Analysis of Reproduction Operator in Bacterial Foraging Optimization Algorithm

Ajith Abraham, Arijit Biswas, Sambarta Dasgupta and Swagatam Das

Abstract— **One of the major driving forces of Bacterial Foraging Optimization Algorithm (BFOA) is the reproduction phenomenon of virtual bacteria each of which models one trial solution of the optimization problem. During reproduction, the least healthier bacteria (with a lower accumulated value of the objective function in one chemotactic lifetime) die and the other healthier bacteria each split into two, which then starts exploring the search place from the same location. This keeps the population size constant in BFOA. The phenomenon has a direct analogy with the selection mechanism of classical evolutionary algorithms. In this article, we provide a simple mathematical analysis of the effect of reproduction on bacterial dynamics. Our analysis reveals that the reproduction event contributes to the quick convergence of the bacterial population near optima.**

I. Introduction

To tackle several complex search problems of real world, scientists have been looking into the nature for years - both as model and as metaphor - for inspiration. Optimization is at the heart of many natural processes like Darwinian evolution, group behavior of social insects and the foraging strategy of other microbial creatures. Natural selection tends to eliminate species with poor foraging strategies and favor the propagation of genes of species with successful foraging behavior, as they are more likely to enjoy reproductive success.

Since a foraging organism or animal takes necessary action to maximize the energy utilized per unit time spent for foraging, considering all the constraints presented by its own physiology such as sensing and cognitive capabilities, environment (e.g. density of prey, risks from predators, physical characteristics of the search space), the natural foraging strategy can lead to optimization and essentially this idea can be applied to real-world optimization problems. Based on this conception, Passino proposed an optimization technique known as Bacterial Foraging Optimization Algorithm (BFOA) [1, 2]. Until date, the algorithm has successfully been applied to real world problems like optimal controller design [1 - 3], harmonic estimation [4], transmission loss reduction [5], pattern recognition [6] and design of active power filters [7].

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One of the major steps in BFOA is the event of reproduction in which the bacterial population is at first sorted in order of ascending accumulated cost (value of the objective function to be optimized), then the worse half of the population containing least healthy bacteria is liquidated while all the members of the better half is split into two bacteria which are placed in the same location. As pointed out by Passino, this phenomenon finds analogy with the selection mechanism incorporated in classical evolutionary algorithms (EA) [1, 2, and 8]. Bacteria in the most favorable environment (i.e., near an optima gain a selective advantage for reproduction through the cumulative cost).

A first step towards the mathematical analysis of the chemotaxis operation in BFOA has recently been taken by Dasgupta *et al.* [9]. This article following the same train of thoughts appears as one approach for mathematical analysis of the reproduction mechanism in BFOA. We focus our attention on reproduction in a simple two-bacterial system working on a one dimensional fitness landscape and verify the role of reproduction in the convergence characteristics of the said population near global optima. Although the analysis may appear to have a limited scope, note that this article is the first of its kind and the issues of multi-bacterial population over a multi-dimensional fitness landscape are topics of further research. Here our primary objective is to provide important insight into the operational mechanism of BFOA acting as a global function optimizer.

II. The Classical Bacterial Foraging Optimization Algorithm

The bacterial swarm proceeds through four principal mechanisms namely chemotaxis, swarming, reproduction and elimination-dispersal. Below we briefly describe each of these processes and finally provide a pseudo-code of the entire algorithm.

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 :

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

where Δ indicates a unit length vector in the random direction.

