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A hybrid approach of support vector regression with genetic algorithm optimization for aquaculture water quality prediction

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ABSTRACT

Water quality prediction plays an important role in modern intensive river crab aquaculture management. Due to the nonlinearity and non-stationarity of water quality indicator series, the accuracy of the commonly used conventional methods, including regression analyses and neural networks, has been limited. A prediction model based on support vector regression (SVR) is proposed in this paper to solve the aquaculture water quality prediction problem. To build an effective SVR model, the SVR parameters must be set carefully. This study presents a hybrid approach, known as real-value genetic algorithm support vector regression (RGA–SVR), which searches for the optimal SVR parameters using real-value genetic algorithms, and then adopts the optimal parameters to construct the SVR models. The approach is applied to predict the aquaculture water quality data collected from the aquatic factories of YiXing, in China. The experimental results demonstrate that RGA–SVR outperforms the traditional SVR and back-propagation (BP) neural network models based on the root mean square error (RMSE) and mean absolute percentage error (MAPE). This RGA–SVR model is proven to be an effective approach to predict aquaculture water quality.

1. Introduction

Aquaculture water is an important aspect of the river crab's habitat in the intensive breeding of river crab, and the water quality determines the growth status and product quality directly. Once the water quality deteriorates and the crabs are in a poor environment, it is very easy for there to be an outbreak of some diseases; also there is the decline in the quality and even a large number of dead river crabs in a short time, which will cause great economic losses to the farmers if remedial measures are not taken in a timely manner. So, taking advantage of modern information technology to have early warnings of water conditions and enable the dynamic change of water is an urgent and important matter.

Aquaculture water is an open, nonlinear, dynamic, complex system. Water quality is affected by many factors such as physics, chemistry, hydraulics, biology, meteorology, and human activities, and the water quality parameters are nonlinear, time varying, random and delayed, because of the interactions between them. Thus, it is difficult to describe them quantitatively using accurate mathematical models and to establish an accurate, perfect, nonlinear prediction model using traditional methods.

Prediction of water quality focuses mainly on lakes, rivers, reservoirs, estuaries, and other large expanses of water using the gray system theory, neural networks, statistical analysis methods, time series models, both in China and elsewhere.

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Partalas et al. studied the greedy ensemble selection family of algorithms for ensembles of regression models to solve the forecasting of water quality [1]; Feifei Li et al. established back-propagation (BP) and autoregressive (AR) versions of the short-term forecasting model to predict dissolved oxygen [2], Eun Hye Naa et al. designed a dynamic three-dimensional water quality model to predict phytoplankton growth patterns in time and space [3]; Han has presented a flexible structure radial basis function neural network (FS-RBFNN) to predict the wastewater biochemical oxygen demand (BOD) index [4].

Palani et al. developed a neural network model to forecast the amount of dissolved oxygen in seawater [5]; Bikash Sarkar proposed a water quality model to predict the changes of temperature in an indoor fish pond [6]; Yu Deng adopted a wavelet neural network model based on wavelet theory and neural network theory to forecast the drinking water permanganate index [7]. However, neural networks suffer from a few weaknesses, which include the need for numerous controlling parameters, difficulty in obtaining a stable solution, and the danger of over-fitting.

Support vector regression (SVR) is a novel learning machine based on statistical learning theory and a structural risk minimization principle, which has been successfully used for nonlinear system modeling [8]. Yunrong Xiang employed a least squares support vector machine (LS-SVM) and a particle swarm optimization model to predict the quality of a drinking water source [9]. Compared with artificial neural networks, an SVM provides more reliable and better performance under the same training conditions [10,11]. Although it has excellent features, SVR is limited in academic research and industrial applications, since the user must define various parameters appropriately. The SVR parameters must be set carefully in order to construct the SVR model efficiently [12–14]. Inappropriately chosen SVR parameters will result in over-fitting or under-fitting, and different parameter settings may also cause significant differences in performance [15]. Thus, selecting the optimal parameters is an important step in SVR design. However, no general guidelines are available to help in selecting these parameters [16–18]. So, we propose a hybrid approach of SVR with real-value genetic algorithm (RGA) optimization is developed by adopting an RGA to determine the SVR free parameters, and so the generalization ability and forecasting accuracy are improved in this study. The approach is used to forecast water quality in a high-density crab culture situation. The traditional SVR model and a BP neural network were also investigated for comparison. The experimental results show that an improvement in predictive accuracy and capability of generalization can be achieved by our proposed approach.

