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Distribution Network Reconfiguration for Power Loss Minimization Using Bacterial Foraging Optimization Algorithm

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Abstract

This paper presents a distribution network reconfiguration based on bacterial foraging optimization algorithm (BFOA) along with backward-forward sweep (BFS) load flow method and geographical information system (GIS). Distribution network reconfiguration (DNR) is a complex, non-linear, combinatorial, and non-differentiable constrained optimization process aimed at finding the radial structure that minimized network power loss while satisfying all operating constraints. BFOA is used to obtain the optimal switching configuration which results in a minimum loss, BFS is used to optimize the deviation in node voltages, and GIS is used for planning and easy analysis purposes. Simulation is performed on the 33-bus system and results are compared with the other approaches. The obtained results show that the proposed approach is better in terms of efficiency and having good convergence criteria.

Index Terms: Feeder reconfiguration, Bacterial foraging optimization, Backward-Forward sweep, Power loss reduction, Radial network, Distribution system, Geographical information system

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1. Introduction

Electric distribution systems are designed radially for effective coordination between feeder's protection systems and to lower the short circuit currents. The distribution feeders have two types of switches: normally closed (sectionalizing) switches and normally opened (tie) switches ([1]; [2]; [3]; [4]; [5]; [6]; [7]). The major concern for distribution utilities is to reduce the power losses in distribution network [8]. Distribution network reconfiguration (DNR) is the most economical method to reduce the power losses in distribution network [9].

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DNR is a process of altering the topological structure of feeders by changing the switching states of normally closed (sectionalizing) switches and normally opened (tie) switches ([10]; [11]). These switching operations must be performed in such a way that resulting network is radial and meets all constraints. With the advancement in computer and automation industry like Geographical Information System (GIS), DNR is being used as a planning and real-time control tool. Regular modification in radial structure of the distribution network is performed, to transfer the loads from one feeder of distribution network to another feeder, in order to improve the operation conditions of overall network and reduce the line losses. Since the daily load variations on each feeder in a distribution network is unpredictable due to mixture of residential, industrial and commercial types of loads.

Loss and reliability are two significant points among several factors in distribution network [12]. Hence feeder reconfiguration helps to transfer the loads from heavily loaded feeders to lightly loaded feeders [10]. These alterations not only reduces the real power losses of the network but also balances the loads among feeders and significantly improves the voltage profiles.

In recent years extensive research has been conducted for power loss minimization in the field of distribution network reconfiguration. Merlin and Back [13] first proposed the distribution network reconfiguration for loss reduction. The method begins with all branches closed to form a meshed network and then procedure of opening the switches is followed to maintain radiality of the network. Shirmohammadi and Hong [14] proposed a heuristic method based on Merlin and Back [13]. The method also starts with all branches closed to form a meshed network and opening of the switch is performed after optimal power flow pattern. The switch having lowest current value for the optimal power flow pattern will be consider first and so on. Many evolutionary and biologically inspired algorithm are presented with time to reduce the losses. Nara et. al [15] proposed Genetic Algorithm (GA) to reduce the network losses using string as a set of switch status, fitness function and penalty factor to limit the voltage and current. Later the approach used by Nara et. al [15] was modified by Zhu et. al [16] by using refined genetic algorithm (RGA). RGA is achieved with some improvements in chromosome coding, fitness function and mutation pattern. Simulated Annealing (SA) method was also proposed by many authors ([17]; [18]) to mitigate the power losses in distribution network reconfiguration. Das et. al [19] uses the concept of heuristic rule and fuzzy multi-objective approach to optimize the network. Although some of these methods are suitable for smaller systems, some have bad convergence property and some are very time consuming due to the use of rigorous mathematics.