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 high level of succinate release an attractant aspertate, which helps them to aggregate into groups and thus move as concentric patterns of swarms of high bacterial density. The cell to cell, signaling in E.coli swarm may be represented with the following function.

$$J_{cc}(\theta^i(j,k,l)) = \sum_{i=1}^{s}[-d_{\text{attractant}}\exp(-w_{\text{attractant}}\sum_{m=1}^{p}(\theta_m - \theta_m^i)^2)] +$$

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

where $\theta = [\theta_1, \theta_2, \ldots, \theta_D]^T$ is a point in the D-dimensional search domain.

iii) **Reproduction:** The least healthy bacteria eventually die while each of the healthier bacteria (those yielding higher value of fitness function) asexually split into two bacteria, which are 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. The pseudo-code of the complete algorithm is given below:

The BFOA Algorithm
Parameters:

[Step 1] Initialize parameters *n, N,* N_C, N_S, N_{re}, N_{ed}, P_{ed}, *C(i)(i=1,2…N),* θ^i.
Where,
n: Dimension of the search space,
N: The number of bacteria in the population,
N_C: chemotactic steps,
N_{re}: The number of reproduction steps,
N_{ed}: the number of elimination-dispersal events,
P_{ed}: elimination-dispersal with probability,
C (i): the size of the step taken in the random direction specified by the tumble.

Algorithm:

[Step 2] Elimination-dispersal loop: *l*=*l*+1
[Step 3] Reproduction loop: *k*=*k*+1
[Step 4] Chemotaxis loop: *j*=*j*+1
[a] For *i* =1,2…N, take a chemotactic step for bacterium *i* as follows.
[b] Compute fitness function, J (*i, j, k, l*).
Let,
$J(i,j,k,l) = J(i,j,k,l) + J_{cc}(\theta^i(j,k,l), P(j,k,l))$
(i.e. add on the cell-to cell attractant–repellant profile to simulate the swarming behavior)
Where, J_{cc} is defined in (2).
[c] Let J_{last}=J (*i, j, k, l*) to save this value since we may find a better cost via a run.
[d] Tumble: generate a random vector $\Delta(i) \in R^n$ with each element $\Delta_m(i), m = 1,2,\ldots, p$, a random number on [-1, 1].
[e] Move: Let

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

This results in a step of size $C(i)$ in the direction of the tumble for bacterium *i.*
[f] Compute J ($i, j+1, k, l$) and let

$$J(i,j,k,l) = J(i,j,k,l) + J_{cc}(\theta^i(j,k,l), P(j,k,l)).$$

[g] Swim
i) Let m=0 (counter for swim length).
ii) While m< N_s (if have not climbed down too long).
• Let m=m+1.
• If J ($i, j+1, k, l$) < J_{last} (if doing better), let J_{last} = J ($i, j+1, k, l$) and let

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

And use this $\theta(i+1,j,k)$ to compute the new J ($i, j+1, k, l$) as we did in [f]
• Else, let m= N_s. This is the end of the while statement.
[h] Go to next bacterium (*i*, 1) if $i \neq N$ (i.e., go to [b] to process the next bacterium).
[Step 5] If $j < N_C$, go to Step 3. In this case, continue chemotaxis, since the life of the bacteria is not over.
[**Step 6**] Reproduction:
[a] For the given *k* and *l*, and for each $i = 1,2,\ldots,N$, let

$$J_{health}^i = \sum_{j=1}^{N_c+1} J(i,j,k,l)$$

be the health of the bacterium *i* (a measure of how many nutrients it got over its lifetime and how successful it was at avoiding noxious substances). Sort bacteria and chemotactic

parameters $C(i)$ in order of ascending cost J_{health} (higher cost means lower health).

[b] The S_r bacteria with the highest J_{health} values die and the remaining S_r bacteria with the best values split (this process is performed by the copies that are made are placed at the same location as their parent).

[**Step 7**] If $k < N_{re}$, go to Step 3]. In this case, we have not reached the number of specified reproduction steps, so we start the next generation of the chemotactic loop.

[**Step 8**] Elimination-dispersal: For $i = 1,2...,N$, with probability P_{ed}, eliminate and disperse each bacterium, and this result in keeping the number of bacteria in the population constant. To do this, if a bacterium is eliminated, simply disperse one to a random location on the optimization domain. If $l < N_{ed}$, then go to [Step 2]; otherwise end.

