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Power system reconfiguration and loss minimization for an distribution systems using bacterial foraging optimization algorithm

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ABSTRACT

In this paper, a method based on bacterial foraging optimization algorithm (BFOA) is proposed for distribution network reconfiguration with the objective of loss minimization. A novel model to simplify a distribution network is presented. The feeder reconfiguration problem is formulated as a non-linear optimization problem, and BFOA is used to find the optimal solution. According to the characteristics of distribution network, some modifications are done to retain the radial structure and reduce the searching requirement. Test results of a 33 bus sample network have shown that the proposed feeder reconfiguration method can effectively ensure the loss minimization, and the BFOA technique is efficient in searching for the optimal solution.

1. Introduction

The problem of reducing power losses in distribution feeders via feeder reconfiguration through BFOA approach is discussed here for a 33 bus distribution network posed in [1,2]. The results of this system provide the significant insight into the useful characteristics. It is known that distribution networks are built as interconnected meshed networks, while in the operation they are arranged into a radial tree structure. Distribution network is divided into subsystems of radial feeders equipped by number of sectionalizing switches and tie switches [3]. The power system can be operated more reliably by changing the configuration of the network [4]. A number of algorithms including mathematical programming and artificial intelligent methods, such as, Refined Genetic Algorithms [5], Ant Colony Search & GA [6], Heuristic Approach [7], and Adaptive Genetic Algorithms (AGAs) [8], have been proposed to reconfigure distribution feeders with the objective of minimizing real power losses while avoiding transformer and feeder overloads and inadequate voltages. The problem is formulated as a non-linear optimization problem where power loss is minimized subject to security and operational constraints. The test results on a sample distribution network are given here suggests that the BFOA approach is better than the results obtained by other methods.

Optimization problems in the steady state analysis of power systems aim at minimizing or maximizing an objective function. Traditional methods like Gauss-Siedel method, Newton Raphson method, Lambda iteration method are used to solve linear, continuous, and differential objective functions. To solve non-linear objective functions, evolutionary algorithms came into existence. The evolutionary algorithms are random, stochastic, and robust algorithms used for optimization of non-linear problems. Among these evolutionary algorithms one of the recent algorithms is bacterial foraging optimization algorithm.

The load on the feeders of a distribution system is generally a combination of industrial, commercial, residential and lighting loads. Substation transformers and feeders undergo peak loading at different times of the day, and therefore, the distribution system becomes heavily loaded at certain times of the day and lightly loaded at other. This is detrimental to the operating conditions of the network and leads to high real losses and poor voltage profile.

Load flow or power flow is the solution for the normal balanced steady-state operating conditions of an electric power system. The program computes the voltage magnitude and angle at each bus in a power system under balanced three phase steady state conditions. Once they are calculated, real and reactive power flows for all equipment interconnecting the buses, are computed. The load flow analysis is implemented on 33-bus test system. The objective function in this case is the loss reduction [9,10]. By using compensation techniques and using Bacterial Foraging Algorithm the losses are reduced in both the systems.

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2. Problem formulation

The paper is aimed at finding a way for load balancing through feeder reconfiguration so that stability and reliability of the distribution network could be enhanced. The objective of this optimization problem can be expressed by the minimization of the power loss as in

$$\Delta P = \mathrm{Re}\{2\Sigma I_i(E_m - E_n) + R_{line}\Sigma|I_i|^2 \quad (2.1)$$

Subject to:

1. No feeder section *can* be left out of service.
2. Radial network structure must be retained always.

$$\Phi(i) = 0 \quad (2.2)$$

3. Bus voltage magnitude should be strictly between upper and lower limits

$$E_{\min} \leqslant E \leqslant E_{\max} \quad (2.3)$$

where ΔP is the net power loss, E_m the voltage at node with higher potential, E_n the voltage at node with lower potential, R_{line} the resistance of the line, and I_i is the current in the line.