In 2012 Kumar and Jayabarathi [20] proposed a method of loss minimization for distribution system reconfiguration using bacterial foraging optimization algorithm (BFOA). The major drawbacks of this methodology are:

- Criteria for selecting switches is not provided
- Newton-Raphson Method is used for load flow analysis (while conventional Gauss-Seidel and Newton-Raphson methods of load flow gives unreliable solutions in distribution network due to radial structure of the network, and has high R/X ratio ([8]; [14]; [16]; [21])
- With the opening of 13th and 14th switches, the load at bus 14 goes out of service, which violates the constraint of distribution network reconfiguration, that no load can be out of service

In this paper BFOA is proposed along with backward-forward sweep (BFS) load flow method and GIS for the minimization of power loss using DNR. The results obtained are very encouraging when proposed algorithm is tested on 33 bus system and BFOA is proven to be an efficient method for distribution network.

The structure of the paper is organized as follows: Section 2 presents the problem formulation. Section 3 provides the necessary details about the backward-forward sweep load flow method. Description of bacterial foraging optimization algorithm is given in Section 4. While Section 5 deals with the implementation of the bacterial foraging optimization. Section 6 presents results of 33-bus system and provides the necessary discussion. The conclusion is outlined in Section 7.

2. Problem Formulation

The problem of distributed network reconfiguration is to find best configuration of radial network having minimum power losses, and meet all operating constraints, which are voltage profile of the network, current capacity of the feeder and radial structure of the distribution network. Since many switching combinations are possible in a distribution network, finding the best configuration is a complex, non-linear, combinatorial, and non-differentiable constrained optimization problem. The objective function for power loss minimization is:

$$Minimize \ f(x) = Min \ (P_{T,Loss}) \tag{1}$$

$$x = [S_{01} S_{02} S_{03} S_{04} S_{05}]$$
⁽²⁾

$$P_{T,Loss} = \sum_{k=1}^{Nbr} P_{Loss}(k, k+1)$$
(3)

where
$$P_{Loss}(k, k+1) = R_k \times \frac{(P_k^2 + Q'_k^2)}{|V_k|^2}$$
 (4)

Subjected to
$$V_{min} \le |V_k| \le V_{max}$$
 (5)

and

$$|I_k| \le |I_{k,max}| \tag{6}$$

Constraints are:

- No feeder section can be out of service
- Network must be radial
 - det(M) = 1 or -1 for radial network
 - \circ det(*M*) = 0 for non-radial network

Where,

 $P_{T,Loss}$: Total real power loss of the system x: Control variable representing open switches vector R_k : Resistance of kth branch P_k : Real power flowing out of bus k Q_k : Reactive power flowing out of bus k $|I_k|$: Current magnitude at kth branch Nbr: Total number of branches with respect to x S_{on} : n = 1, 2, 3, 4, 5 representing the open switches f(x): Total real power loss of the network with respect to x $|V_k|$: Voltage magnitude at kth bus V_{min} : Bus minimum voltage limit ($V_{max} = 0.9$ p.u) V_{max} : Bus maximum voltage limit ($V_{max} = 1.05$ p.u) $|I_{k,max}|$: Maximum current magnitude at kth branch M: Bus incidence matrix The differences in power losses, and voltage drops can be measured from the simulation of the network using power flow before and after the network reconfiguration. Conventional Gauss-Seidel and Newton-Raphson methods of load flow gives unreliable solutions in distribution network due to radial structure of the network, and have high R/X ratio ([8]; [14]; [16]; [21]). Therefore a BFS load flow method is used in this paper. The BF sweep load flow is explained by Ehsan and Javad [22]. A brief description of BF sweep [8] is described in section 3.

3. Backward-Forward Sweep Load Flow Method

In order to evaluate the objective function of the problem a BFS load flow method is used. The first step of BFS uses graph theory to convert the topological structure of the distribution network into meaningful matrices [Ehsan and Javad]. Later steps are as follows:

- The vector V_k containing the nodes voltages is defined. At first all elements of vector is assigned a value 1 pu or 1.05 pu with zero angle. Where $k \in [1, Nbr]$ with respect to the control variable x.
- The current at each nodes I_k is calculated by the following equation:

$$I_L(i) = \left[\frac{P_L(i)}{V(i)}\right]^* \tag{7}$$

where $I_L(i)$, $P_L(i)$ and V(i) are current, apparent power and voltage of the load at node *i*.