III. Analysis of the Reproduction Step in BFOA

Let us consider a small population of two bacteria that sequentially undergoes the four basic steps of BFOA over a one-dimensional objective function. The bacteria live in continuous time and at the t-th instant its position is given by $\theta(t)$. Below we list a few assumptions that were considered for the sake of gaining mathematical insight.

Assumptions:

i) The objective function J(θ) is continuous and differentiable at all points in the search space.
ii) The analysis applies to the regions of the fitness landscape where gradients of the function are small i.e., near to the optima.
iii) At the start of reproduction, the two bacteria remain close to each other and one of them must not superpose on another (i.e. $|\theta_2 - \theta_1| \mapsto 0$ may happen as time progresses but $\theta_2 \neq \theta_1$ never occurs. Suppose P and Q represent the respective positions of the two bacteria as shown in Figure 1).
iv) The portion of the function we are concerned is assumed to be monotonously decreasing or increasing and the bacteria system lives in continuous time.

3.1 Analytical Treatment

In our two bacterial system $\theta_1(t)$ and $\theta_2(t)$ represent the position of the two bacteria at time t and $J(\theta_1), J(\theta_2)$ denote the cost function values at those positions respectively. In this two bacterial system, when reproduction takes place the virtual bacterium with a relatively larger value of the cost function (for a minimization problem) is liquidated while the other is split into two. These two offspring bacteria start moving from the same location. Hence in effect during reproduction the least healthy bacteria shift towards the healthier bacteria. Health of a bacterium refers to the accumulated cost function value, possessed by the bacterium until that time instant. The two-bacterial system working on a single dimensional fitness landscape has been depicted in Figure 1.

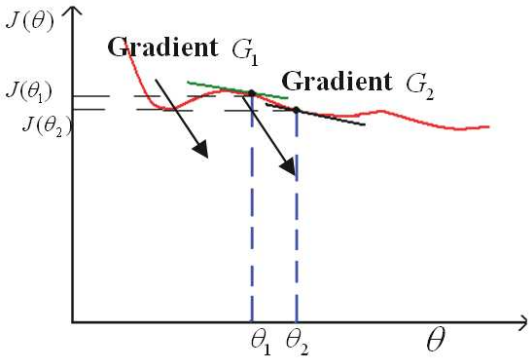

Fig 1: A two-bacterium system on arbitrary fitness landscape

To simulate the bacterial reproduction we have to take a decision on which bacterium will split in next generation and which one will die. This decision may be mathematically implemented with the help of the well-known unit step function $u(x)$, which is defined as,

$$u(x) = 1; \text{ if } x > 0$$
$$= 0; \text{ if } x < 0$$

Although at $x = 0$, $u(x)$ has a jump discontinuity, its value may be assumed as 0.5 for $x = 0$.

At a particular time instant the displacement of the bacteria due to reproduction are modeled with the help of the following pair of equations, (Now onwards we write $\theta_1(t)$ and $\theta_2(t)$ as θ_1 and θ_2 respectively),

$$\frac{\Delta\theta_1}{\Delta t} = u[\int_0^t J(\theta_1)dt - \int_0^t J(\theta_1 + \Delta\theta_1)dt].(\theta_2 - \theta_1) \quad (1)$$

$$\frac{\Delta\theta_2}{\Delta t} = u[\int_0^t J(\theta_2)dt - \int_0^t J(\theta_2 + \Delta\theta_2)dt].(\theta_1 - \theta_2) \quad (2)$$

$\int_0^t J(\theta_1)dt$ represents the health of the first bacterium at the time instant t and $\int_0^t J(\theta_1 + \Delta\theta_1)dt$ represents the health corresponding to $(\theta_1 + \Delta\theta_1)$ at the time instant *t*. We are going to carry out calculations with the equation for bacterium (1) only as the results for other bacterium can be obtained just from symmetry. Now let us consider this $\Delta\theta_1$ displacement occurs in time Δt. Then the average velocity of the bacterium is $\frac{\Delta\theta_1}{\Delta t}$. But as we consider $\Delta\theta_1 \to 0, \Delta t \to 0$, we get the instantaneous velocity $\frac{d\theta_1}{dt}$.

