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# Short-term Load Forecasting using Support Vector Machines Augmented by an Improved Bacterial Foraging Algorithm

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*Abstract*— **In this paper, the short-term load forecasting problem is addressed using a Support Vector Machine (SVM) Model. In order to optimize the parameters of the model, an improved Dynamic Bacterial Foraging Algorithm (DBFA) is utilized. Load forecasting is a very significant task for the power system operation and planning. An accurate prediction of loading has a great impact on the system's stability, reliability, economic dispatch and other operational aspects. Tuning the parameters of the SVM model is a key factor for the algorithm to converge since it is based on gradient searches. Specifically, Kernel function and penalty factor of the basic SVM model are highly dependent on prior experience. In this perspective, the DBFA was applied to optimize the model's parameter selection procedure using historical data as training sets for the SVM model. The proposed model was validated using applicable historical load data of a total of 30 days as the training and testing samples. A comparison of the results with those obtained by the basic SVM model was performed to administrate the effectiveness and superiority of the model.**

*Index Terms:* **BFA, short-term load forecasting, SVM.**

## I. INTRODUCTION

Load forecasting is the prediction of the load demand over a period of time. Depending on the forecasting period, load forecasting could be classified as short-term, medium-term or long term. For the short-term load forecasting, this period could range from one hour to a couple of weeks [1]. From this standpoint, the significant role the load forecasting plays in power system operation and planning is highly evident. An accurate load forecasting maintains the balance between the power generation and load demand of the system. The solutions of various power system operational problems such as load flow, economic load dispatch and unit commitment as well as security and contingency studies, are based on the load forecasting [2]. It is obvious that the accuracy of load forecasting is affected by the load uncertainty. This is understandable since the load forecasting depends on the load historical data. The accuracy of the forecasting is influenced by many factors such as weather conditions, political events and social activities [3].

In the literature many techniques have been proposed and applied to solve the load forecasting problem. These methods could be classified into two types [4]. The first is statistical-calculus-based methods such as time series method, regression method and auto regressive integrated moving average. The second type is the heuristic non-calculus-based methods including fuzzy logic [5], artificial neural networks [6], and support vector machine models [7, 8]. In spite of the simplicity and easy implementation, the methods of the first type have some drawbacks that are associated with the nonlinearities of the load data patterns. The artificial intelligence-based methods have shown good behavior when dealing with nonlinear load data sets.

SVM is one of the non-deterministic techniques that was introduced by Vladimir Vapnik [9]. It is a technique that uses a set of training data to create a classification or regression functions. The mechanism of the SVM is derived from the statistical learning theory [10, 11]. To have a kind of classifier, the SVM applies a separating hyperplanes. For the spaces that cannot be separated in a linear manner, the SVM model transforms this space to another one with high dimensional characteristics. Therefore, the margin of the classifier is maximized according to the training data set and a linear separating hyperplanes are created optimally [9, 12, 13]. The mechanism of the SVM algorithm as a supervised learning scheme is based on generating a learning function from a set of training data with a limited number of training samples [14]. SVM have shown significant advantages such as the easy training process and limited number of parameters required. However, the statistical-based methods are generally known to have some difficulties when dealing with nonlinear problems and high dimensional data. Differently, SVM models have proved ability to tackle this kind of problems and

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overcome this weakness [15]. On the other hand, the weakness of the SVM is the selection of its parameters appropriately. This issue is very crucial for the training, learning and generalization processes. As a matter of fact, the determination of these parameters highly depends on the previous experience what raises a problematic issue. In order to find a solution to this problem, some optimization techniques have been proposed and implemented. Particle swarm optimization algorithm (PSO), for instance, is one of these heuristic optimizers [15, 16]. Bacterial Foraging Algorithm (BFA) is a heuristic non-calculus-based optimization method. The BFA is a mimic approach which is inspired by the foraging behavior of the *E coli* bacteria [17]. The original BFA has been applied to power system problems to find optimal or near optimal solutions. However, when it was utilized for large-scale nonlinear optimization problems, it showed poor convergence behavior [18, 19]. Effective and successful enhancements have been proposed and introduced to the basic BFA aiming to improve its convergence characteristics [20-27].

