

Journal of Computers: A Radial Basis Function Neural Network Model Based on a Genetic Algorithm for the Prediction of Nuclear Leakage



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Abstract. In recent years, nuclear accidents have spurred the improvement of nuclear power plants, because nuclear pollution has resulted in considerable environmental damage. This paper describes a radial basis function (RBF) neural network prediction model based on a genetic algorithm to predict concentrations of nuclear leakage in case of nuclear accidents. The prediction model uses various factors impacting the concentrations of nuclear leakage as input and concentrations of nuclear leakage concentrations as output. We used data from the Hong Yanhe Nuclear Power plant in the Liaoning Province for a simulation experiment, and compared the proposed prediction model with a RBF prediction model based on a traditional genetic algorithm. The results demonstrated that the prediction model had a smaller error than the output from the traditional model.

Keywords: nuclear leakage prediction, genetic algorithm, RBF neural network

1 Introduction

With the transformation of the international energy strategy, nuclear power has the potential to ease the crisis of energy shortage. However, nuclear leakage and nuclear pollution incidents caused by mismanagement or technological factors have resulted in great harm, such as the accident and subsequent leakage at Japan's Fukushima plant [1]. Hence, monitoring and treatment of nuclear pollution has become a top priority for the nation's economic development and environmental protection plans.

The concentration of nuclear radiation is influenced by wind speed, wind direction, total cloud cover / low cloud cover, nuclide category, particle density, and other meteorological factors related to the environment and the nuclide itself, and these factors have certain interactions, resulting in a very complex nonlinear relationship between these factors and the nuclear concentration [2]. It is difficult to establish a precise model for the relationship between the factors and to obtain appropriate forecasting results using traditional mathematical models and statistical methods.

The radial basis function (RBF) neural network model is one of several prediction methods [3], which determines the mapping relationship between the network input factors and the output (the prediction) by using historic sample data for learning and training. RBF neural networks are self-learning, self-organizing, and adaptive, possess fast training speed, and deliver local approximation and global convergence [4].

RBF neural networks partition the input data according to the distance from the input factor to the center value of the basis function, and combine the output value of RBF linearly based on weighting the connections in order to obtain the prediction results.

Many papers have been published to date on the use of RBF neural networks for prediction and evaluation of data in many fields of study [5-8]. However, conventional RBF neural networks use a

piecewise training method, which can complete the training process, but destroys the integrity of the RBF neural network [9-11]. Therefore, this paper proposes a RBF neural network model based on optimization by using an improved genetic algorithm. This model encodes the three key parameters of the RBF neural network uniformly, adapts the number of hidden units in real time, and changes the genetic strategy adaptively based on the probability of crossover and mutation operations [12-14]. The proposed prediction model uses various factors impacting the concentration of nuclear leakage as input and the concentration of nuclear leakage as output. The results were validated by using historic leakage data.

The remainder of the paper is structured as follows: section 2 introduces the RBF neural network; section 3 describes the RBF neural network prediction model based on the improved genetic algorithm; section 4 compares and analyzes the proposed prediction model with the conventional model; and section 5 describes the conclusions.

2 RBF Neural Network

RBF neural networks are based on the theory of the propagation process in the human nervous system, and the models have been applied widely due to their suitable characteristics of local approximation and global optimization [15]. The topology structure of a RBF neural network is shown in Fig. 1. The first layer is called the input layer, and it includes the nodes for the input data, in which the number of nodes equal the dimension of the set of input parameters. The second layer is the central layer, called the hidden layer, in which the number of nodes is adapted dynamically based on the specific requirement of the study. The third layer is called the output layer, which represents the transformation of the data into results based on the input data [16]. In summary, in RBF neural networks, the mapping process between input layer and hidden layer can be viewed as a nonlinear transformation, while the mapping process between hidden layer and output layer can be viewed as a linear transformation [17-18].