- The current of the last branch is the current of the last node. So starting from the last node to the first one by using Kirchhoff's current law (KCL) (backward sweep), the current of the network branches $J_{1 \times Nbr}$ are calculated.
- Voltage drop of the network is calculated by the following equation $V_d = ZJ$. Where Z is the impedance, $d \in [1, Nbr]$ and V_d is voltage drop of each branch.
- Since the voltage of reference node is taken as 1 or 1.05 pu. The voltage of next node is calculated by subtracting the corresponding voltage drop from the voltage of previous node (forward sweep) and V_k will be updated.
- The procedure from step 2 is repeated until convergence criteria are satisfied. The convergence criteria is

$$\Delta V_k = V_k(itr) - V_k(itr - 1) < \varepsilon \tag{8}$$

where *itr* is number of iteration and ε is the threshold.

4. Bacterial-Foraging Optimization Algorithm

Inspiration from the natural creatures and nature has been taken from many years to solve the complex real world problems, and the algorithm which are inspired from the natural biological behaviour are called Biological Inspired Algorithms (BIA). The BIA inspired from the foraging behaviour of bacteria (*E.coli*) is called Bacterial Foraging Optimization Algorithm (BFOA), proposed by Passino ([23]; [24]). Since its inception BFOA has been widely accepted as global optimization algorithm for real world problems such as transmission loss reduction [25], learning of artificial neural networks [26], active power filters [27], optimal controller design ([23]), and harmonic estimation [28]. Foraging is a process of moving the bacteria towards more nutrients region through neutral medium, and avoiding the poisonous substances. The main steps of BFOA are as follows ([29]):

Step 4.1) Initialize the problem and algorithm parametersStep 4.2) ChemotaxisStep 4.3) ReproductionStep 4.4) Elimination-dispersion

These steps are described in the following sections:

4.1. Initialize the problem and algorithm parameters

Initialize the positions of 'N' (say) number of bacteria. Let it be $X^1, X^2, X^3, \ldots, X^N$ corresponding to 'N' bacterium $b^1, b^2, b^3, \ldots, b^N$. The position vector $X^1, X^2, X^3, \ldots, X^N$ is the initial population for the optimization problem, specified as follows:

Minimize f(s)

(9)

Subject to $s_k \in Y_k$, $k=1, 2, 3, \ldots M$

Where f(s) is the objective function, s is the control variable which is set of all decision variable s_k and M is number of decision variables, Y_k is the set of all possible range of values corresponding to the decision variable s_k . The initial position of the bacteria is initialized randomly with the array of open switches as X

$X = \begin{bmatrix} & \cdot & - & - & \cdot & \cdot & \cdot & \cdot & \cdot \\ & \cdot & - & - & \cdot & - & \cdot & \cdot & \cdot \\ & \cdot & \cdot & - & \cdot & - & \cdot & \cdot & \cdot & \cdot \end{bmatrix}$		$\begin{bmatrix} X^1 \\ X^2 \\ X^3 \end{bmatrix}$	а а	$\begin{bmatrix} x_1^1 \\ x_2^1 \\ x_3^1 \end{bmatrix}$	$x_1^2 \\ x_2^2 \\ x_3^2$	$x_1^3 \\ x_2^3 \\ x_3^3$		x_1^{M-} x_2^{M-} x_3^{M-}	$\begin{array}{cccc} ^{1} x_{1}^{M} & ^{-1} \\ ^{1} x_{2}^{M} \\ ^{1} x_{3}^{M} \end{array}$
	<i>X</i> =	•	=	.	•	•	•	•	•
		•			:	:	:	:	:

The other parameters required for BFOA is also specified in this step. These are Number of bacteria (N), Chemotactic step size(c), Swimming length (Ns), Elimination/dispersal probability (P_{ed}), Attractant factor (A), and Repellent Factor (R).

