

Figure 5: Reaching global point with help of position updating process

So, in the process the velocity factor V_j is binding with position updating process and also is pilot to determine the best position according to the previous best positions. Update best bacteria position and add the velocity according to reach the best position, the velocity factor desired by depending upon according to position of best and other bacteria. The velocity factor V_j also gives direction to global best value or its used to identify global best value.

Step length

The basic BFA shows a step size is a constant parameter and it's suitable to finding the solution in single and small optimization problems. However, when applied to multiple objective problems and dynamic environmental problems it shows poor performance. The basic BFA with fixed step size is failure in reaching the optimal point for the following reasons. The first case, if step size is very high then the accuracy gets low although the bacterium reaches the locality of optimum point quickly and it moves around the maxima for the remaining chemotactic steps. The second case, if the step size is very small, it takes many chemotactic steps to reach the optimum point and its lead to slow convergence and rate of convergence decreases. Meanwhile to reach the optimal point it takes convergence time and number of iterations increases. So, in order to reach the optimal point, speed of convergence and search ability the controlling of step length is essential. In this paper the proposed RBFA following consideration in determining step length process with help of search dimensions, If deviation is very high then the step size must be increased and if the deviation is small in which case the bacterium is close to the optimum point the step size is to be reduced and also improve the performance the swim walk considered instead of the constant step. The Figure.5 shows effect of best fitness of solution and reaching the global point with minimum of time.

For a each bacteria, the location of the *i*th bacterium at the *j*th chemotactic step, *r*th reproduction step and *l* th elimination / dispersal event is represented by $X_{id}(j,k,l) \in \Re^{p}$. After a tumble, the location of the *i*th bacterium is represented by

$$X_{id}\left(j+1,r,l\right)=X_{id}\left(j,r,l\right)+\mathrm{L}\left(\mathrm{i},j\right)\phi\left(j\right) \tag{8}$$

Where

$$\mathrm{L}\left(\mathrm{i},j\right)=\mathrm{L}_{\mathrm{id}}\left(j\right)\mathrm{W}_{\mathrm{id}}\left(j\right)$$

The J(i,j,k,l) is cost function of corresponding X_{id} (j,k,l).The fitness value of the i_{th} bacterium at $X_{id}(j,k,l)$ is represented by j_{id} (j,k,l). In this paper the minimum fitness value j_{min} is defined as the global optimum.

In a run, consecutive steps of size L(*i,j*) is the same direction as the tumble is taken, in condition X_{id} $(j+1,k,l)$ the cost function J $(i,j+1, k,l)$ is better (lower) than J(i,j,k,l). In this condition, the fitness value of the i_{th} bacterium in the r_{th} step of the run Ns indicates the maximum number of steps in a run and also r is smaller than N_s. This swimming operation is repeated as long as a lower cost is obtained until a maximum preset number of steps, N_s, is reached.

In BFA the step length *L* is a constant and it ensures accuracy and speed of the search. The size of the step length is dynamically adjusted in the reproduction and elimination-dispersal process, which ensures the bacteria moving towards the global optimum quickly at the beginning, and converging to the global optimum accurately in the end. So the i_{th} bacteria in d_{th} dimension search space the step length controlling vector is given by

$$\mathrm{L}\left(\mathrm{id}\right)=\min\left\{\left(\mathrm{L}\left(\mathrm{id}\right)-\mu\right),\mathrm{n}\right\} \tag{9}$$

Where

μ - step length vector, n = constant controlling the decreasing rate of the step length. The value of 'n' is desired by according to position updating process and Chemotaxis process.

Computational Algorithm and Pseudo Code of RBFA

The multi disciplinary multi-objective optimization problem is can be solved by using Refined BFA.

Read system data.

Randomly initialize the position of each bacterium in the domain, set the position and fitness value of the best bacterium. Initialize the parameters: S, p, N_c, N_S, $N_{re,}$ $N_{c,}$ $P_{ed,}$ L (id), α, μ, $V_{j,}$ and n.