θ_2

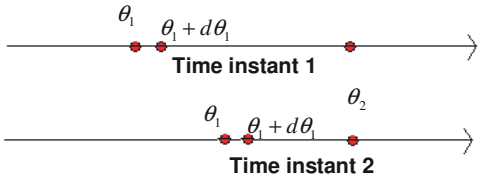

Fig. 2: Change of position of the bacteria during reproduction (one-dimensional system)

Since we are considering only the monotonous part of any function, so if θ_2 is at a better position, then any position, in-between θ_1 and θ_2, has a lesser objective function value compared to θ_1. So we may conclude $J(\theta_1 + d\theta_1)$ is less than $J(\theta_1)$. Again we can imagine that $\int_0^t J(\theta_1 + d\theta_1)$ is less than $\int_0^t J(\theta_1)$ as t is not too high, the functional part under consideration is monotonous and change of $\theta_1 + d\theta_1$ with respect to t is same as that of θ_1.

So we write the equation (1) corresponding to bacterium 1 as,

$$\Rightarrow \underset{\substack{\Delta t\to 0\\ \Delta\theta_1\to 0}}{Lt} \frac{\Delta\theta_1}{\Delta t} = \underset{\substack{\Delta t\to 0\\ \Delta\theta_1\to 0}}{Lt} u[-\int_0^t \frac{J(\theta_1+\Delta\theta_1)-J(\theta_1)}{\Delta t}dt](\theta_2-\theta_1)$$

$$\Rightarrow \frac{d\theta_1}{dt} = u[-\int_0^t (\frac{dJ}{d\theta_1}\frac{d\theta_1}{dt})dt](\theta_2-\theta_1)$$

$$\Rightarrow v_1 = u[-\int_0^t G_1 v_1 dt](\theta_2-\theta_1) \qquad (3)$$

[where $v_1 = \frac{d\theta_1}{dt}$ and G_1 is the gradient of J at $\theta = \theta_1$.]

Now in equation (1) we have not yet considered the fact that the event of reproduction is taking place at t=1 only. So we must introduce a function of time $r(t) = 2 * u(-(t-1)^2)$ (unit step) ($u(-(t-1)^2)$ is multiplied with 2 for getting $r(t) = 1$, not 0.5, when t=1) in product with the right hand side of equation (1). This provides a sharp impulse of strength 1 unit at time t = 1. Now it is well known that $u(x)$ may be approximated with the continuous logistic function $\phi(x)$, where

$$\phi(x) = \frac{1}{1+e^{-kx}}$$

We note that, $u(x) = \underset{k\to\infty}{Lt}\ \phi(x) = \underset{k\to\infty}{Lt}\ \frac{1}{1+e^{-kx}}$

Figures 3 (a) and (b) illustrate how the logistic function may be used to approximate the unit step function used for decision-making in reproduction.

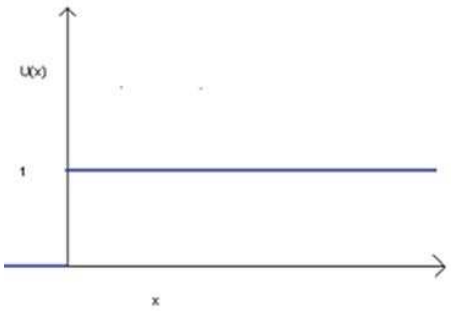

Figure 3 (a): Unit step function

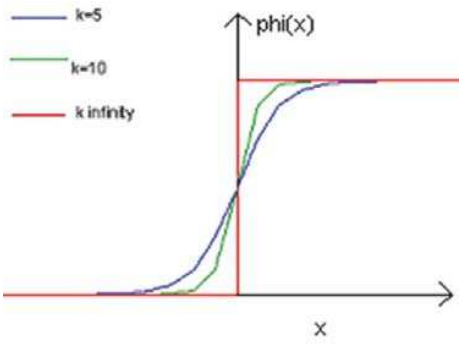

Fig. 3 (b): The logistic function

Following this we may write:

$$u(-(t-1)^2) \approx \frac{1}{1+e^{k(t-1)^2}}$$

For moderately large value of k, since $t \to 1$, we can have $|k(t-1)^2| << 1$ and thus $e^{k(t-1)^2} \approx 1 + k(t-1)^2$. Using this approximation of the exponential term we may replace the unit step function $r(t)$ with another continuous function $g(t)$ where

$$g(t) = \frac{2}{2+k(t-1)^2} \qquad \text{(We can take k=5)}$$

Which is not an impulsive function just at t=1 rather a continuous function as shown in figure 4.Higher value of k will produce more effective result. Due to the presence of this function we see that $v_1 (i.e, \frac{d\theta_1}{dt})$ will be maximum at t=1 and decreases drastically when we move away from t=1 in both sides.

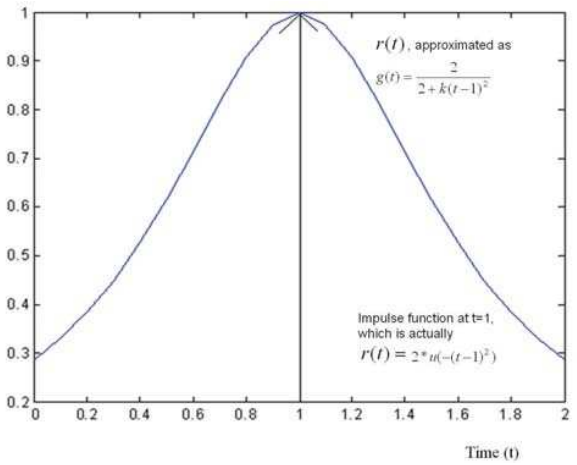

Fig 4: Function r (t) and g(t)

So equation (3) is modified and becomes,

$$v_1 = u[-\int_0^t G_1 v_1 dt](\theta_2 - \theta_1)\frac{2}{2+k(t-1)^2} \quad (4)$$

For ease of calculation we put, the term within the unit step function as

$$\text{i.e., } M = -\int_0^t G_1 v_1 dt$$

So equation (4) reduces to,

$$v_1 = u(M)(\theta_2 - \theta_1)\frac{2}{2+k(t-1)^2} \quad (5)$$

$$\text{Now, } u(M) = \lim_{C\to\infty} \frac{1}{1+e^{-CM}}$$

We take a smaller value of C for getting into the mathematical analysis (say C=10). Since, we have the region, under consideration with very low gradient and the velocity of the particle is low, (so product $G_1 v_1$ is also small enough), and the time interval of the integration is not too large (maximum 2seconds), so we can write, by expanding the exponential part and neglecting the higher order terms

$$u(M) = \frac{1}{1+(1-CM)}$$

$$= \frac{1}{2(1-CM/2)}$$

Substituting the above expression in equation (5) we get,

$$v_1 = \frac{1}{2(1-CM/2)}(\theta_2 - \theta_1)\frac{2}{2(1+(k/2)(t-1)^2)}$$

$$\Rightarrow \frac{v_1}{\theta_2 - \theta_1}((1+(k/2)(t-1)^2) = \frac{1}{2}(1+\frac{CM}{2}) \quad (6)$$

[$\because |\theta_2 - \theta_1| \to 0$ but $|\theta_2 - \theta_1| \neq 0$] [$\because \left|\frac{CM}{2}\right| << 1$,

neglecting higher order terms, $(1-\frac{CM}{2})^{-1} \approx (1+\frac{CM}{2})$]