Eq. (2.1) corresponds to the objective function to be optimized and represents total real power loss of the distribution system. Eq. (2.2) considers voltage constraints for each node of the system. Eq. (2.3), deals with the radial topology constraint. It ensures radial structure of the *i*th candidate topology.

In this study, feeder switching status and consequently, network configuration [11], are adjusted to keep losses at a minimum [12,13] in the area. I_i is the current flowing through sectionalizing switches in the simplified model. The above objective function is also solved by traditional mathematical programming method.

3. Bacterial foraging optimization algorithm

Bacterial foraging optimization algorithm (BFOA) has been widely accepted as a global optimization algorithm of current interest for distributed optimization and control. BFOA [14] is inspired by the social foraging behavior of *Escherichia coli*. BFOA has already drawn the attention of researchers because of its efficiency in solving real-world optimization problems arising in several application domains. The underlying biology behind the foraging strategy of *E. coli* is emulated in an extraordinary manner and used as a simple optimization algorithm. This chapter starts with a lucid outline of the classical BFOA. Then it analyses the dynamics of the simulated chemotaxis step in BFOA with the help of a simple mathematical model.

3.1. Steps of Bacterial Foraging Algorithm

There are three steps in Bacterial Foraging Algorithm after the search strategies like swimming and tumbling. They are

- Chemotaxis.
- Reproduction.
- Elimination and dispersal.

3.1.1. 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 [15] the movement of the bacterium may be represented by

$$\theta^i(j+1,k,l) = \theta^i(j,k,l) + C(i)\frac{\Delta(i)}{\sqrt{\Delta^\tau(i)\Delta(i)}} \quad (3.1)$$

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

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

$$\begin{aligned} J_{cc}(\theta, P(j,k,l)) &= \sum_{i=1}^{s} J_{cc}\theta, \theta^i(j,k,l) \\ &= \sum_{i=1}^{s}\left[-d_{attrac\tan t}\exp\left(-w_{attrac\tan t}\sum_{m=1}^{p}(\theta_m - \theta^i)\right)\right] \\ &\quad + \sum_{i=1}^{s}\left[-d_{repellant}\exp\left(-w_{repellant}\sum_{m=1}^{p}(\theta_m - \theta^i)\right)\right] \end{aligned} \quad (3.2)$$

$d_{\text{attractant}}$, $w_{\text{attractant}}$, $d_{\text{repellant}}$, $w_{\text{repellant}}$ are the coefficients.

3.1.2. Reproduction

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

3.1.3. 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.

3.2. Fitness indicator (health)

As suggested by Chen et al. [16], each bacterium in the colony has to permanently maintain an appropriate balance between *exploration* and *exploitation* states by varying its own run-length unit adaptively. The adaptation of the individual run-length unit is done by taking into account the decision indicator of fitness improvement (health) The criteria that determine the adjustment of individual run-length unit and the entrance into one of the states (i.e., exploitation and exploration) are the following. (i) *Criterion-1*: if the bacterium discovers a new, promising domain, the run-length unit of this bacterium is adapted to another smaller one. Here, "discovers a new promising domain" means this bacterium registers a fitness improvement beyond a certain precision from the last generation to the current. Following *Criterion-1*, the bacterium's behavior will self-adapt into exploitation state. (ii) *Criterion-2*: if the bacterium's current fitness is unchanged for a number *Ku* (user defined) of consecutive generations, then this bacterium's run-length unit is augmented and this bacterium enters exploration state. This situation means that the bacterium searches an unpromising domain.

4. Implementation of Bacterial Foraging Algorithm to minimize the power loss

The steps of the Bacterial Foraging Algorithm applied to reduce the power loss are as follows:

Step 1: Initialization of the following parameters:

P: dimension of the search space: number of parameters used in the objective function. Every dimension signifies a parameter: ($P = 3$).
P_1: E_m.
P_2: E_n.
P_3: R_{line}.
P_4: I_i.
S: the number of bacteria in the population (20).
N_c: number of chemotactic steps (10).
N_s: the length of a swim when it is on a gradient (4).
N_{re}: the number of reproduction steps (4).
N_{ed}: the number of elimination/dispersal events (2).
P_{ed}: the probability that each bacterium will be eliminated/dispersed (0.75).
$C(i, j)|_{j=1}$: initial run-length unit (0.05 $*$ ones (s, 1)).
$C(N_c)$: the run-length unit at the end of the chemotactic steps ($j = N_c$).
θ^i: the initial random location of each bacterium.