4.2. Chemotaxis

It is the tendency of the bacteria to move towards the sources of Nutrients. It consists of two stages which are as following:

(a) Tumbling:

It is the tendency of the bacteria to change their positions in search of Nutrients. Let X_{new}^i be the next position of the ith bacteria whose current position is X^i . They are related as described below.

$$X_{new}^i = X^i + c\phi \tag{11}$$

Where

$$\varphi = \frac{\Delta}{\sqrt{\Delta^T \Delta}} \Delta \in \mathbf{R}^m$$

such that each element of the vector Δ is in the range [-1 1]. φ is the unit walk in random direction. 'c' is called as chemotactic step size. The new positions are computed for i = 1, 2, ... N.

(b) Swimming:

Bacterium will tend to keep on moving in the particular direction if it is in the direction that is rich in nutrients.

Mathematically if $f(X_{new}^i) < f(X^i)$, then another swimming in the same direction (φ) is taken by the ith bacteria and it can be continued up to N_s steps. After the completion of N_s steps bacteria goes to the step 4.3. If $f(X_{new}^i) \ge f(X^i)$, bacteria comes out of the tumbling stage and goes to the step 4.3.

 $f(X^i) < 0$ can be treated as the presence of nutrients, $f(X^i) = 0$ can be treated as neutral while $f(X^i) > 0$ can be treated as presence of toxic substances. In nature there is the social communication between bacterium such that they are neither close together nor far away from each other. This is done by releasing the chemical by the bacteria. The chemical signal can be either attractant or Repellent. If the chemical signal released by the particular bacteria is attractant in nature, then it attracts other bacteria to come to its position. On the contrary if the chemical signal released by the particular bacteria is repellent in nature, it doesn't allow other bacteria to come to its position.

The social communication between bacterium can be simulated using the modified objective function to be computed for the ith position corresponding to the ith position bacteria as given below.

$$fmod(X^{i}) = f(X^{i}) + fsocial(X^{i})$$
⁽¹²⁾

where *fmod* is the modified objective function computed for the ith position X^i corresponding to the ith bacteria. $f(X^i)$ is the actual objective function value computed for the ith position X^i corresponding to the ith bacteria. *fsocial*(X^i) is the attractant cum repellent signal computed for the ith position X^i corresponding to the ith bacteria as displayed below.

Let
$$d_{ij} = \left\| X^i - X^j \right\|^2$$
(13)

$$fsocial(X^{i}) = m\left(\sum_{j=1}^{N} e^{-Rd_{ij}} - \sum_{j=1}^{N} e^{-Ad_{ij}}\right)$$
(14)

Note that if the first term $\sum_{j=1}^{N} e^{-Rd_{ij}}$ is reduced if distance between the ith position and others are made large and hence it acts as the repellent signal. Similarly the second term $-\sum_{j=1}^{N} e^{-Ad_{ij}}$ is reduced if the distance between the ith position and others are made small and hence it acts as the attractant signal. 'R' is the repellent factor and 'A' is the attractant factor.

4.3. Reproduction

After step 4.2, best 'N/2' (50%) bacteria measured in terms of its health are survived. The survived bacterium are subjected to reproduction to obtain 'N' bacterium as described below.

Health of the bacteria is measured in terms of f(X). If the functional value f(X) is less, then the corresponding bacteria is healthier. Compute $f(X^i)$ for i=1,2,3,... N and arrange them in ascending order. First 'N/2' bacterium and the corresponding positions are selected. Let the positions be $[P^1, P^2, P^3, ..., P^{N/2}]$. Every bacteria is split

into two bacterium and are placed in the same positions. Thus new set of positions corresponding to 'N' bacterium are given as $[P^l, P^l, P^2, P^2, P^3, P^3, \dots, P^{N2}, P^{N2}] = [Q^l, Q^2, Q^3, \dots, Q^N]$ (say). Go to step 4.2. Repeat 4.2 and 4.3 for finite number of iterations. Then Go to step 4.4.