In this paper, a modified DBFA, is presented and used to optimize the parameters of the SVM model. The modification proposes a dynamic behavior so that the BFA gains better convergence characteristics. The SVM model based on the modified DBFA optimizer was established and applied for the short-term load forecasting problem. The reminder of the paper is organized as follows: The SVM and the basic BFA as well as the modified DBFA are briefly discussed in Section II and Section III respectively. In Section IV, the proposed Model is presented. Simulation results are shown in Section V. The conclusion is drawn in Section VI.

## II. SUPPORT VECTOR MACHINES (SVM)

The SVM is applied so that it nonlinearly maps input data to a higher dimensional hyperspace. Next, a linear estimated regression is obtained. Given a data set as $D=\{(x_i, y_i) \mid i=1,2,...,n\}$, where $x_i, y_i \in R_n$ represent the input and output variables respectively. The input data is mapped to a feature space and hence the linear regression is performed according to:

$$f(x)=[\omega \times \varphi(x)]+b \tag{1}$$

where φ(x) is a nonlinear mapping from the input space to a high-dimensional feature space. The coefficients b is a threshold value. The following objective optimization function is applied to determine the regression function:

$$\begin{aligned} &\min\left\{\frac{1}{2}\|\omega\|^2 + C\sum_{i=1}^{n}\left(\xi_i^* + \xi_i\right)\right\} \\ &\textit{subject to}: \; y_i - \omega.\varphi(x) - b \le \varepsilon + \xi_i^*; \\ &\qquad \omega.\varphi(x) + b - y_i \le \varepsilon + \xi_i; \\ &\qquad \xi_i \xi_i^* \ge 0 \end{aligned} \tag{2}$$

The parameter C in Equation (2) is the penalty factor which is a balancing weighting factor and error training parameter. $\varepsilon$ is the loss function, $\xi_i$ and $\xi_i^*$ are the relaxation factors. The factor is given by:

$$\xi_i^* = \begin{cases} 0, |f(x)-y_i| \le \varepsilon \\ |f(x)-y_i| - \varepsilon, \; |f(x)-y_i| > \varepsilon \end{cases} \tag{3}$$

The regression equation coefficient is expressed as:

$$\omega = \sum_{i=1}^{n}(\alpha_i - \alpha_i^*)x_i \tag{4}$$

where $\alpha_i$ and $\alpha_i^*$ are called lag range factors. The SVM regression function is obtained by:

$$f(x) = \sum_{i=1}^{n}(\alpha_i - \alpha_i^*)K(X_i, X) + b \tag{5}$$

The Kernel function *K* $(X_i, X)$ in Equation (5) can be one of a variety of kernel functions such as the polynomial or radial basis. In general, kernel function could be any function that satisfies the Mercer condition [28].

## III. THE BACTERIAL FORAGING ALGORITHIM (BFA)

### *A. The basic bacterial foraging algorithm (BFA)*

The BFA is a non-deterministic-based optimization method which is inspired by the foraging behavior of the *E coli*. Bacteria [17]. BFA was proposed to find the optimal solution vector for non-differentiable and non-gradient complex objective functions. The chemotaxis process is performed through swimming and tumbling. In the BFA, a tumble is represented by a unit length in a random direction, $\phi(j)$ which specifies the movement after a tumble. The size of the step taken in randomly in any direction is represented by the constant run-length unit, *C (i)*. For a population of a number of bacteria, the location of the $i^{th}$ bacterium at the $j^{th}$ chemotactic step, $k^{th}$ reproduction step and $l^{th}$ elimination/dispersal event is represented by $\theta^i(j,k,l) \in \Re^p$. At this location the cost function is given by $J(i,j,k,l)$, which is also known as the nutrient function. After a tumble, the location of the $i^{th}$ bacterium is represented by [17]:

$$\theta^i(j+1,k,l) = \theta^i(j,k,l) + C(i,j)\phi(j) \tag{6}$$

When at $\theta^i(j+1,k,l)$ the cost function $J(i,j+1,k,l)$ is less than $J(i,j,k,l)$, another step of size *C(i,j)* in the same direction is taken. This operation is repeated as long as a lower cost is obtained until a maximum number of steps, $N_s$, is reached. The cost function of each bacterium is affected by a kind of swarming that is performed by the cell-to-cell signaling released by the bacteria groups to form swarm patterns. This swarming is expressed as [17]:

$$\begin{aligned} J_{cc}\left(\theta, P(j,k,l)\right) &= \sum_{i=1}^{S} J_{cc}^{i}\left(\theta, \theta^i(j,k,l)\right) \\ &= \sum_{i=1}^{S}\left[-d_{attract}\exp\left(-\omega_{attract}\sum_{m=1}^{p}(\theta_m-\theta_m^i)^2\right)\right] \\ &+ \sum_{i=1}^{S}\left[h_{repellant}\exp\left(-\omega_{repellant}\sum_{m=1}^{p}(\theta_m-\theta_m^i)^2\right)\right] \end{aligned} \tag{7}$$

where $d_{attract}$, $\omega_{attract}$, $h_{repellant}$ and $\omega_{repellant}$ are coefficients represent the characteristics of the attractant and repellant signals released by the cell and $\theta_m^i$ is the $m^{th}$ component of $i^{th}$ bacterium position $\theta^i$. $P(j,k,l)$ is the position of each member of the population of the S bacteria and defined as [17]:

$$P(j,k,l) = \left\{\theta^i(j,k,l) \mid i = 1,2,...,S\right\} \tag{8}$$

where $S$ is the size of the bacteria population. The function which represents the cell-to-cell signaling effect is added to the cost function [11]:

$$J(i,j,k,l) + J_{cc}(\theta, P) \tag{9}$$

A reproduction process is performed after taking a maximum number of chemotactic steps, $N_c$. The population is halved so that the least healthy half dies and each bacterium in the other healthiest one splits into two bacteria which takes the same position [17]:

$$S_r = \frac{S}{2} \tag{10}$$

After $N_{re}$ reproduction steps an elimination/dispersal event takes place for $N_{ed}$ number of excisions. In this operation each bacterium could be moved to explore another parts of the search space. The probability for each bacterium to experience the elimination/dispersal event is determined by a predefined fraction $p_{ed}$.

### *B. Modified dynamic bacterial foraging algorithm*

The length unit step in the basic BFA is fixed constant. This could be sufficient for small linear optimization problems. However, for large non-convex problems satisfactory convergence characteristics may not be guaranteed. Better dynamic properties are required for high-dimensional search spaces to achieve good convergence behavior. In order to reach the desired results using this modified algorithm, the run-length parameter is attuned so that it could have the required dynamic and adaptive characteristics. The key element which governs the local and global search capability of the algorithm. Consequently, balancing the exploration and exploitation of the search could be guaranteed by adapting the run-length unit. An adaptive nonlinear dynamic function is augmented to implement the swim walk as a substitute of the fixed length unit step. This function is formulated as [20]:

$$C(i,j+1) = \left(\frac{C(i,j) - C(N_C)}{N_C + C(N_C)}\right)(N_C - j) \tag{11}$$

where $j$ is the chemotactic step index and *Nc* is the maximum number of chemotactic steps while *C(Nc)* is the initial predefined parameters.