The structure of the paper is as follow. In Section 2, we introduce the real-value genetic algorithm (RGA) and support vector regression (SVR), and then the hybrid RGA–SVR model is proposed. Section 3 describes the data source and experimental setting and explains the process for determining the parameters of the RGA and SVR models. Section 4 discusses the results and analysis of the hybrid RGA–SVR model used in on-site aquaculture water quality prediction. Section 5 concludes the study, and suggests directions for future investigations.

2. Methodology

2.1. Genetic algorithms (GAs)

GAs are stochastic search techniques that can search large and complicated spaces using ideas from natural genetics and the evolutionary principle [19,20]. The idea of this method, which was inspired by the theory of natural evolution, was first proposed by Holland [21]. A genetic algorithm works with a population of individual strings (chromosomes), each representing a possible solution to a given problem. Each chromosome is assigned a fitness value according to the result of the fitness function. Highly fit chromosomes are given more opportunities to reproduce and the offspring share features taken from their parents. The GA is a simple but powerful tool for finding the global solution to an optimization problem. It is suitable for large-scale and complex nonlinear optimization problems, and it has the tendency to find the global optimal solution [22].

The procedure of a GA can be summarized in the following steps.

1. Choose a randomly generated population.
2. Calculate the fitness of each chromosome in the population.
3. Create the offspring by genetic operators: selection, crossover, and mutation.
4. Judge the stopping criteria. If the stopping criteria are met, the genetic algorithm would be stopped. Otherwise, repeat steps 2–4 using the generated offspring as the new starting population.

There are two types of coding method for GAs. They are real and binary-coded GAs. However, binary coding has some disadvantages, such as needing more memory, not being so flexible, and requiring a large amount of decode computation, so it is difficult to solve large-scale multi-parameter optimization problems using a binary coding genetic algorithm in a small-memory computer [23].

In contrast to the binary genetic algorithm (BGA), the real-value genetic algorithm (RGA) uses a real value as a parameter of the chromosomes in the population without the coding and encoding process prior to calculating the fitness value [24]. Thus, the RGA is more straightforward, faster, and more efficient. GAs have been used in a number of applications in engineering and social science. They have recently been applied, for example, to the optimization of the parameters of support vector machines for predicting bankruptcy [23], parallel searching for an optimal feature subset [25], and efficient selection and assignment of material handling equipment [26].

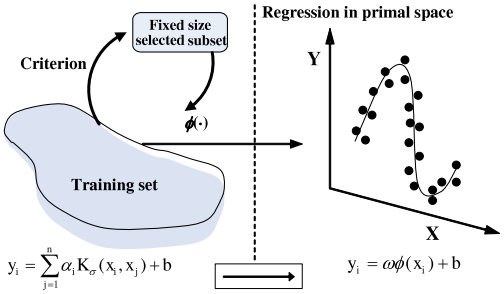

Fig. 1. Mapping input space x into high-dimensional feature space (from [27]).

2.2. Support vector regression

Support vector regression(SVR) is a promising technique. It follows the principle of structural risk minimization, which has been successfully used for data classification and regression ect nonlinear systems modeling [18]. We briefly introduce the basic idea of SVR.

In a typical regression problem, consider a training set $G = \{(x_i, y_i)\}_i^n \subset R^d \times R$, where x_i and y_i are the input variable vector and output variable, respectively, of the ith pair, and n denotes the total number of data patterns. SVR [17] is a kernel method that performs nonlinear regression based on the kernel trick. Essentially, each input $x_i \in R^d$ is mapped implicitly via a nonlinear feature map $\phi(\cdot)$ to some kernel-induced feature space F where linear regression is performed (see Fig. 1).

In SVR [17,8,28], the aim is to find a function $f(x)$ that has at most ε deviation from the actually obtained targets y_i for all the training data. Any deviation larger than ε is not accepted. To fulfill the stated goal, SVR considers the following linear estimation function:

$$f(x) = \omega\phi(x) + b$$
$$\phi : R^n \to F, \qquad \omega \in F, \tag{1}$$

where ω and b are coefficients; $\phi(x)$ denotes the high-dimensional feature space, which is nonlinearly mapped from the input space x.