4.4. Elimination-dispersion

In real world process, some of the bacterium (i.e.) with probability 'Pd' are dispersed to new locations. This is achieved as follows.

Generate the random vector of size 1xN. Sort the elements of the vector in an ascending order. Find the index corresponding to the first NxPd sorted numbers. Choose the positions of the bacterium corresponding to the obtained index. They are replaced as per the randomly generated positions on the optimization domain. The positions thus obtained are treated as the current best positions. Go to step 4.2. Repeat the steps 4.2–4.4 for the finite number of iterations. The best value in each iteration can also be tracked and the best among them can be declared as the optimal solution.

5. Implementation of Bacterial-Foraging Optimization Algorithm in distribution network reconfiguration

Objective function value must be minimum in order to achieve the best switching combination. The efficiency and reliability of distribution network can only be achieve by limiting the switching operations, because increasing the number of switching operations increases load flow studies, and thus becomes extremely inefficient not only from computational point of view, but it also becomes impractical as a real-time feeder reconfiguration strategy [16]. Conventional optimization methods becomes inefficient and impractical due to large search space. In order to limit the search space, all possible radial structure of the network (which meets all operating constraints) are generated and subsequently objective function are evaluated [30]. GIS is used in this paper for easy analysis, planning, and for obtaining all possible radial structures of the distribution network. Fig 1 and Fig 2 shows the 33-bus radial distribution network before and after the reconfiguration. One switch from every loop (Loop 1 to Loop 5) as shown in Fig 1 and Fig 2 must be open to maintain the radiality of the network. The open switches vectors from Fig 1 and Fig 2 are as follows:

$$X^1 = [33 \ 34 \ 35 \ 36 \ 37]$$
 and $X^2 = [7 \ 9 \ 14 \ 32 \ 37]$



Fig.1. A 33-bus Radial Distribution Network Before Reconfiguration

Distribution Network Reconfiguration for Power Loss Minimization Using Bacterial Foraging Optimization Algorithm



Fig.2. A 33-bus Radial Distribution Network After Reconfiguration

Similarly other possible radial network are generated without violating the operating constraints using GIS. GIS based distribution network is shown in the Fig 3.



Fig.3. GIS Based Distribution Network

The initial positions of the bacteria is populated randomly with open switches vectors for N (20) number of bacteria as shown below:

[X ¹]		7	9	14	24	30	L
X^2		7	13	30	35	37	
X^3		10	14	17	20	27	
X^4		6	13	16	35	37	
X^5		4	10	17	21	24	
X^6		7	9	14	32	33	
X^7		8	12	29	33	37	
X ⁸		2	8	10	25	36	l
X ⁹		7	11	26	34	36	
X^{10}		11	14	16	19	26	
X^{11}	=	7	9	21	25	36	
X^{12}		8	14	28	32	33	
X^{13}		33	34	35	36	37	
X^{14}		9	13	21	24	30	
X^{15}		3	10	13	26	34	
X^{16}		9	12	16	19	24	
X^{17}		5	10	17	23	27	
X^{18}		11	14	18	28	36	
X^{19}		16	19	21	26	34	
X^{20}		L 7	10	14	28	32	
	X^{1} X^{2} X^{3} X^{4} X^{5} X^{6} X^{7} X^{8} X^{9} X^{10} X^{11} X^{12} X^{13} X^{14} X^{15} X^{16} X^{17} X^{18} X^{19} X^{20}	$\begin{bmatrix} X^{1} \\ X^{2} \\ X^{3} \\ X^{4} \\ X^{5} \\ X^{6} \\ X^{7} \\ X^{8} \\ X^{9} \\ X^{10} \\ X^{11} \\ X^{12} \\ X^{13} \\ X^{14} \\ X^{15} \\ X^{16} \\ X^{17} \\ X^{18} \\ X^{19} \\ X^{20} \end{bmatrix}$	$\begin{bmatrix} X^{1} \\ X^{2} \\ X^{3} \\ X^{4} \\ X^{5} \\ X^{6} \\ X^{7} \\ X^{8} \\ X^{9} \\ X^{10} \\ X^{11} \\ X^{12} \\ X^{13} \\ X^{14} \\ X^{15} \\ X^{16} \\ X^{17} \\ X^{18} \\ X^{19} \\ X^{20} \end{bmatrix} = \begin{bmatrix} 7 \\ 7 \\ 10 \\ 6 \\ 4 \\ 7 \\ 8 \\ 33 \\ 9 \\ 5 \\ 11 \\ 16 \\ 7 \end{bmatrix}$	$\begin{bmatrix} X^{1} \\ X^{2} \\ X^{3} \\ X^{4} \\ X^{4} \\ X^{5} \\ X^{5} \\ X^{6} \\ X^{7} \\ X^{7} \\ X^{8} \\ X^{9} \\ X^{10} \\ X^{11} \\ X^{11} \\ X^{12} \\ X^{13} \\ X^{14} \\ X^{15} \\ X^{15} \\ X^{16} \\ X^{16} \\ X^{16} \\ X^{17} \\ X^{18} \\ X^{19} \\ X^{20} \end{bmatrix} = \begin{bmatrix} 7 & 9 \\ 7 & 13 \\ 10 & 14 \\ 7 & 9 \\ 8 & 14 \\ 7 & 9 \\ 8 & 14 \\ 33 & 34 \\ 9 & 13 \\ 3 & 10 \\ 9 & 12 \\ 5 & 10 \\ 11 & 14 \\ 16 & 19 \\ 7 & 10 \end{bmatrix}$	$\begin{bmatrix} X^1 \\ X^2 \\ X^3 \\ X^4 \\ X^5 \\ X^6 \\ X^7 \\ X^6 \\ X^7 \\ X^8 \\ X^7 \\ X^8 \\ X^7 \\ X^8 \\ X^1 \\ X^1 \\ X^1 \\ X^{12} \\ X^{12} \\ X^{13} \\ X^{14} \\ X^{15} \\ X^{16} \\ X^{16} \\ X^{17} \\ X^{18} \\ X^{19} \\ X^{20} \end{bmatrix} = \begin{bmatrix} 7 & 9 & 14 \\ 7 & 13 & 30 \\ 4 & 10 & 17 \\ 7 & 9 & 14 \\ 8 & 12 & 29 \\ 2 & 8 & 10 \\ 7 & 11 & 26 \\ 11 & 14 & 16 \\ 7 & 9 & 21 \\ 8 & 14 & 28 \\ 33 & 34 & 35 \\ 9 & 13 & 21 \\ 3 & 10 & 13 \\ 9 & 12 & 16 \\ 5 & 10 & 17 \\ 11 & 14 & 18 \\ 16 & 19 & 21 \\ 7 & 10 & 14 \end{bmatrix}$	$\begin{bmatrix} X^1 \\ X^2 \\ X^3 \\ X^4 \\ X^5 \\ X^5 \\ X^6 \\ X^6 \\ X^7 \\ X^7 \\ X^8 \\ X^7 \\ X^8 \\ X^1 \\ X^1 \\ X^{10} \\ X^{11} \\ X^{11} \\ X^{12} \\ X^{13} \\ X^{13} \\ X^{14} \\ X^{15} \\ X^{16} \\$	$ \begin{bmatrix} X^1 \\ X^2 \\ X^3 \\ X^4 \\ X^5 \\ X^6 \\ X^6 \\ X^7 \\ X^8 \\ X^1 \\ X^1 \\ X^{11} \\ X^{12} \\ X^{13} \\ X^{13} \\ X^{14} \\ X^{15} \\ X^{16} \\ X^{16} \\ X^{17} \\ X^{16} \\ X^{16} \\ X^{17} \\ X^{18} \\ X^{16} \\ X^{19} \\ X^{20} \end{bmatrix} = \begin{bmatrix} 7 & 9 & 14 & 24 & 30 \\ 14 & 17 & 20 & 27 \\ 7 & 9 & 14 & 32 & 33 \\ 8 & 12 & 29 & 33 & 37 \\ 2 & 8 & 10 & 25 & 36 \\ 7 & 11 & 26 & 34 & 36 \\ 11 & 14 & 16 & 19 & 26 \\ 7 & 9 & 21 & 25 & 36 \\ 8 & 14 & 28 & 32 & 33 \\ 33 & 34 & 35 & 36 & 37 \\ 9 & 13 & 21 & 24 & 30 \\ 3 & 10 & 13 & 26 & 34 \\ 9 & 12 & 16 & 19 & 24 \\ 5 & 10 & 17 & 23 & 27 \\ 11 & 14 & 18 & 28 & 36 \\ 16 & 19 & 21 & 26 & 34 \\ 7 & 10 & 14 & 28 & 32 \end{bmatrix} $