## IV. SVM BASED ON A MODIFIED DBFA OPTIMIZER

The penalty factor and Kernel function of the SVM model are optimized using the modified DBFA according to the following steps:

Step 1: Input experimental data
Step 2: Initiate the population size of the DBFA, the parameters of the SVM including the penalty factor and the Kernel function
Step 3: Select the maximum number of chemotactic steps, the chemotactic step index…etc
Step 4: Normalize and specify training and testing subsets of labeled data
Step 5: Calculate the fitness value in the training process from the input data and according to the Kernel function
Step 6: Find the optimal or near optimal solution vector
Step 7: Check if the results are better (percentage error)
Step 8: If not satisfying repeat Step 5
Step 9: If satisfied or the highest number of iteration is reached, the output is the optimal
Step 10: The optimal parameters are encoded to the SVM model to implement the forecasting task

The process of optimizing the parameters of the SVM model using the modified DBFA is shown in Figure 1.

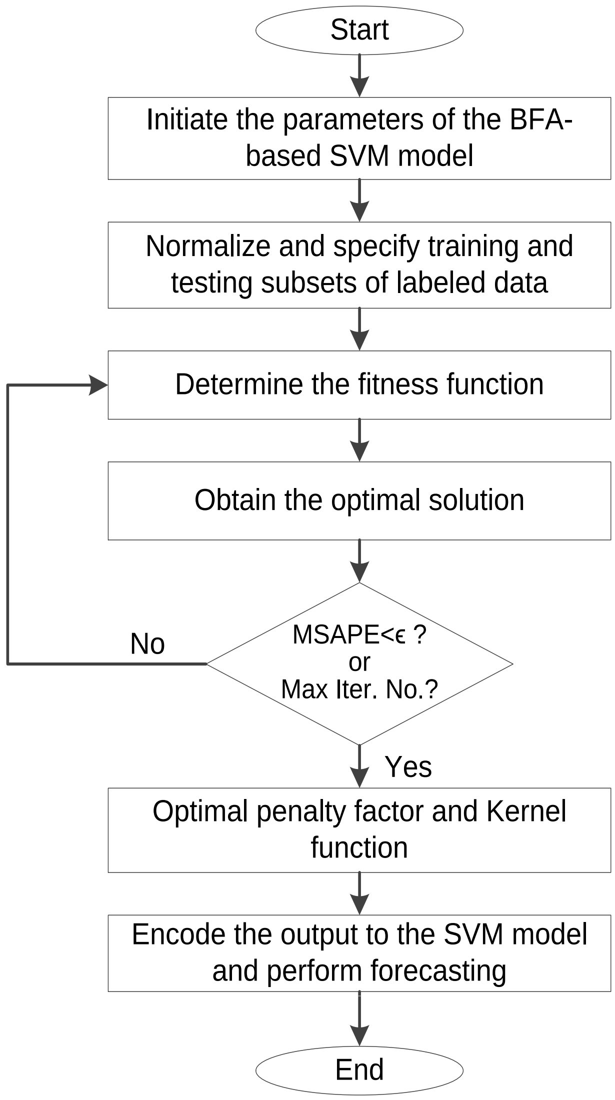


Figure 1. Flow chart of parameter selection optimization

## V. SIMULATION RESULTS

The proposed DBFA-based SVM model was applied to obtain a day-ahead load forecasting. The algorithm was implemented and coded in MATLAB and executed on an Intel Core i7-8750H 2.20GHz personal computer with 8 GB RAM. In order to check for consistency, 30 runs were independently conducted. A specified set of data for one month, September 15 to October 14, 2015, were collected for a selected zone [29]. The data set were divided into three subsets; training, testing and forecasting. The first 25 days were employed for training, while the next 4 days were utilized as the testing data set. The data of the last day were forecasted by implementing the proposed model based on the training and testing subsets. Afterward, the forecasted data were compared to the actual data for the same day. The basic SVM model was also executed to determine the load forecasting for the same day using the same data and testing subsets. The results obtained by the DBFA-based SVM and the traditional SVM were compared in order to demonstrate the superiority of the proposed model. The comparison was carried out in terms of the load power, as shown in Figure 2, and the absolute percentage error as illustrated by Figure 3.