Now the equation given by (6) is true for all values of t in [0, 2], So we can differentiate both sides of it with respect to t and get,

$$\Rightarrow \frac{(\theta_2-\theta_1)\frac{dv_1}{dt} - v_1(\frac{d\theta_2}{dt} - \frac{d\theta_1}{dt})}{(\theta_2-\theta_1)^2}((1+(k/2)(t-1)^2) +$$

$$\frac{v_1}{\theta_2-\theta_1}k(t-1) = \frac{1}{4}\frac{d(CM)}{dt} \quad (7)$$

$$\text{Now, } \frac{d(CM)}{dt} = \frac{d(-C\int_0^t v_1 G_1 dt)}{dt} = -Cv_1G_1$$

[By substituting the expression for M and applying the Leibniz theorem for differentiating integrals]

So from (7), we get,

$$\frac{(\theta_2-\theta_1)\frac{dv_1}{dt} - v_1(\frac{d\theta_2}{dt} - \frac{d\theta_1}{dt})}{(\theta_2-\theta_1)^2}((1+(k/2)(t-1)^2)$$

$$+\frac{v_1}{\theta_2-\theta_1}k(t-1) = -\frac{1}{4}Cv_1G_1$$

Substituting $\frac{d\theta_1}{dt} = v_1$ and $\frac{d\theta_2}{dt} = v_2$ after some further manipulations (where we need to cancel out $(\theta_2 - \theta_1)$, which we can do as $|\theta_2 - \theta_1| \to 0$ but $|\theta_2 - \theta_1| \neq 0$ according to assumption (iii)), we get,

$$\frac{dv_1}{dt} = -\frac{v_1^2}{\theta_2 - \theta_1} - v_1[\frac{k(t-1)}{1+(k/2)(t-1)^2}$$

$$+\frac{CG_1(\theta_2-\theta_1)}{4(1+(k/2)(t-1)^2)} - \frac{v_2}{\theta_2-\theta_1}]$$

$$\Rightarrow \frac{dv_1}{dt} = -Pv_1^2 - Qv_1 \quad (8)$$

where, $P = \frac{1}{\theta_2 - \theta_1}$ and

$$Q = (\frac{k(t-1)}{1+(k/2)(t-1)^2} + \frac{CG_1(\theta_2-\theta_1)}{4(1+(k/2)(t-1)^2)} - \frac{v_2}{\theta_2-\theta_1})$$

The above equation is for the first bacterium and similarly we can derive the equation for the second bacterium, which appears like,

$$\frac{dv_2}{dt} = -P'v_2^2 - Q'v_2 \quad (9)$$

Where, $P' = \frac{1}{\theta_1 - \theta_2}$

and $Q' = (\frac{k(t-1)}{1+(k/2)(t-1)^2} + \frac{CG_2(\theta_1-\theta_2)}{4(1+(k/2)(t-1)^2)} - \frac{v_1}{\theta_1-\theta_2})$

3.2 Physical Significance

A possible way to visualize the effect of the dynamics presented in equations (8) and (9) is to see how the velocities of the bacteria vary over short time intervals over which the coefficients P and Q can be assumed to remain

fairly constant. The velocity of bacteria 1 (v_1) has been plotted over five short time intervals in Figure 5 (P and Q are chosen arbitrarily in those intervals). Note that at the time of reproduction (t=1) the graph is highly steep indicating sharp decrease in velocity.

Now if we study the second term in the expression of Q from equation (8) i.e. the term $\frac{CG_1(\theta_2-\theta_1)}{4(1+(k/2)(t-1)^2)}$, as $G_1 \to 0$, $(\theta_2-\theta_1)$ is also small and C is not taken to be very large. At the denominator also we have got some divisors greater than 1. So the term becomes insignificantly small and all we can neglect it from Q. In equation (9) also we can similarly neglect the term $\frac{CG_2(\theta_1-\theta_2)}{4(1+(k/2)(t-1)^2)}$ from Q'. Again we assume, the velocity of both the particles to be negative for the time being. So we can replace, $v_1 = -|v_1|$ and $v_2 = -|v_2|$ in Q and Q' in equations (8) and (9). After doing all this simplifications for getting a better mathematical insight, equations (8) and (9) become,