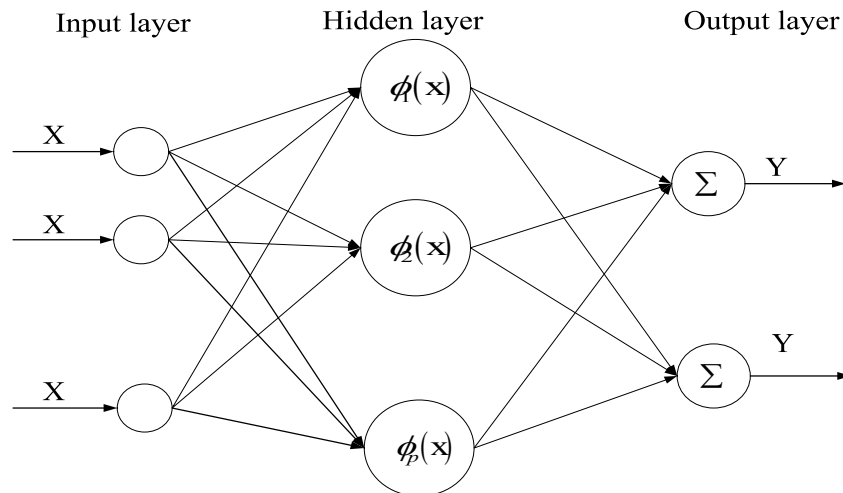


Fig. 1. RBF neural network topology structure

RBF neural networks can be expressed by formula (1):

$$y = \sum_{i=1}^{n_c} w_i \phi \left(\|x - c_j\|_{R^p} / \sigma_i \right) \tag{1}$$

where $x \in R^p$, $X^T = [x_1, x_2, \dots, x_p]$ is the input vector of the neural network; w_i is the weight of the connection for each hidden unit; c_i is the center of the i_{th} basis function in the hidden layer; σ_i is the width of the i_{th} RBF; b is the threshold of the output layer; n_c is the number of hidden units; $\|\cdot\|_{R^p}$ is the distance between input x and the center c_i ; $\phi(\cdot)$ is the RBF which is always replaced by a Gaussian function, as expressed by formula (2), where σ is the width of the Gaussian function.

$$\exp\left(-\frac{\|x - c_i\|^2}{\sigma}\right) \quad (i=1,2,\dots,k) \quad (2)$$

The weight of the connection can be obtained by calculating a pseudo-inverse matrix, as expressed by formula (3), where d is the expected response vector, A^+ is the pseudo-inverse matrix of A and it is unique.

$$W = A^+ d \quad (3)$$

Matrix A is determined by formula (4):

$$\begin{cases} A = \{a_{ji}\} \\ a_{ji} = \exp\left(-\frac{M}{d_m^2} \|X_j - C_i\|\right) \quad (j=1,2,\dots,N; i=1,2,\dots,M) \end{cases} \quad (4)$$

The pseudo-inverse matrix of A can be computed by formula (5):

$$A^+ = (A^T A)^{-1} A^T \quad (5)$$

All of the hidden units include two key parameters in a RBF neural network, i.e., the center and the corresponding width of the RBF. These values influence the ability of local approximation of the RBF to a large degree. If the value used for the center is not reasonable, the convergence speed of the network will be slow and the network will disperse. The value used for the width can restrict the response range of the input data. Aside from these two important parameters, the weight between the hidden layer and the output layer is also an important parameter.

3 The RBF Neural Network Model Based On An Improved Genetic Algorithm

In summary, there are three required training parameters for the RBF neural network, the center of the RBF, its width in all hidden units, and the connection weight between the hidden layer and the output layer. Determining appropriate values for the three parameters is the key to improving the nonlinear approximation ability of the RBF neural network. Therefore, this paper is proposing an improved genetic algorithm to find optimal solutions for the three parameters both globally, and for the purpose of developing a RBF neural network model for the prediction of nuclear leakage.

3.1 Improved genetic algorithm

Selection of the initial population. In this paper, we determined the data center and width based on a k-means value clustering algorithm, and we obtained weights for the connections by using the pseudo-inverse matrix. Although the set of initial populations obtained in this manner may not be optimal, the set may be viewed as an approximate solution, which can be improved upon with genetic manipulation and search efficiency to obtain an optimum solution with higher accuracy.

Coding. The commonly used segmentation approach can destroy the integrity of the RBF neural network. In order to solve this problem, we used unified coding for the three parameters in the RBF neural network, namely, we wrote the codes of the three parameters into the same chromosome. In the RBF neural network, the width is changed along with the center, and the value of the connection weight is associated with the width and center values. Therefore, coding was based on the center, width, and connection weight in sequential order. In addition, we assumed that the preset number of hidden units was p . When executing the iterative optimization at each step in time, we adjusted p according to the learning effect until the training phase was terminated. Normally, a smaller value of p would be chosen and increased gradually during the training phase. In this paper, we adopted a real encoding method. The specific coding string structure diagram is as shown in Fig. 2.