The coefficients w and b can be estimated by minimizing the regularized risk function

$$R(f) = C\frac{1}{n}\sum_{i-1}^{n} L_\varepsilon(f(x_i) - y_i) + \frac{1}{2}\|\omega\|^2 \tag{2}$$

$$L(f(x, y)) = \begin{cases} |f(x) - y| - \varepsilon & |f(x) - y| \geq \varepsilon \\ 0 & \text{otherwise,} \end{cases} \tag{3}$$

where $||\omega^2||/2$ is the Euclidean norm, and it is adopted to estimate the flatness of a function, which can avoid over-fitting. The parameter ε is the difference between actual values and values calculated from the regression function. This difference can be viewed as a tube around the regression function. C denotes a cost function measuring empirical risk; it indicates a parameter determining the trade-off between the empirical risk and the model flatness. The constant $C > 0$ stands for the penalty degree of the sample with error exceeding ε. $L_\varepsilon(f(x_i) - y_i)$ is called the ε-insensitive loss function. C and ε are user-defined parameters in the empirical analysis [18].

The two positive slack variables ξ and ξ^* represent the distance from actual values to the corresponding boundary values of the ε-tube. A dual problem can then be derived by using the optimization method to maximize the function:

$$\max R(\alpha_i, \alpha_i^*) = \sum_{i-1}^{n} y_i(\alpha_i - \alpha_i^*) - \varepsilon\sum_{i-1}^{n}(\alpha_i + \alpha_i^*) - \frac{1}{2}\sum_{i=1}^{n}\sum_{j-1}^{n}(\alpha_i - \alpha_i^*)(\alpha_j - \alpha_j^*)K(x_i - x_j) \tag{4}$$

$$\text{Subject to } \sum_{i-1}^{n}(\alpha_i + \alpha_i^*) = 0, \quad a_i, a_i^* \in [0, C]. \tag{5}$$

Here, a_i and a_i^* are Lagrange multipliers, representing solutions to the above quadratic problem that act as forces pushing predictions towards the target value y_i. Only non-zero values of the Lagrange multipliers in Eq. (4) are useful in forecasting the regression line, and they are called the support vectors.

Then, we can obtain the optimal linear regression hyperplane by using the above-mentioned maximization function [18]:

$$f(x) = \sum_{i-1}^{n}(\alpha_i - \alpha_i^*)\langle x_i, x\rangle + b. \tag{6}$$

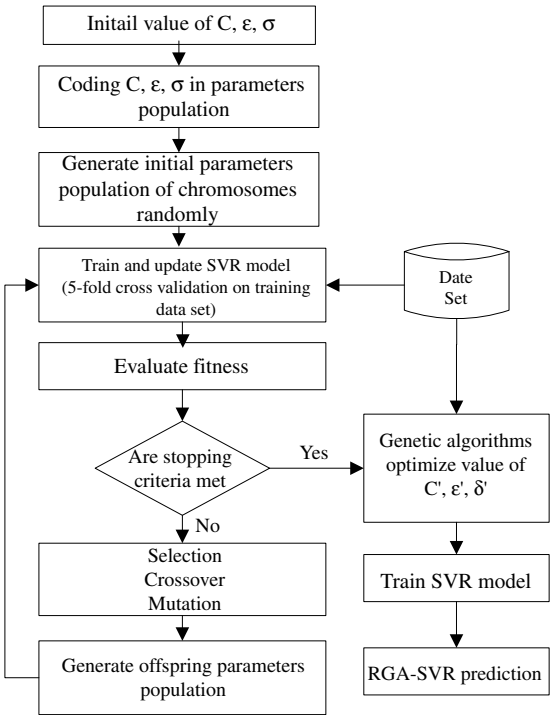

Fig. 2. RGA–SVR model.

To solve the nonlinear regression problem, the solution can be found by mapping the original problems to linear ones in a characteristic space of high dimension by a kernel function, which is denoted as $k(x_i, x_j) = \phi(x_i)\ \phi(x_j)$. Typical examples of the kernel function are the polynomial kernel ($K(x, y) = (x \times y + 1)^d$) and the Gaussian kernel ($K(x, y)) = \exp(-(x - y)^2/2\sigma^2$) [18]. In these equations, d represents the degree of the polynomial kernel, and σ^2 indicates the bandwidth of the Gaussian kernel. These parameters must be selected accurately, since they determine the structure of high-dimensional feature space and govern the complexity of the final solution. In this study, a radial basis function (RBF) is used as the kernel function in the SVR, where σ is the width of radial basis function.