(15)

The updated positions of the bacteria will be obtained from the chemotaxis step given in 4.2 for the chemotactic step size c (1). If objective function value at updated position for *i*th bacteria is less than the objective function value at previous position for the same bacteria, then bacteria will keep on updating their position with same value of φ up to Ns (5) steps. After this step the bacteria is arranged with the sorted objective function values in ascending order. First half (N/2 or 50%) of the bacteria will survive and these bacterium reproduce to obtain N (100%) bacterium as discussed in section 4.3. While in the last step, N*Pd number of bacteria will be dispersed and these blanked spaces will be filled with the randomly generated open switches vectors, where Pd (0.75) is the probability of dispersion. This procedure is repeated until the termination criteria is satisfied. Both the attractant and repellent factor is taken as 2 in this simulation.

6. Results and Discussion

The proposed optimization method is tested on 33-bus radial distribution network. Simulation has been performed in MATLAB and ArcGIS. The distribution network consists of 33-buses, five normally open tie switches and 32 normally closed sectionalizing switches. The normally open tie switches are 33-37, and the normally closed sectionalizing switches are 1-32. The line and load data is given in Table 2. The network base is V = 12.66 kV, S = 10 MVA and total real and reactive power loads on the system are 3715 kW and 2300 kVAr. The minimum bus voltage is 0.9134 p.u at bus 18 and have initial power loss of the system is 202.7kW. Distribution network before reconfiguration is shown in Fig 1.

After reconfiguration the open switches vector obtained by the proposed algorithm is 7, 9, 14, 32, and 37. The minimum bus voltage is 0.9406 p.u at bus 32 and have real power loss of the configured network is 135.67 kW. After reconfiguration overall 33.07% reduction in power loss and 2.89% improvement in minimum voltage are achieved as compared to the original configuration. Distribution network after reconfiguration is shown in Fig 2.The voltage and angle at each bus before and after reconfiguration is shown in Table 1.

Fig 4 shows the voltages angles while Fig 5 shows the voltages profiles at different buses before and after reconfiguration in 33-bus radial distribution network. In Fig 6 power loss before and after reconfiguration is

shown. Even after the transfer of loads from one branch to another the power losses reduced at every branch after the reconfiguration. These improvement in power losses reduction after reconfiguration is clear indication of load balancing.

The proposed method is compared with the method proposed by Shirmohammadi and Hong [13], Zhu et. al [15] and Rao et. al [28]. The comparison table is shown in Table 3 and the convergence graph is shown in Fig 7.