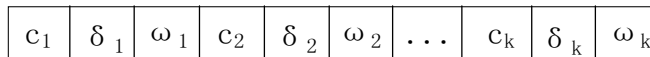


Fig. 2. The chromosome encoding

The confirmation of fitness function. The individual fitness is a standard parameter used to evaluate whether an individual is appropriate or not in the genetic process. The purpose of using a RBF neural network model for forecasting is to determine the existence of a minimum value for the objective function. However, there is a close relationship between the objective function and the error value between the expected output and the actual output. Therefore, we can determine the fitness function as shown in Formula (6):

$$fitness = \frac{1}{\sum_{i=1}^N \sum_{j=1}^K (Y_j(i) - \bar{Y}_j(i))^2} \tag{6}$$

Where,

$Y_j(i)$ — The actual output of the training data i in the j_{th} output units;

$\bar{Y}_j(i)$ — The expected output of the training data i in the j_{th} output units;

N — The number of input data

K — The number of output nodes

Selecting operation. This paper adopted a roulette wheel selection approach. Firstly, we calculated the fitness function value of each individual in the population and obtained the accumulated sum $\sum fitness$. Then, according to the obtained individual fitness value, we developed the corresponding relationship between this individual and a certain interval in $[0, \sum fitness]$. Next, we generated a number randomly in $[0, \sum fitness]$ by using a random number generator, so that the interval of this number represented the hit rate of the individual.

Based on the above selection algorithm, we adopted the best reservation mechanism, namely, we calculated the fitness values of all individuals of the current generation of the population and sorted them, retaining the individual with the largest fitness. When the fitness of the optimal individual in the population was smaller than the fitness of retained individuals, namely, when populations evolved towards an undesirable direction, we replaced the current optimal individual with the retained individual.

Crossover operation. In this paper, the crossover operator was computed using the two-point arithmetic crossover method because of the real-time coding method. Firstly, we chose the chromosome pairs which conduct the crossover operation by randomly pairing and generating two random numbers to select the real encoded position of the crossover operation in the chromosomes. Next, we ensured two pairs of real numbers for the crossover operation to reproduce the next population. In this paper, the crossover possibility is denoted as P_c .

Mutation operation. This paper used the two-point-bit mutation operator. Firstly, two random numbers were generated to determine the position of the mutation operation. Then, according to the range of parameters represented by the above position, two real numbers were generated randomly and were used to replace the real number in the position of the corresponding genes on the chromosome. The generation of new offspring by mutation operation involves in the inheritance of the next generation. In this paper, the mutation probability is denoted as P_m .

In previous genetic algorithms, the probabilities of the crossover operation P_c and the mutation operation P_m have been set generally to a fixed value. If P_c is larger, new individuals generate faster, but it is likely that individuals with high fitness are eliminated. On the converse, the search speed of the genetic algorithm will be greatly affected and cannot meet the requirements of rapid optimization, if P_m is smaller, and it will be difficult to generate new individuals. On the contrary, it will lead to the genetic algorithm become to a pure search problem.

To solve these problems, this paper has adopted an adaptive genetic strategy which means that the probabilities of the crossover and mutation operations can adapt based on the evaluation results of the

group in the genetic process. Using the average fitness of the population as a benchmark, the values of P_c and P_m were reduced to protect excellent individuals from elimination, when the fitness of one individual was larger than the average fitness. On the converse, the values of P_c and P_m were increased to accelerate the speed with which new individuals replaced poor individuals. We adjusted the values of P_c and P_m using formula (7) and (8), where $P_{c\max}$ and $P_{c\min}$ denote the maximum value and the minimum value of the crossover probability, respectively, and $P_{m\max}$ and $P_{m\min}$ denote the maximum value and the minimum value of the mutation probability, respectively. f' denotes the individual with larger fitness value based on the two individuals of the crossover operation, f_{avg} denotes the average fitness of the population, and f_{\max} denotes the largest fitness value of the population.

