A Bacterial Foraging Optimized Finite Difference Time Domain Method

Vipul Sharma
E&C Engg Dept, Gurukul Kangri University,Haridwar, India

S.S. Pattnaik
NITTTR, Chandigarh

Tanuj Garg
E&C Engg Dept, Gurukul

ABSTRACT
Bacterial foraging optimization algorithm (BFOA) has attracted a lot of attention as a high performance optimizer because of its faster convergence and global search approach. Since its inception, BFOA has been applied successfully to wide variety various applications leading to faster convergence with higher accuracy. This paper presents one such application of the algorithm i.e. optimization of finite difference time domain method (FDTD). The hybrid algorithm has been applied for simulation of rectangular cavity resonator. The results show excellent performance.

General Terms
Optimized EM Simulation.

Keywords
Optimization tools, germ intelligence, FDTD, CAD.

1. INTRODUCTION
.Prof. K.M. Passino introduced an optimization technique known as Bacterial Foraging Optimization Algorithm (BFOA or simply BFO) based on the social foraging behaviour of Escherichia Coli (E. Coli) bacteria present in human intestine, in 2002 [1],. Since then, the BFO has been used by researchers in many successful applications such as optimal control engineering [1, 2], image processing [3], network scheduling [4], electrical load forecasting [5] etc have been reported till date. BFOA coupled with method of moment (MOM) has also been used in antenna applications [6-9]. Basic concept of BFO is discussed as follows.

The Bacterial Foraging is an evolutionary algorithm which estimates cost function after each iterative step of the program as the program execution proceeds and leads to progressively better fitness (less cost function). The foraging strategy of E. Coli. Bacteria is governed by four processes. These are chemotaxis, swarming, reproduction and elimination and dispersal. Chemotaxis is achieved by swimming and tumbling. When the bacterium meets favourable environment (rich in nutrients and noxious free), it continues swimming in the same direction. Decrease in cost function represents favourable environment, while increase in cost function represents unfavourable environment. When it meets unfavourable environment it tumbles (changes direction). In swarming, the bacteria move out from their respective places in ring of cells by bringing mean square error to the minimal value.

Chemotaxis and Swarming

Suppose m1,m2,m3 are the parameters to be optimized. They represent axis of space coordinates (like x,y,z axis in rectangular coordinate system). Now let fi,j,k,l(m1,m2,m3) represents position of ith bacterium at a point in m1,m2,m3 coordinate system, in jth Chemotaxis, kth reproduction and lth elimination and dispersal step. Also let C(i) represents unit run-length of a bacterium. Then movement of ith bacterium in jth chemotaxis step can be represented by equation (1) [].

$$f^{i,j+1,k,l}(m1,m2,m3) = f^{i,j,k,l}(m1,m2,m3) + C(i)\frac{del(i)}{\sqrt{del^T(i)\ del(i)}} \quad \ldots\ldots\ldots\ldots\ldots\ldots (1)$$

where del(i) is three elements direction vector (because position of bacteria being represented by three coordinates which are basically optimization parameters). Each element of del (i) is a random number lying between [-1, 1]. If ith bacterium meets favourable environment which is represented by less value of cost function at that point in space coordinates, it swims which means direction vector will remain same as was in previous (j-1th) chemotaxis step. Otherwise, del (i) is assigned with a new value which is a random number lying between [-1,1].

After each chemotaxis step, the bacteria move and reach new points in space (whose coordinate axis are optimization parameters). Each point represents a set of optimization parameters. Here, at these present locations, fitness of each bacterium is evaluated which further decides next movement of the bacterium. Fitness of ith bacterium is represented by Cost function Pi,j,k,l. Better fitness mean less value of Cost function.