After the load flow solution by Newton Raphson method, we have calculated the pre and post fault currents. The net power loss is calculated using the calculated load flow values.

Step 2: Elimination/dispersal loop, $l = l + 1$.

From the calculated power loss values, the $S/2$ values of losses will be eliminated by this loop.

Step 3: Reproduction loop, $k = k + 1$.

$S/2$ values of loss values having least values will be reproduced, keeping net strength of power loss bacteria constant.

Step 4: Chemotaxis loop, $j = j + 1$.

For $i = 1, 2, \ldots, S$, execute the chemotactic step for each bacterium as follows:

Evaluate the objective function used in Eq. (3.1) and is equaled to $J(i, j, k, l)$.

Let $J_{last} = J(i, j, k, l)$ so that lower ΔP could be found.

Tumble: Generate a random vector $\Delta(i)$ and $\Delta_m(i)$, $m = 1, 2, \ldots, p$ is a random number in the range of $[-1,1]$.

Compute $\Phi(i)$

$$\Phi(i) = \frac{\Delta(i)}{\sqrt{\Delta^{\tau}(i)\Delta(i)}} \tag{4.1}$$

Move using

$$\theta^i(j+1,k,l) = \theta^i(j,k,l) + C(i)\frac{\Delta(i)}{\sqrt{\Delta^{\tau}(i)\Delta(i)}} \tag{4.2}$$

Compute $J(i, j+1, k, l)$ compute $J_{cc}(\theta, P(j+1, k, l))$ 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 $J(i, j+1, k, l)$. Hence the bacteria takes one step and fetches a new ΔP.

Go to the next bacterium ($i = i + 1$ if $i = S$).

Update the run-length unit using

$$C(i,j+1) = \left(\frac{C(i,j) - C(N_c)}{N_c + C(N_c)}\right)(N_c - j) \tag{4.3}$$

Compute the best (lower) power obtained ($J_{\text{best}}(j)$).

Compute the difference in power is achieved in the current chemotactic step (Diff(j))

$$(\text{Diff}(j) = J_{\text{best}}(j) - J_{\text{best}}(j-1)) \tag{4.4}$$

If $j < N_c/n$ (e.g. $n = 2$).

If $|\text{Diff}(j) - \text{Diff}(j-h)| < \varepsilon$, $h = 1, 2, \ldots, h_m$, $h_m < N_c/n$. $j = N_c$ (i.e. end chemotactic operations).

Table 5.1
33 Bus network data.

S. No.	From bus i	To bus $i+1$	$R_{i,i+1}$	$X_{i,i+1}$	P (kW)	Q (kVAR)
1	1	2	0.0922	0.0477	100	60
2	2	3	0.493	0.2511	90	40
3	3	4	0.366	0.1864	120	80
4	4	5	0.3811	0.1941	60	30
5	5	6	0.819	0.707	60	20
6	6	7	0.1872	0.6188	200	100
7	7	8	1.7114	1.2351	200	100
8	8	9	1.03	0.74	60	20
9	9	10	1.04	0.74	60	20
10	10	11	0.1966	0.065	45	30
11	11	12	0.3744	0.1238	60	35
12	12	13	1.468	1.155	60	35
13	13	14	0.5416	0.7129	120	80
14	14	15	0.591	0.526	60	10
15	15	16	0.7463	0.545	60	20
16	16	17	1.289	1.721	60	20
17	17	18	0.732	0.574	90	40
18	2	19	0.164	0.1565	90	40
19	19	20	1.5042	1.3554	90	40
20	20	21	0.4095	0.4784	90	40
21	21	22	0.7089	0.9373	90	40
22	3	23	0.4512	0.3083	90	50
23	23	24	0.898	0.7091	420	200
24	24	25	0.896	0.7011	420	200
25	6	26	0.203	0.1034	60	25
26	26	27	0.2842	0.1447	60	25
27	27	28	1.059	0.9337	60	20
28	28	29	0.8042	0.7006	120	70
29	29	30	0.5075	0.2585	200	600
30	30	31	0.9744	0.963	150	70
31	31	32	0.3105	0.3619	210	100
32	32	33	0.341	0.5302	60	40
33	21	8	2.0000	2.0000	–	–
34	9	14	2.0000	2.0000	–	–
35	12	22	2.0000	2.0000	–	–
36	18	33	0.5000	0.5000	–	–
37	25	29	0.5000	0.5000	–	–