$$\frac{dv_1}{dt} = -Pv_1^2 - Qv_1 \qquad (10)$$

where, $P = \frac{1}{\theta_2-\theta_1}$ and

$$Q = \left(\frac{k(t-1)}{1+(k/2)(t-1)^2} + \frac{|v_2|}{\theta_2-\theta_1}\right)$$

$$\frac{dv_2}{dt} = -P'v_2^2 - Q'v_2 \qquad (11)$$

where, $P' = \frac{1}{\theta_1-\theta_2}$ and

$$Q' = \left(\frac{k(t-1)}{1+(k/2)(t-1)^2} + \frac{|v_1|}{\theta_1-\theta_2}\right)$$

Now, for $\theta_2 > \theta_1$ P and Q are both positive. That means the first bacterium slows down very quickly. Whereas the second particle has P' and Q' (assuming the other term independent of $(\theta_1-\theta_2)$ in Q' is lesser than this) both negative. That means this bacterium accelerates. This acceleration is hopefully towards the first bacterium.

Since the rate of change of velocity of bacterium 1 and 2 are dependent on $(\theta_2-\theta_1)$ and $(\theta_1-\theta_2)$ respectively, it is evident that the distance between the two bacteria guides their dynamics. If we assume, $\theta_2 > \theta_1$ and they don't traverse too long, the first bacterium is healthier (less accumulated cost) than the second one, when the function is decreasing monotonically in a minimization problem and also the time rate change of first bacterium is less than that of the second (as depicted in Figure 6 clearly, where we take $f(x) = x^2$).

So at the time of reproduction, in a two bacteria system, the healthier bacterium when senses (since it is a grouped dynamics, so one must have the knowledge about the other one) that it is in a better position compared to its fellow bacterium, it hopes that the optima might be very near so it slows down and its search becomes more fine-tuned. This can be compared with the real bacterium involved in foraging. Whenever it senses that food might be nearby then it obviously slows down and searches that place thoroughly at cost of some time [10-12].

The second bacterium moves away from that place with a high acceleration quite naturally getting the information from the first bacterium that the fitter place is away from its present position. In biological system for grouped foraging when one member of the group share information from its neighbors it tries to move towards the best position found out by the neighboring members [11, 12].

Thus we see that reproduction was actually included in BFOA in order to facilitate grouped global search, which is explained from our small analysis. Another interesting thing that we observe is the acceleration, which is dependent on the distance between the two bacteria. When they come closer to each other, acceleration (that means the force with which the healthier bacteria attracts the weaker one) increases gradually. This reminds us about the *gravitational force*, which is also inversely proportional between the distance of two objects, and body with larger mass attracts the lesser one. So in our bacterial system the health of the bacteria can be equivalent to the mass and also we can find an analogy between the reproduction phenomenon and universal gravitational force.

IV. Conclusions and Future Research

This paper has presented a simple mathematical analysis of the reproduction step used in the BFOA. For a two bacterial system, it has formulated the effect of the reproduction on bacterial dynamics in the form of two coupled differential equations. Although it was not possible to have an explicit solution of the equations (as their coefficients vary with time in a complex manner), important conclusions regarding the search strategies of the bacterial population at the time of reproduction could be reached at from the analysis.

We would like to point out that this paper is a first step towards the mathematical analysis of BFOA, which appears as an attractive global optimization technique these days. Future research should focus on extending the analysis presented here, to a group of bacteria working on a multi-dimensional fitness landscape and also include effect of the chemotaxis and elimination-dispersal events in the same.