Reproduction:

Health status (fitness) of each bacterium is calculated after each complete chemotaxis process. It is overall sum of cost function $\sum_{j=1}^{Nc} P^{i,j,k,l}$, where NC is total number of steps in a complete chemotaxis process. Locations of healthier bacteria represent better sets of optimization parameters. Then, to further speed up and refine the search, more number of bacteria is required to be placed at these locations in the optimization domain. This is done in reproduction step. Healthiest half of bacteria (with minimum value of cost function) are let to survive, while the weaker half die. Each surviving bacterium splits up into two and these two are placed at the same location. In this way population of bacteria remains constant.

Elimination and Dispersal Event

The chemotaxis process performs local search and reproduction speeds up convergence of search parameters. But, chemotaxis and reproduction may not be enough to reach the global minimum point (best optimized set of parameters).

The bacteria may also get trapped in local minima assuming it to be the best fitness position in the surrounding patch. To avoid this to happen, elimination and dispersal event is performed. The bacterium having probability Ped (probability of elimination and dispersion) is eliminated from present location and one bacterium is placed (dispersion) at a random location so as to realize global search. The population of bacteria still remains constant.

Followings are the step by step procedure of Bacterial Foraging Algorithm:

Initialize parameters

D = Dimension of search. It is number of parameters to be optimized. If three parameters are to be optimized, say m1,m2,m3, then D is equal to three.

B= Number of bacteria in the population. It is equal to number of sets of points obtained by discretizing the optimization parameter. Suppose m1,m2,m3 each parameter is discretized to give ten values in range [1, 2]. Then each set represents a point in space (m1,m2,m3-coordinates). Hence, there exist ten points (locations) in the optimization domain. So, ten bacteria are required to be placed at these points to start the search.

NC = Number of chemotaxis steps a bacterium has to move in a complete chemotaxis procedure before going for reproduction.

Ns = Number of swimming steps

Nre = Number of reproduction steps

Ned = Number of elimination and dispersal steps

Ped = Elimination and dispersal probability

C(i) = Unit run-length

fi,j,k,l (m1,m2,m3)= Position vector of ith bacterium, in jth chemotaxis step, in kth reproduction step and lth elimination and dispersal step at a point in m1,m2,m3-coordinates for the assumption given above.

Step 1: Elimination and dispersal loop l = l+1

Step 2: Reproduction loop l = l+1

Step 3: Chemotaxis loop j = j+1

For i= 1,2,3.....B, a chemotaxis step for ith bacterium will be as follows:

Calculate fitness function Pi,j,k,l.

Save this value in Plast= Pi,j,k,l so that we can find better fitness (cost) via run.

Tumble: Generate direction vector del (i) is assigned with a new value which is a random number lying between [-1,1].

Move using equation (1)

$$f^{i,j+1,k,l}(m1,m2,m3) = f^{i,j,k,l}(m1,m2,m3) + C(i)\frac{del(i)}{\sqrt{del^T(i)\ del(i)}}$$

Calculate fitness function Pi,j,k,l

Swim : (i) Initialize swim counter sc = 0.

(ii) If sc< Ns

If Pi,j,k,l < Plast , Let Plast= Pi,j,k,l, and use equation (1) given in step e) to move in the same direction.

Use the new generated location fi,j,k,l for new values of m1,m2,m3 to calculate Pi,j,k,l and continue in the loop.

Else sc=Ns

Do the same process for next bacterium i=i+1, go to step (b) if i≠S.

Step 4: If j< Nc, go to step 3 for next chemotaxis step as the chemotaxis process is not complete.

Step 5: Reproduction. With current values of k,l, compute overall fitness (cost function) $\sum_{j=1}^{Nc} P^{i,j,k,l}$ for each ith bacterium and sort the fitness in descending order. Higher value of cost function means less fitness.

Step 6: Half of the bacteria with less fitness die and the rest half reproduce. They split into two and placed at the same locations of their parents. So, population remains constant.

Step 7: If k< Nre, go to step 2. Increment the reproduction counter and start new chemotaxis process.

Step 8: Elimination-dispersion. Eliminate the bacterium with probability Ped and disperse one at a random location in the optimization space.

Step 9: If l< Ned, go to step1. Otherwise end.