$$P_c = \begin{cases} P_{c\max} - \frac{(P_{c\max} - P_{c\min})(f' - f_{avg})}{f_{\max} - f_{avg}}, & f' \geq f_{avg} \\ P_{c\max}, & f' < f_{avg} \end{cases} \quad (7)$$

$$P_m = \begin{cases} P_{m\max} - \frac{(P_{m\max} - P_{m\min})(f' - f_{avg})}{f_{\max} - f_{avg}}, & f' \geq f_{avg} \\ P_{m\max}, & f' < f_{avg} \end{cases} \quad (8)$$

3.2 Nuclear leakage prediction model based on the RBF neural network

Based on the optimization of neural network parameters by using the improved genetic algorithm, the entire design process of the prediction model for nuclear leakage is as follows:

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- 1 Initialize populations with a k-means clustering algorithm and pseudo-inverse matrices, and
 - 2 generate the initial population.
 - 3 Randomly select K samples as initial cluster centers.
 - 4 **While** (the distribution result of each type is changed)
 - 5 {
 - 6 For each sample, calculate the Euclidean distance between sample and center
 - 7 Classify each sample according to the nearest principle
 - 8 Calculate the arithmetic mean of all samples for each type of sample as a new clustering center.
 - 9 }
 - 10 Establish the pseudo inverse matrix of the output of the hidden layer nodes, obtain the connection
 - 11 weights by Formula (3). Thus obtain the initial population.
 - 12 Real-number encode the initial populations and set the numbers of iterations and hidden layer
 - 13 nodes.
 - 14 **While** (the number of iterations does not reach the prescribed value)
 - 15 {
 - 16 Calculate the fitness function values of each gene string in the populations.
 - 17 **If** (the fitness values of individuals does not reach the required precision)
 - 18 Crossover and mutate the individuals, and adjust P_c and P_m appropriately.
 - 19 The number of iterations plus 1.
 - 20 **Else**
 - 21 Decode chromosomes and record the center value, the width, and the connection weights of
 - 22 the basis function.
 - 23 **Break.**
 - 24 }
-

After completing the above training phase, we obtained the final RBF neural network prediction model for nuclear leakage, and determined the calculation error between the result and actual output by using test samples.

4 Simulations

We used one thousand samples based on monitoring data from a wireless sensor network from the Hong Yanhe nuclear power plant in the Liaoning Province of China as well as meteorological data for the corresponding period. These data were divided randomly into two groups according to a 4:1 ratio. One group was used to forecast the training samples established by the model, denoted as training sample A. The other group was used to verify the accuracy of the prediction model, denoted as training sample B. The traditional RBF neural network model and the improved RBF neural network model based on the genetic algorithm were trained based on the sample A. The two models we developed were validated by the sample B. Finally, the validation results of the two models were compared.

The network training of the model terminates when the fitness value is smaller than 0.01. The initial number of hidden layer neural units was set to 5. The maximum number of iterations was set to 100. The traditional RBF neural network model and the improved RBF neural network model based on the genetic algorithm were trained using the sample A, and the training results are shown in Fig. 3 and Fig. 4. We observed that the improved RBF neural network based on the genetic algorithm had a faster convergence speed than the traditional model, meaning the required training period was shorter.

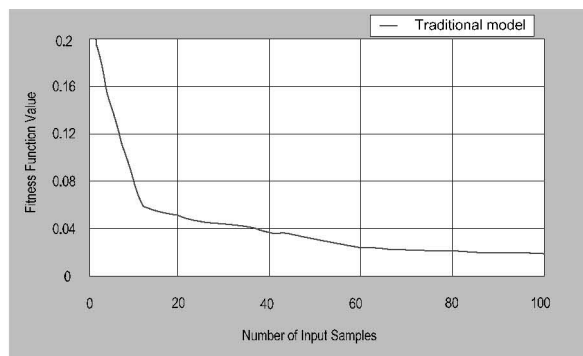


Fig. 3. Diagram of the traditional RBF neural network training process

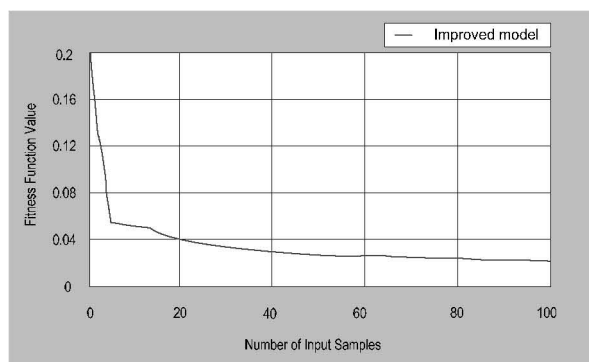


Fig. 4. Diagram of the improved RBF neural network based on a genetic algorithm training process