Hence, the nonlinear regression function is

$$f(x) = \sum_{i-1}^{n} (\alpha_i - \alpha_i^*) K(x_i, x) + b. \tag{7}$$

2.3. RGA-based optimization of the SVR model

The SVR generalization performance (estimation accuracy) and efficiency depend on the hyperparameters (C, ε, and kernel parameter σ^2) being set correctly. However, no general guidelines are available to select these parameters. Most researchers still follow a standard procedure (trial and error) using the Grid algorithm, building a few SVR models based on different parameter sets first, then testing them on the validation set to obtain the optimal parameters. However, this procedure is time consuming; we attempted to use it, but were unable to converge at the global optimum. Therefore, we adopted a real-value genetic algorithm (RGA) to seek the optimal parameters of SVR in order to improve the efficiency of prediction. In the proposed RGA–SVR model, the values of the SVR parameters C, ε, and σ are directly coded in the chromosome with real-value data; we dynamically optimize the values of the SVR parameters through the RGA evolutionary process, and use the acquired parameters to construct an optimized SVR model in order to proceed with the forecasting.

Fig. 2 shows the framework of optimizing the SVR parameters with a real-value genetic algorithm, which is summarized as follows.

Step 1 (Code the chromosome). The SVR parameters C, ε, and σ are directly coded to generate the chromosome randomly. Here, the range of C is defined as [1,100], the range of ε is defined as [0.0001, 0.01], and the range of σ is defined as [0, 1]. The population size is 30.

Step 2 (Fitness definition). The fitness of the training data set is easy to calculate, but is prone to over-fitting. This problem can be handled by using a cross-validation technique. In this context, a five-fold cross-validation technique is used to overcome the over-fitting phenomenon [12]. In five-fold cross-validation, the training data set is randomly divided into five mutually exclusive subsets (folds) of approximately equal size ($k = 5$ suggested by Duan et al. [12]). The regression function is built

with the given set of parameters $\{C, \varepsilon, \sigma\}$, using four subsets as the training set. The performance of the set of parameters $\{C, \varepsilon, \sigma\}$ is measured by the root mean square error (RMSE) on the last subset. The above procedure is repeated five times such that each subset will be used once for validation. Averaging the RMSE over the five trials gives an estimation of the expected generalization error for training sets of size $(4 - k/5)$, where k is the number of training data sets.

Therefore, the fitness function is defined as the RMSE cross-validation on the training data set, given as follows:

$$\text{Min } f = \text{RMSE}_{\text{cross\_validation}} = \frac{1}{5}\sum_{i-1}^{5}\sqrt{\frac{5}{m}\sum_{j=1}^{k/5}(\alpha_j - p_j)^2}. \tag{8}$$

Here, a_j and p_j are the actual value and the predicted value, respectively. A solution with a smaller $\text{RMSE}_{\text{cross\_validation}}$ of the training data set has a smaller fitness value, and thus has a better chance of surviving in the successive generations.

Step 3 (Genetic algorithm operators). In the operators, a standard roulette wheel operation is performed to select excellent chromosomes to reproduce. Single-point crossover is randomly adopted to exchange genes between two chromosomes: the probability of creating new chromosomes in each pair is set to 0.5. The mutation operation follows the crossover operation, and determines whether a chromosome should be mutated in the next generation [29,25]. Each chromosome in the new population is subject to mutation with a probability of 0.02.

Step 4 (Stopping criteria). If the new population does not meet the termination condition, steps 3–4 are repeatedly executed until C, ε and σ are satisfied with minimum model error. The best C, ε, and σ would be output according to the optimum fitness function value.

3. Data collection and pre-processing of water quality in aquaculture river crab

3.1. Data acquisition

The pond being studied is monitored by a water quality monitoring system based on a wireless network system in real time. It has been equipped at China Agricultural University–YiXing Aquaculture Digital System Research Center in YiXing city, Jiangsu province, China.

The system consists of four parts: the data collection node, which detects the aquatic ecotope parameters using the wireless sensor, such as pH, dissolved oxygen (DO), electrical conductivity (EC), water temperature (WT), solar radiation (SR), air temperature (AT), and wind speed (WS); the routing nodes, which transfer the collected water quality parameter; the on-site monitoring center, which assists the on-site administrator in monitoring the water quality; and the remote monitoring center, which provides decision support. The data collection node connects to the intelligent sensor directly through an RS485 connector and sends the data from the intelligent sensor to the routing node through the wireless network. Then the routing node sends the data to the onsite monitoring center through the wireless network and to the remote monitoring center by General Packet Radio Service (GPRS). The system has operated in a stable manner for more than one year and has obtained many water quality parameters.