Fig.4. Voltages Angles at Different Buses Before and After Reconfiguration in 33-bus Radial Distribution Network



Fig.5. Voltage Profile of the 33-Radial Distribution Network Before and After Reconfiguration



Fig.6. Power Losses at Every Branch in 33-Bus Radial Distribution Network Before and After Reconfiguration



Fig.7. Convergence Characteristics of BFOA for 33-Bus Radial Distribution Network

Table 1. Voltage Profile and Voltages Angles Before and After Reconfiguration in 33-bus Radial Distribution Network

Table 2. Network Data for 33 bus System

1 1 2 0.0922 0.0470 100.0	60.0 40.0
1 1 2 0.0922 0.0470 100.0	60.0 40.0
	40.0
2 2 3 0.4930 0.2511 90.0	
3 3 4 0.3660 0.1864 120.0	80.0
4 4 5 0.3811 0.1941 160.0	30.0
5 5 6 0.8190 0.7070 60.0	20.0
6 6 7 0.1872 0.6188 200.0	100.0
7 7 8 0.7114 0.2351 200.0	100.0
8 8 9 1.0300 0.7200 60.0	20.0
9 9 10 1.0440 0.7400 60.0	20.0
10 10 11 0.1966 0.0650 45.0	30.0
11 11 12 0.3744 0.1238 60.0	35.0
12 12 13 1.4680 1.1550 60.0	35.0
13 13 14 0.5416 0.7129 120.0	80.0
14 14 15 0.5910 0.5260 60.0	10.0
15 15 16 0.7463 0.5450 60.0	20.0
16 16 17 1.2890 1.7210 60.0	20.0
17 17 18 0.7320 0.5740 90.0	40.0
18 18 19 0.1640 0.1565 90.0	40.0
19 19 20 1.5042 1.3554 90.0	40.0
20 20 21 04095 0.4784 90.0	40.0
21 21 22 0.7089 0.9373 90.0	40.0
22 3 23 04512 03083 900	50.0
23 23 24 0.8980 0.7091 420.0	200.0
24 24 25 0.8960 0.7011 420.0	200.0
25 6 26 02030 01034 600	25.0
26 26 27 02842 01447 600	25.0
27 27 28 10590 0.9337 60.0	20.0
28 28 29 0.8042 0.7006 120.0	70.0
29 29 30 0.5975 0.2585 200.0	600.0
30 31 0974 09630 1500	70.0
31 31 32 03/05 0.3619 2100	100.0
32 32 0.5105 0.5077 210.0	40.0
33 21 8 2 0000 2 0000	-0.0
34 9 15 2,000 2,000	
35 12 22 2 0000 2 0000	
26 18 23 0 5000 0 5000	
27 25 20 0 5000 0.5000	

Table 3. Comparison Table of 33-bus Radial Distribution Network

Methods	Open switches	Power loss (kW)	Percentage of loss reduction
Proposed BFOA	7, 9, 14, 32, 37	135.67	33.07%
Rao et. al (Harmony Search Algorithm) [28]	7, 10, 14, 36, 37	138.06	31.89%
Zhu et. al (Refined Genetic Algorithm) [15]	7, 9, 14, 32, 37	139.53	31.16%
Shirmohammadi and Hong [13]	7, 10, 14, 33, 37	141.54	30.17%

7. Conclusions

In this paper BFOA is proposed along with BFS and GIS to minimize the real power loss through reconfiguration and improving the voltage profile of the distribution network. The simulation is performed on IEEE 33-bus radial distribution network and results are compared with the other methods proposed by Rao *et. al*, Zhu *et. al*, and Shirmohammadi and Hong. It can be shown from the table that the loss reduction achieved by BFOA is approx. 2-3 % more than the existing approach and having good convergence characteristic. Power loss reduction at every branch is shown in Fig 6 and is clear indication of load balancing. After reconfiguration 2.89% improvement in voltage profile can also be seen from the Table 1. The efficiency and good convergence characteristic of the proposed approach proves that it can be used in large-scale network.

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Distribution Network Reconfiguration for Power Loss Minimization Using Bacterial Foraging Optimization Algorithm



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