Randomly initialize the position of each bacterium in the domain, set the position and fitness value of the best bacterium as $X_{id}^{b}(j,k,l)$ and j_{min} (j, k, l) respectively.

FOR (each bacterium i=1: S)

FOR (chemotactic loop j=1: $N_{c)}$

FOR (dimensions=1: π)

FOR (reproduction loop k=1: N_{re})

FOR (elimination-dispersal loop l=1: N_{ed})

Evaluate the cost function *J(i,j,k,l)*

Let $J_{last} = J(i,j,k,l)$ so that a lower cost could be found Calculate J^{i} (j, k, l) and set it as J_{last};

Tumble

Search direction identified with help of identification process according to RBFA

For bacterium I, set J*i*(j,r) as Jlast. A random vector $\Delta(i)$, with each element $\Delta_m(i)$, m=1,2….. p, a random number in the range [-1,1].

Move

Move to a random direction $\frac{\Delta}{\sqrt{\Delta' \times \Delta}}$ by a unit walk, the new position is calculated by equation and start another chemotactic step.

Compute $J(I,j+1,k,l)$ and use to compute J_{cc} (θ, P $(j+1,k,l)$) then use to find the new $J(i,j+1,k,l)$.

Swim: let *m* = 0 (counter for swim length)

While $m< N_s$ (no climbing down too long)

Let $m=m+1$

If $J(I,j+1,k,l)<J_{last}$ *let* $J_{last} = J(I,j+1,k,l)$ then take another step in the same

direction and compute the new J(I,*j*+1,*k*,*l*).

Swim:

Update X_{id}(j+1, k, l).

Recalculate J^i(j+1, k, l);

IF ($J_{current}$< J_{last})

WHILE (J^i_{r+1}(j+1, k, l)<J^i_r(j+1, k, l)

and r<N_s)

Set J^i_r (j+1, k, l) as j_{last};

Run:

Update X_{id} (j+1, k, l)

Set new J^i_{r+1}(j+1, k, l) as $J_{current}$;

Swim:

Update X_{id} (j+1, k, l)

Recalculate J^i_{r+1}(j+1, k, l);

END WHILE

END IF

END FOR (bacterium)

Calculate J_{min} (j+1, k, l)

END FOR (chemotaxis)

Sum:

Evaluate the sum of the fitness value J^i_{health} for the i_{th} bacterium.

Sort
Sort bacteria according to their health J^i_{health} in ascending order.

Split
The bacteria with the highest J^i_{health} values, computed by die while the other S_r with the lowest values split and take the same location of their parents

Eliminate other then health bacteria are to be eliminated.

Update:

Update the step length L (i,j).

END FOR (reproduction)

Disperse:

Disperse certain bacteria to random places in the optimization domain with probability P_{ed}.

Update:

Update the step length L (id)
END FOR (elimination-dispersal)
END

If it's optimal solution is achieved means, the program will stopped.