2. Methodology and Results (The BFO-FDTD)

Finite Difference Time Domain (FDTD) is the most widely used algorithm for EM simulation. This is because of its inherent simplicity in realizing discrete form Maxwell's equations. But, in spite of that, FDTD suffers with a limitation that it takes too long to converge to a solution. First, generalized regression neural network (GRN) was used to reduce the convergence time. But the GRN itself is not complete solution. GRN is to be trained with sample values using spread constant. A value of spread constant is to be obtained by hit and trial to get the network trained very close to the sample values. The spread constant can be optimized using BFO and thus saving a lot of time and efforts. The resultant algorithm which hybrid of BFO and GRN FDTD can also be called as BFO GRN FDTD or simply BFO FDTD. The hybrid algorithm is quite usable for complex heterogeneous problem like detection of skin cancer in human being. Figure 1 presents the model used in this work. An air-filled rectangular cavity resonator is modeled having PEC(perfect electric conductor) boundary condition. The length, width, and height of the cavity are 10.0 cm (x-direction), 4.8 cm (y-direction), and 2.0 cm (z-direction), respectively. The model is gridded 50x24x10 in x, y and directions respectively. The cavity is excited at (26,13,5) location in grids, with differentiated Gaussian pulse given by J(t)=J0*(t-t0)*exp(-(t-t0)^2/tau^2), where tau=50 psec. Specifications of BFO parameters taken in the BFO FDTD model are as follows:

B=10; D =1; Ns=3; Nc=4; Nre=2 ; Ned=4 ; Ped=0.25; run-length unit = 0.5.

The results of simulation are shown in Figure 2 (a) and 2(b). Figure 7.2 (a)shows the values electric field in the volume and Figure 7.2 (b) compares the electric field values obtained from conventional FDTD and BFO optimized GRN FDTD. The program converges to null value of mean square error upto tenth decimal point. Optimized value of spread constant

obtained from BFO came out to be 0.3889.