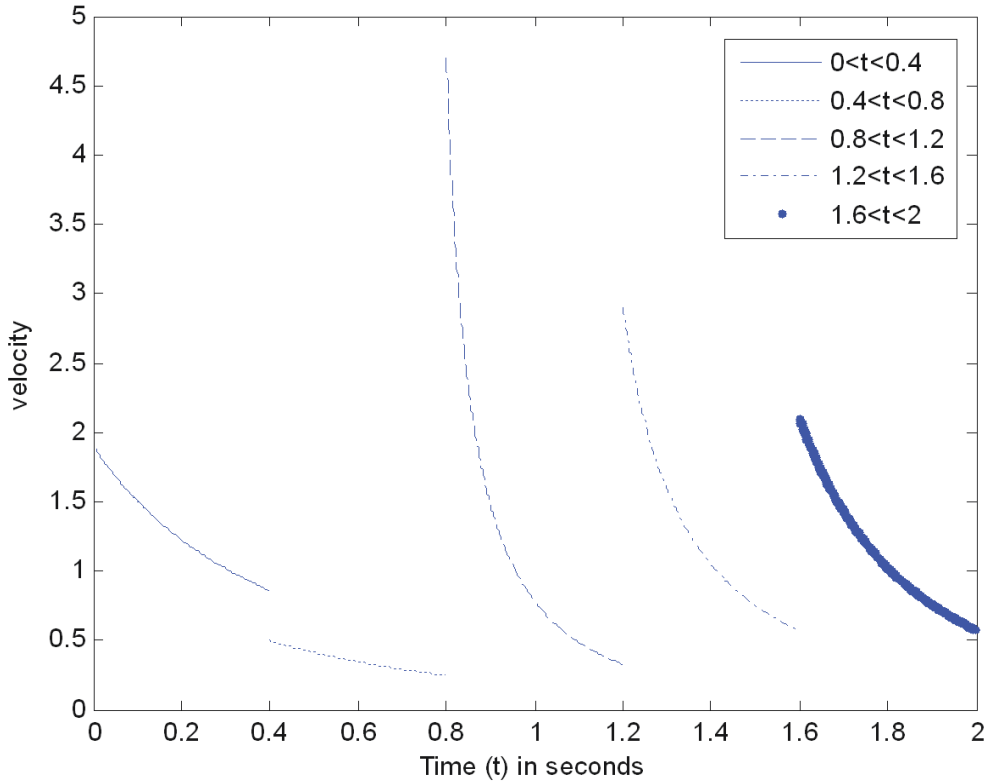

Fig 5: Piece-wise change in velocity over small time intervals

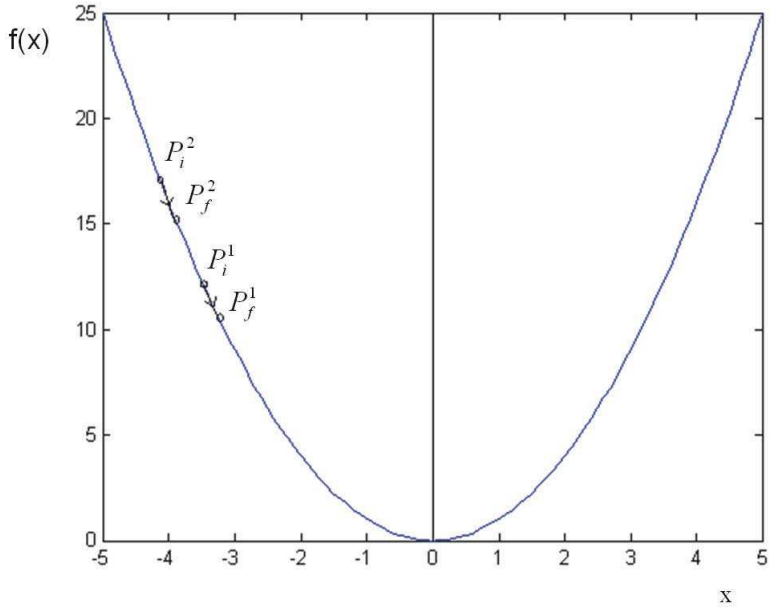

Fig 6: Initial and final positions of the two bacteria (after one chemotactic lifetime). P_i^k = Initial position of k[th] bacterium, P_f^k = Final position of k[th] bacterium after one chemotactic lifetime (k=1,2).

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