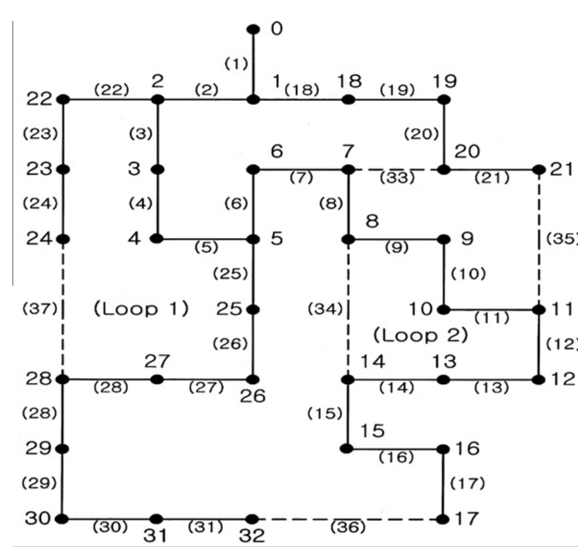

Fig. 5.1. 33-Bus final radial configuration of distribution system.

Table 6.1
Power loss results using BFOA with various switch statuses.

Switch status		Power loss (kW)
Closed	Open	
1,2,3,4,5,6,8,10,11,12,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,33,34,35,36	7,9,13,14,32	135.78
1,2,3,4,5,6,8,9,10,12,15,16,17,18,19,20,21,22,23,24,25,26,27,29,30,31,33,34,35,36,37	7,11,13,14,28,32	151.63
1,2,3,4,5,6,8,9,11,12,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,33,34,35,36	7,10,13,14,32	140.28
1,2,3,4,5,7,6,8,9,10,12,15,16,17,18,19,20,21,22,23,24,25,26,27,29,30,32,33,35,36,37	11,13,14,28,31	162.12
1,2,3,4,5,7,8,9,10,12,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,32,33,35,36	6,11,13,14,31	179.87

Step 5: If $j < N_c$ go to step 4 ($j = j + 1$).

Step 6: Reproduction.

For the given k and l, evaluate the health of each bacterium i as follows:

$$J(i)health = \sum_{i=1}^{N_c+1} J(i,j,k,l) \tag{4.5}$$

The health of the bacterium i measures how many nutrient it got over its lifetime. Sort all bacteria according to their health J^i_{health} in ascending order. Hence all the bacteria are arranged in such a way that the best bacteria have least ΔP and it increases in the coming bacteria.

The bacteria with the highest J^i_{health} values, computed by $S_r = S/2$ die while the other S_r with the lowest values split and take the same location of their parents.

Step 7: If $k < N_{re}$, go to step 3 ($k = k + 1$).

Step 8: Elimination/dispersal: with probability P_{ed}, randomly eliminate and disperse each bacterium i, keeping the size of the population constant. So the dispersed bacterias gives brand new values to the parameters of the objective function (ΔP).

Step 9: If $l < N_{ed}$, go to step 2 ($l = l + 1$), otherwise end.

These are the steps in BFO algorithm implemented in minimizing the power loss. Bacterial Foraging Algorithm is Robust, Stochastic and is one of the most efficient evolutionary algorithm.