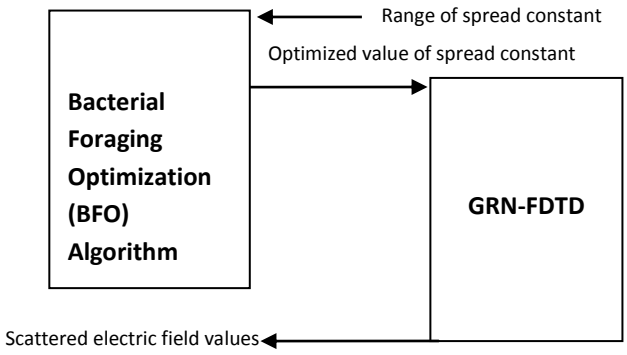

Figure 1 BFO GRN FDTD simulation model

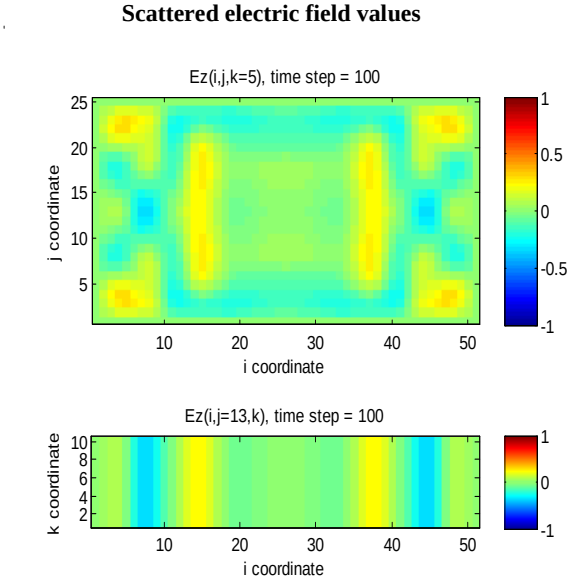

Figure 2 (a) Electric field obtained from BFO-FDTD

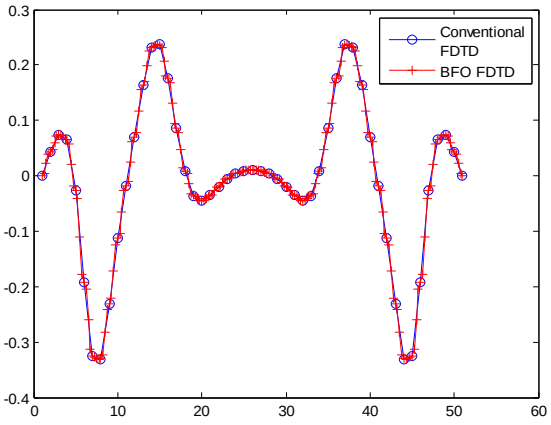

Figure 2 (b) Comparison of electric field values obtained from BFO FDTD and Conventional FDTD

3. CONCLUSION

Starting with basic review of BFOA, this paper presents its application to simulation of electromagnetic environment. First, finite difference time domain method FDTD is used to simulate electric field values at given number of points in space and then GRN is used to predict the values at all possible points. BFOA has been used to optimize spread of GRN. This hybrid version of FDTD (BFO-FDTD) leads to faster convergence with high accuracy.

4. REFERENCES

[1] Passino K.M., "Biomimicry of Bacterial Foraging", IEEE Control System Magzine, Vol. 22, 2002, pp. 52-67.

[2] W. Korani, " Bacterial Foraging Oriented By Particle Swarm Optimization Strategy for PID Tuning", GECOO 2008, 12-16 July, 2008, Atlanta, USA, pp. 1823-1826.

[3] K.M. Bakwad, S.S. Pattnaik, B.S. Sohi, S. Devi, B.K. Panigrahi, G.S. V.R. Sastri, "Bacterial Foraging Optimization Technique Cascaded with Adaptive Filter to Enhance Peak Signal to Noise Ratio from Single Image", IETE Journal of Research, Vol 55 (4), Jul-Aug 2009.

[4] W. Liu, H. Chen, H. Chen and M. Chen, "RFID Network Scheduling Using an Adaptive Bacteria Foraging Algorithm", Journal of Computer Information Systems (JCIS), Vol. 7(4), 2011, pp. 1238-1245.

[5] Y. Zhang, L. Wu and S. Wang, "Bacterial Foraging Optimization Based Neural Network for Short term Load Forecasting", JCIS, Vol. 6(7), 2010, pp. 2099-2105.

[6] B. B. Mangraj, I.S. Misra and A.K. Barisal, "Optimizing Included Angle of symmetrical V-Dipoles for Higher Directivity Using Bacteria Foraging Optimization Algorithm", PIER B, Vol. 3, 2008, pp. , 295-314

[7] G.S. V.R. Sastri, S.S. Pattnaik, O.P. Bajpai, S.Devi, C.V. Sagar, P.K. Patra and K.M. Bakwad, "Bacterial Foraging Optimization Technique to Calculate Resonant Frequency of Rectangular Microstrip Antenna", Int. J. RF Microwave Computer Aided Eng., Vol. 18, 2008, pp. , 383-388.

[8] G.S. V.R. Sastri, S.S. Pattnaik, O.P. Bajpai, S.Devi, K.M. Bakwad, "Velocity Modulated Bacterial Foraging Optimization Technique (VMBFO)", Applied Soft Computing Journal, Vol. 11 (1), January 2011, pp. 154-165.

[9] G.S. V.R. Sastri, S.S. Pattnaik, O.P. Bajpai, S.Devi, K.M. Bakwad and P.K. Patra "Intelligent Bacterial Foraging Optimization Technique to Calculate Resonant Frequency of RMA", IJMOT, Vol 4(2), March 2009, pp.67-75.

[10] A. Biswas, S. Dasgupta, S. Das and A. Abraham, " Synergy of PSO and BFO-A Comparative Study on Numerical Benchmarks", International Symposium on Hybrid Artificial Intelligent Systems (HAIS), November, 2007, Salamanca, Spain, pp. 255-263.

