



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.

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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

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

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

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

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

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

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-effector. The cells when stimulated by a high level of *succinate*, release an attractant *aspartate*, 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

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

$d_{\text{attractant}}$, $w_{\text{attractant}}$, $d_{\text{repellant}}$, $w_{\text{repellant}}$ 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 K_u (user defined) of consecutive generations, then this bacterium’s run-length unit is

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