Results and Discussions

Table.1: Complex mathematical functions

functions	Search space	Globally minimal function value
$f_1(x) = \sum_{i=1}^{n} ix_i^4 + rand[0,1)$	$[-1.28,1.28]^n$	0
$f_2(x) = -20\exp\left(-0.2\sqrt{\frac{1}{n}\sum_{i=1}^{n} x_i^2}\right) - \exp\left(\frac{1}{n}\sum_{i=1}^{n}\cos(2\pi x_i)\right) + 20 + \exp(1)$	$[-32,32]^n$	0
$f_3(x) = \left(0.002 + \sum_{j=1}^{25}(j + \sum_{i=1}^{2}(x_i - a_{ij})^6)^{-1}\right)^{-1}$	$[-65.54,65.54]^n$	0.99800436
$f_4(x) = [1 + (x_1 + x_2 + 1)^2(19 - 14_{x1} + 3x_1^2 - 14x_2 + 6x_1x_2 + 3x_2^2)] \times [30 + (2x_1 + 3x_2)^2 X(18 - 32_{x1} + 12x_1^2 + 48x_2 - 36x_1x_2 + 27x_2^2)]$	$[-2,2]^n$	3.000000
$f_5(x) = -\sum_{i=1}^{4} c_i exp\left[-\sum_{j=1}^{3} a_{ij}(x_j - p_{ij})^2\right]$	$[0,1]^n$	-3.862776
$f_6(x) = \sum_{i=1}^{n-1}[100\,(x_{i+1} - x_1^2)^2 + (x_i - 1)^2]$	$[-30,30]^n$	0
$f_7(x) = \sum_{i=1}^{30}[x_i^2 - 10\cos(2\pi x_i) + 10]$	$[-5.12,5.12]^n$	0
$f_8(x) = \frac{1}{4000}\sum_{i=1}^{30} x_1^2 - \prod_{i=1}^{30}\cos\left(\frac{x_i}{\sqrt{i}}\right) + 1$	$[-600,600]^n$	0
$f_9(x) = 0.1\{sin^2(\pi 3x_1) + \sum_{i=1}^{n}(x_i - 1)^2[1 + sin^2.(3\pi x_{i+1})] + (x_n - 1)^2[1 + sin^2(2\pi x_n)]\} + \sum_{i=1}^{n} u(x_i, 5,100,4)$	$[-50,50]^n$	0

Test functions

Twenty five commonly used test functions [16] [23] are selected for validity analysis of proposed algorithm. The selected all mathematical functions are complex in nature, out of twenty five functions nine high dimensional and multimodal functions [24] are taken for evaluation and comparing the results. The characteristics of those test functions are like search space and globally minimum point are listed in Table.1.Here, some of the functions having many local optima and these functions really challengeable during the evaluations.

Comparison of results with similar bio-inspired algorithms

In fact, today's world the real time optimization problems solution towards to bio-inspired algorithms. Because all the real time problems are multi disciplinary problem and multi objective problems, practically these type problems are high dimensional, varying environments in nature and consist of many local optima. In order to strengthen the local search ability and to ability to track or attain the global optimal quickly, the bio-inspired algorithms are well suitable.

The evaluation of test function solution with proposed algorithm and performance of proposed algorithm are compared with other bio- inspired algorithms like Ant Colony Algorithm (ACO), Particle Swarm Optimization (PSO), basic Bacterial Foraging Algorithm (BFA) and Modified version of Bacterial Foraging Algorithm (MBFA). All the above mentioned algorithms are executed to solve the nine test functions and the results are given in Table.2. The proposed algorithms and all other algorithms are executed 50 runs for each test functions. The programs were coded with MATLAB 7.0 software package and executed via Pentium-IV Computer. The results of Best Mean (Best) and Standard Deviation (Std) of all the functions and comparison of results are given in Table.2.

Experimental setup and function optimization

In this section mainly focused about function optimization and how the validity analysis carried out. The different algorithms are taken for validity analysis and listed in above section. In all the experiments, the basic BFA, MBFA and proposed algorithm are considered same bacteria size and maximum numbers of generations are varied according to the function and trapping level of local minima. The initial solution is generated randomly according to the function and is given in Table.1. In this validity analysis of proposed algorithm are considered twenty five functions out of these nine functions are results taken for final.

Function $f_1(x)$ is Quartic function: the function f_1 is noisy unimodal functions consist of only one local minima and globally minimum point is $f_1(0) = 0$.