[11] Hanning Chen, Yunlong Zu, and Kunyuan Hu, "Adaptive Bacterial Foraging Optimization", Abstracts and Applied Analysis, Vol. 2011, 2011, pp. 1-27.

[12] K.R.Mahmoud, "Design Optimization of A Bow-Tie Antenna For 2.45 GHz RFID Readers Using A Hybrid BSO-NM Algorithm", PIER 100, 2010, pp. 105-117

[13] T Datta, I.S. Misra, B. B. Mangraj, S. Imtiaj, "Improved Adaptive Bacteria Foraging Algorithm in Optimization of Antenna Array for Faster Convergence", PIER C, Vol. 1, 2008, pp. 143-157.

[14] M. O'Halloran, R. Coceicao, D. Byrne, M. Glavin and E. Jones, "FDTD Modeling Of The Breast: A Review", PIER B, Vol. 18, 2009, 1-24.

[15] S.C. Hagness, A. Taflove and J. E. Bridges, "Two Dimensional FDTD Analysis of a Pulsed Microwave Confocal System for Breast Cancer Detection: Fixed Focus and Antenna Array Sensors", IEEE Trans. Biomed. Eng. Vol.45, 1998, pp. 1470-1479.

[16] E.C. Fear, X. Li, S.C. Hagness and M.A. Stuchly, "Confocal Microwave Imaging for Breast Cancer Detection : Localization of Tumors in three dimensions", IEEE Trans. Biomed. Eng. Vol.47, 2002, pp. 812-822.

[17] E.C. Fear, S.C. Hagness, P.M. Meaney and M.A. Stuchly, "Breast Cancer Detection with Near-Field Imaging", IEEE Microwave Magazine, March 2002, pp. 48-56.

[18] X. Li and S.C. Hagness, "A Confocal Microwave Imaging Algorithm for Breast Cancer Detection", IEEE Microwave and Wireless Components Letters, Vol. 11, 2001, 130-132.

[19] Pratik Mehta, Kundan Chand, D. Narayanswamy, D. G. Beetner, R. Zoughi and W.V. Stoecker, "Microwave Reflectrometry as a Novel Diagnostic Tool for Detection of Skin Cancers", IEEE Trans. Inst. Meas., Vol.55(4), August 2006, pp.1309-1316.

[20] D.M. Hagl, D. Popovic, S.C. Hagness, J.H. Booske and Michal Okoniewski, "Sensing Volume of Open-Ended Coaxial Probes for Dielectric Characterization of Breast Tissue at Microwave Frequencies", IEEE Trans. Microwave Theory Tech., Vol. 51(4), 2003, pp. 1194-1206.

[21] Ding, W. and Marchionini, G. 1997 A Study on Video Browsing Strategies. Technical Report. University of Maryland at College Park.

[22] Fröhlich, B. and Plate, J. 2000. The cubic mouse: a new device for three-dimensional input. In Proceedings of the SIGCHI Conference on Human Factors in Computing Systems

[23] Tavel, P. 2007 Modeling and Simulation Design. AK Peters Ltd.

[24] Sannella, M. J. 1994 Constraint Satisfaction and Debugging for Interactive User Interfaces. Doctoral Thesis. UMI Order Number: UMI Order No. GAX95-09398., University of Washington.

[25] Forman, G. 2003. An extensive empirical study of feature selection metrics for text classification. J. Mach. Learn. Res. 3 (Mar. 2003), 1289-1305.

[26] Brown, L. D., Hua, H., and Gao, C. 2003. A widget framework for augmented interaction in SCAPE.

[27] Y.T. Yu, M.F. Lau, "A comparison of MC/DC, MUMCUT and several other coverage criteria for logical decisions", Journal of Systems and Software, 2005, in press.

[28] Spector, A. Z. 1989. Achieving application requirements. In Distributed Systems, S. Mullender