5. 33-Bus distribution system

Table 5.1 gives us the system data for a 33 bus distribution system given in Fig. 5.1.

Due to their inherent characteristics, BFO algorithms are well suited for combinatorial optimization problem. The results obtained in this paper for loss minimization [17,18] demonstrate the effectiveness of BFO algorithm in solving combinatorial optimization problems. Effectiveness of this method can be further demonstrated by applying this method to larger systems. Other variations of the system can also be implemented to determine their effectiveness for the reconfiguration problem.

Table 6.2
Power loss results using BFOA compared with other methods using 33 bus network. Loss in base configuration – 202.71 kW.

Methods	Switches open	Power loss (kW)
BFOA	7,9,13,14,32	135.78
Shirmohammadi and Hong [3]	7,10,14,32,37	141.54
ZHU (Refined genetic algorithm) [5]	7,9,14,32,37	139.55
Ant Colony Search & GA [6]	7,9,14,28,32	137.00
Martín and Gill [7]	7,9,14,32,37	139.55
AG Algorithm (Swarnkar, Gupta, Niari) [8]	7,9,14,32,37	139.55
Gomes et al. [9]	7,9,14,32,37	136.57
Goswami and Basu [10]	7,9,14,32,37	136.57
Mcdermott et al. [11]	7,9,14,32,37	136.57
Gomes et al. [12]	7,10,14,32,37	136.66

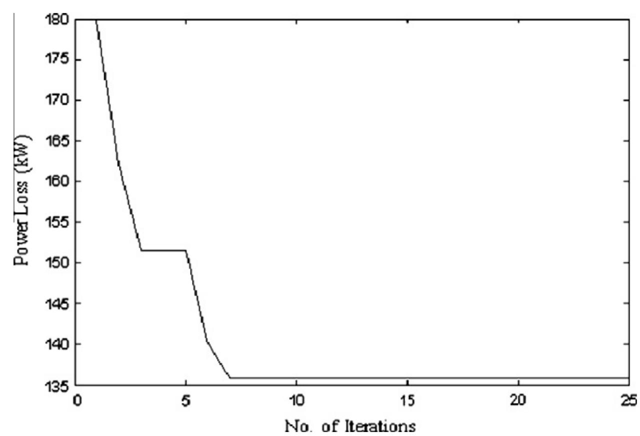

Fig. 6.1. Convergence characteristics of power loss using BFOA.

6. Results and comparisons

For assumed series fault at bus number 13, Table 6.1 shows the results obtained by using BFOA. It is observed that the power loss is minimum when the switches 7,9,13,14,32 are at open. If the configuration changes the power loss will increase. Power loss is calculated using BFOA with various switch statuses and it is given in Table 6.1.

The proposed method is compared with the methods proposed by Gomes et al. [9], Goswami and Basu [10], Mcdermott et al. [11] and various other prevalent methods for the same 33-bus test system. For effective comparison, the results of the proposed method along with other methods are shown in Table 6.2. Here the power loss is minimized and this method gives 4.1% of improved result as mentioned in other methods. In the initial configuration, the power loss is 202.71 kW and after reconfiguration using proposed method, the power loss is 135.78 kW which is very less while comparing with other methods. Approximately 33% of power loss is minimized as compared with original configuration. So the proposed method is highly suitable for restoration and reconfiguration. Fig. 6.1 shows the graph of power loss results using BFOA for the test system.

7. Conclusion

A bacterial foraging optimization algorithm is proposed in this paper is to configure distribution network to keep the load balancing so that the power loss is minimum. The problem is formulated as a non-linear optimization problem with an objective function of minimizing power loss subject to security constraints. Test results have shown that using BFOA method, the feeder reconfiguration problem can be solved efficiently and the power loss is minimized effectively by reconfiguring the system. The fast and effective convergence of this approach proves that it is a highly suitable technique to use in service restoration procedures of distribution automation system (DAS).

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