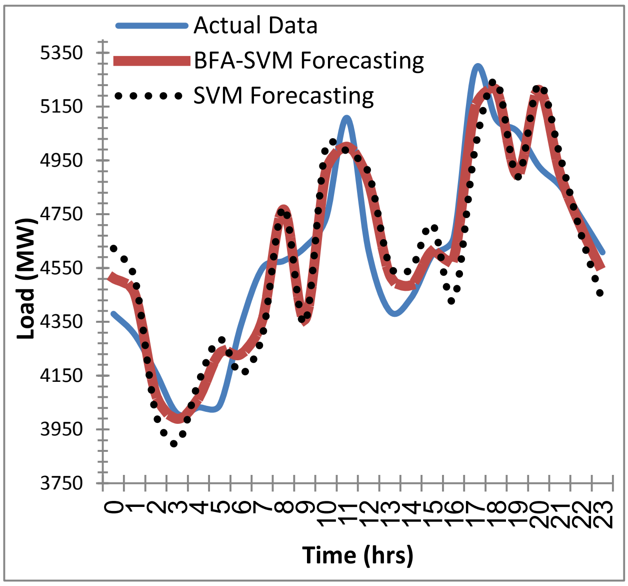


Figure 2. Comparison of forecasting results

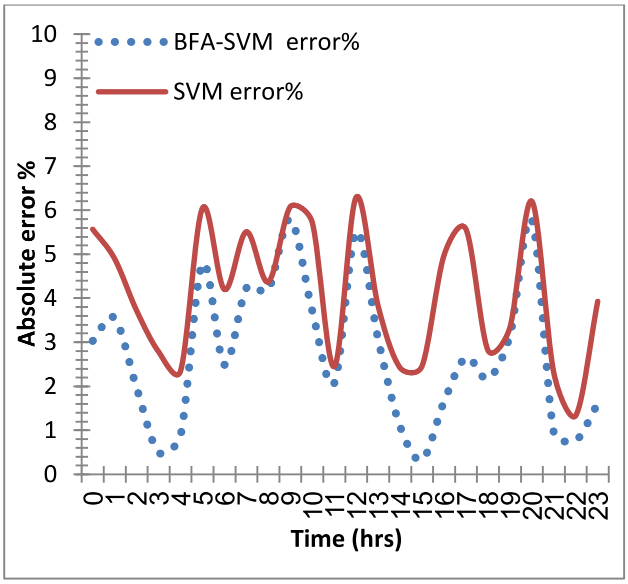


Figure 3. Comparison of forecasting error percentage

The Mean absolute percent error (MAPE) of the results obtained by both the DBFA-SVM model and the basic SVM model were compared as shown in Table 1. The comparison demonstrated that the proposed model proved to be effective with less MAPE as shown in the table.

Table 1. MAPE Comparison of the two models

| | Basic SVM Model | DBFA-SVM model |
|---|---|---|
| Maximum absolute percent error (%) | 6.29561411 | 5.80018399 |
| Minimum absolute percent error (%) | 1.33356981 | 0.328775702 |
| Mean absolute percent error (%) | 4.13023463 | 2.746637501 |

# VI. CONCLUSION

In this paper an improved SVM model is proposed to determine a day-ahead load forecasting. The traditional SVM model is associated with some shortcomings regarding the selection of its parameters. In order to tackle this problem, a modified DBFA was employed to find the optimal selection of the penalty factor and Kernel function of the SVM model. Both the basic and proposed DBFA-SVM models have been established and implemented to determine the load forecasting. The results obtained by the two models were compared on basis of predicted load and the mean absolute percentage error (MAPE). The comparison demonstrated the effectiveness and superiority of the proposed model with a tolerated error percentage.

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