Fig. 5 and Fig. 6 respectively show the changes in nuclear pollution concentration with number of input samples using the traditional RBF neural network model and the improved RBF neural network model based on a genetic algorithm. In terms of differences between the target and prediction values of nuclear pollution concentration, the improved neural network model was superior to the traditional model in terms of prediction effect. The data in Table 1 show the advantages of the proposed model. Although both models can predict nuclear pollution concentration, it was observed that the overall performance of the improved RBF neural network based on a genetic algorithm was better than that of the traditional

RBF neural network.

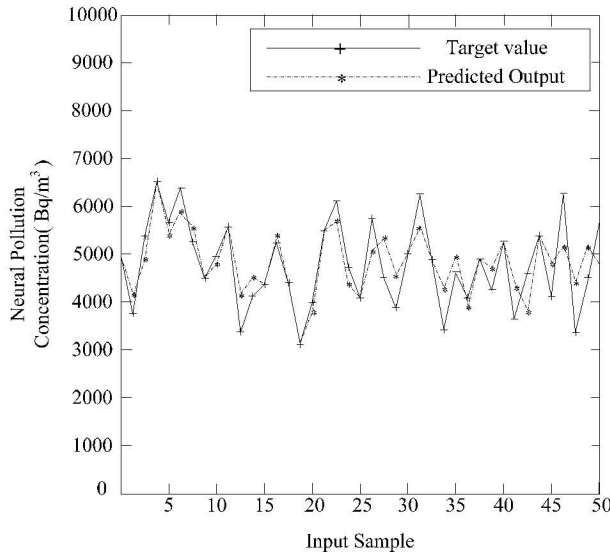


Fig. 5. Target and predicted values for pollution concentration using a traditional RBF neural network

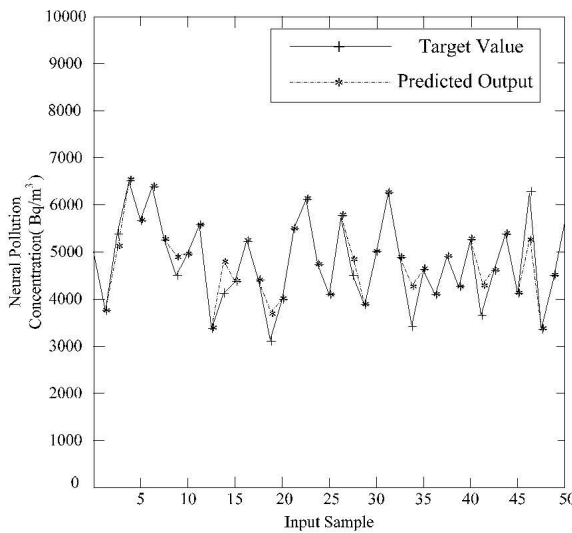


Fig. 6. Target and predicted values for pollution concentration using improved RBF neural network

Table 1. Performance for the two models

Model Category	sample set	hidden nodes	mean absolute percentage error	root-mean-square error
Traditional RBF neural network	A	8	0.007394	2.045×10^{-7}
	B		0.004930	0.003624
RBF neural network based on improved genetic algorithm	A	8	0.005635	3.2156×10^{-7}
	B		0.002245	0.001973

5 Conclusion

This paper adopted a neural network approach to predict the concentration of nuclear pollution, and proposed an improved RBF neural network model based on a genetic algorithm. The purpose of the model was to address the problem of nuclear pollution diffusion. The improved model optimizes the neural net-

work parameters by using an improved genetic algorithm, and enhances the ability for nonlinear approximation of a RBF neural network. Based on our simulation results, the proposed model had a faster convergence rate and more accurate forecasting results than the traditional RBF neural network

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