Table 2: Comparisons of Results

S. no	Functions	Algorithms	STD	Best
1	$f_1(x)$	ACO	0.0010000	0.0000001
		BFA	1.51798e-2	3.7049e-3
		MBFA	4.436e-4	5.0456e-4
		PSO	3.35672e-2	5.0125e-2
		RBFA	4.8141e-5	4.0053e-5

2	$f_2(x)$	ACO	4.1567e-3	1.97742e-4
		BFA	3.74e-5	9.45e-4
		MBFA	3.001e-17	3.256e-16
		PSO	6.78e-5	9.39e-4
		RBFA	7.89e-15	9.40e-15
3	$f_3(x)$	ACO	0.42152	0.998006
		BFA	3.29e-4	0.998300
		MBFA	3.04e-4	0.998300
		PSO	2.69e-4	0.998100
		RBFA	3.62e-4	0.998300
4	$f_4(x)$	ACO	1.6822e-5	3.03
		BFA	3.1875e-12	3.00002
		MBFA	2.96e-13	3.00003
		PSO	3.32e-15	3.00
		RBFA	2.723e-15	3.0001
5	$f_5(x)$	ACO	1.98e-15	-3.8626
		BFA	2.94e-12	-3.8617
		MBFA	2.69e-12	-3.8627
		PSO	3.657e-3	-3.8627
		RBFA	2.056e-15	-3.8628
6	$f_6(x)$	ACO	NA	NA
		BFA	6.45e1	1.98e1
		MBFA	7.94e2	2.46e1
		PSO	3.23e1	3.59e-1
		RBFA	3.023e1	3.62e-1
7	f7(x)	ACO	3.245e1	7.98e1
		BFA	1.83e1	2.69e1
		MBFA	1.49e2	5.89e1
		PSO	5.25e1	1.58e1
		RBFA	0	0
8	$f_8(x)$	ACO	0.06163	0.08396
		BFA	0.7768	0.3634
		MBFA	0.01237	0.01849
		PSO	0.1570	7.946×10^{-7}
		RBFA	0	0
9	$f_9(x)$	ACO	0.06363	1.674e-12
		BFA	1.31e-1	2.76e-3
		MBFA	1.14e1	3.23e-2
		PSO	2.7279e-6	4.226e-6
		RBFA	1.35e-7	9.35e-7

The function $f_2(x)$ is a multimodal function: usually the multimodal function consist many local minima. In this case search dimension and search space is very important, the proposed algorithm plays better role in this type of multimodal functions and because of efficient in handling the chemotaxis behavior via step length calculation and search direction. Finally, proposed algorithm finds better results and speed of convergence is high compared to other algorithms. The globally minimal point is zero.

The function $f_3(x)$ is a Spiky function: The spiky also multimodal function but with few local optima and global optimal point is 0.99800436.

The function $f_4(x)$ is a Goldstein Price function: The function has only one local optima. This particular function, initially step length calculation is fixed but obtaining the best solutions is fast according to time taken even though fixed step length. Finally the results of best is not accurate, hence the step length is adjusted accordingly to search space. The globally minimum point is 3.00.

The $f_5(x)$ is also multimodal function with consists of few local minima and this function is very high complex function. The proposed algorithm finds very high precision value but convergence time is high compared with ACO and PSO, the BFA and MBFA also good enough in the convergence characteristics of this particular function. The globally optimal point is -3.862776.

The function $f_6(x)$ is a Generalized Rosenbrock's function: It is a unimodal function, in this initially the bacteria are scattering in the manner. In order to reach the search space dimension is easy, it means able to track the local solution is easy. But, in this case find the global point is difficult. The other algorithms are hard to find out the global point is difficult and also in time, the proposed algorithm has enough strength to reach the global point and because of position updating process and it's consist of velocity factor. So, convergence speed is high and time taken is very less. The globally optimal point is zero.

The function $f_7(x)$ is a Generalized Rosenbrock's function: It's a multimodal and it is highly complex functions, this particular function is difficult to find the global point. Because, if search dimension is increases means meantime local minima also increases.

The function $f_8(x)$ Generalized Griewank functions and the function $f_9(x)$ Generalized Penalized functions are multimodal functions with consist of many local minima and difficult to find the global point. The function $f_9(x)$ is convergence is very slow. The globally optimal point of both the function is zero.

The comparison of results in Table.2 shows the proposed RBFA can locate the optimal solutions is in the manner of searching the E-coli bacteria action, the proposed algorithm can find the better results in all the test functions and is compared with all other algorithms. The standard deviations is very small, less number of iterations, function evaluation time very less like way the proposed algorithm is best for all the levels.

Speed of convergence

Normally, the basic BFA adopts slow level search and time consuming process, it's because of the chemotaxis process is not so updated according to the search dimension, environment and also bacteria travels keep on randomly selected directions. Finally, end results shows time consuming process. The proposed RBFA algorithm gives the solution of chemotaxis behavior via search direction and search dimension, able to track the more nutrient areas and the step length calculation is used to improve the local search ability. So, the proposed algorithm tends to increase convergence speed. The compare to BFA, MBFA algorithms, the proposed algorithm is best for handling of tumble run process and with help of this process attaining the global solution is very easy.

According the speed of convergence the RBFA is faster than PSO and it's because of the position updating process is very easy in the proposed algorithm and single step process but in the PSO is updating best bacterium according to the current best position and historically best position. The velocity vector is able direct the best bacteria position to other bacteria according position updating process in proposed algorithm and the severity of complexity to attain the solution is same for BFA and MBFA but according to the performance and speed of convergence the RBFA is better. The RBFA algorithm also addresses the gathering of bacteria and repealing effect. The best bacterium position is updated concurrently is very much important and is lead to improve the level of communicating the global position among the bacteria.

The correct tuned value of attraction factor is to improve the convergence effect from local to global optima and velocity factor is additional effect given best bacteria to reach the global position with effective manner. So the above mentioned factors are lead to increase the speed of convergence and these effects comparable to other algorithms like PSO and ACO. Out of nine functions, the function f_5 takes more time consuming. The RBFA takes 0.35 seconds higher than that of other algorithms.

Parameters values and stopping criteria

The parameter selections of all the algorithms for evaluation of test functions are given below. The parameter PSO are, c is varies from 1.8 to 2.0 and w is decreased from 0.8 to 0.4. The parameters of BFA, MBFA and RBFA are given below. The number of bacteria is equal to 50, the chemotaxis step N_c is varies from 1 to 100, the Number of reproduction N_{re} is various from 1 to 50, the elimination-dispersal loop N_{ed} is various from 1 to 50, the attraction factor α is various from 0.001 to 0.85, the step length various from 0.01 to 3, the controlling factor n is varies from 0.01 to 0.0001 and step length vector μ is varies from 0.01 to 0.0005. The basic BFA algorithm, $d_{attract}$-depth of the attractant effect is 0.01, $\omega_{attract}$ -measure of the width of the attractant is 0.04, height of the repellent effect is 0.01 and $\omega_{repellant}$ -measure of the width of the repellent is 10.0. The probability of elimination –dispersal for BFA algorithm 0.02 and RBFA algorithm is 0.25.

Generally, the stopping criteria depends upon the function evaluation, here the PSO algorithm stops when the maximum number of generations is 10,000 runs. ACO algorithm stops when the best solution is found. BFA, MBFA and RBFA are having different stopping criteria in functions f_2, f_5, f_6 and f_8. But, the other function is terminated when reaching global solution. The comparison of results shows the RBFA algorithm is more suitable for multimodal functions. So, in this extension of this work, the RBFA algorithms' is applied real time multi-objective electric power systems problems.

Conclusion

In this paper, a novel bio-inspired algorithm RBFA has been proposed which is based on social behavior of E-coli bacteria. In this algorithm the step length calculation, position updating process, search direction and search dimension are introduced to solve the multi-disciplinary and multi- objective high dimensional problems. Finally the performances of proposed algorithms have been tested for a set of complex mathematical functions and results of these functions are compared with other bio-inspired algorithms. The evaluation of result proves the effectiveness of proposed algorithm improved in speed of convergence and improvement in optimal accuracy in all the levels.

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