The data used in this paper spanned 15 days, from 5 July 2010 to 20 July 2010. The sampling interval is 10 min. At each 10 min interval, the dates change little, so we choose the dates every half hour as the forecast value, which means 48 sets of data collected per day, the total number of samples is 720.

The water quality data for aquaculture water quality prediction were split into two parts: the first 600 sets of water quality data were used for RGA–SVR modeling training and the last 120 sets of data as testing data to analyze the prediction performance of RGA–SVR.

3.2. Data pre-processing

In order to eliminate dimension differences, the following formula was used for data standardization and normalization, and then all input and output data were standardized and normalized to the range [0, 1].

$$x' = \frac{x - x_{\min}}{x_{\max} - x_{\min}}. \tag{9}$$

Here, x denotes the original data point, and $x_{\min}$ and $x_{\max}$ are the minimum and maximum values in the data set, respectively.

3.3. The design of an aquaculture water quality forecasting model based on RGA–SVR

For the SVR model, no standard procedure exists to determine the free parameters, C, ε, and σ. So the proposed RGA–SVR model dynamically optimizes the values of the SVR parameters C, ε, and σ. First, the RGA and five-fold cross-validation were applied for searching, obtaining better combinations of the SVR parameters when the $\text{RMSE}_{\text{cross\_validation}}$ value of the five-fold cross-validation is at its minimum. Then, the water quality forecasting model based on RGA–SVR is constructed.

The structure of aquaculture water quality forecasting system based on GA–SVR is shown in Fig. 3.

The water quality forecasting system is composed of data acquisition, data standardization pre-processing, forecasting, testing results, and application.

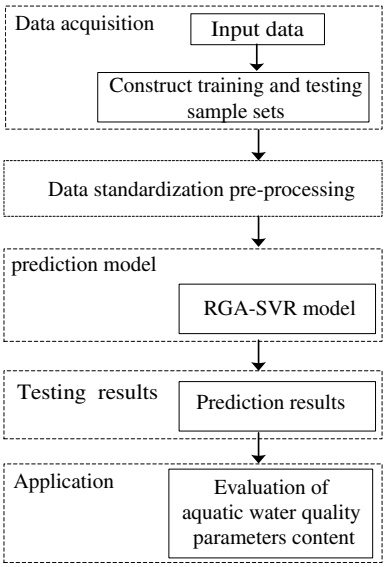

Fig. 3. Sketch map of relation between spatial resolution and local variance.

Table 1
Performance measure indicator comparison for different approaches (DO content).

Forecasting model parameters	RGA–SVR (C, ε, σ) = (5.671, 0.00025, 0.013)	SVR (C, ε, σ) = (7.832, 0.00043, 0.024)	BP-NN (learning rate = 0.086, sigmoid)
MAPE (%)	4.53	6.71	32.69
RMSE	0.0279	0.0653	0.324

Table 2
Performance measure indicator comparison for different approaches (water temperature).

Forecasting model parameters	RGA–SVR (C, ε, σ) = (5.671, 0.00025, 0.013)	SVR (C, ε, σ) = (7.832, 0.00043, 0.024)	BP-NN (learning rate =0.086, sigmoid)
MAPE (%)	2.631	5.753	23.276
RMSE	0.0195	0.051	0.283

4. Experimental results and discussion

4.1. Experimental results

During the experiments, since dissolved oxygen and water temperature are the most important factors affecting the growth of the river crab, we selected dissolved oxygen and temperature as the targets for water quality prediction. In our aquaculture water quality forecasting based on the RGA–SVR model, we adopt the current monitoring water quality values DO_i, pH_i, EC_i, WT_i, WS_i, SR_i as the RGA–SVR model input parameters, to predict DO_{i+1} and WT_{i+1} values, respectively, then the subsequent monitoring values DO and WT are compared and analyzed.

For evaluating and comparing the performance of the hybrid RGA–SVR approach, traditional SVR and BP neural network methods were also used for comparison. For the BP neural network, the learning rate is 0.086 and activation function is sigmoid: 5000 thousand training epochs were also adopted as the stopping criterion. We employed the mean absolute percentage error (*MAPE*) and root mean square error (RMSE) to evaluate the forecasting accuracy. The smaller the values of these errors, the better the performance of the forecasting model. The forecasting results are shown in Fig. 4 and Fig. 5. Fig. 4 shows the forecasting results of DO content for half-hourly time intervals (the ordinate gives the DO in units of mg/L, and the abscissa shows the training sample collection time points).

The prediction results of water temperature for half-hourly time intervals are shown in Fig. 5. Tables 1 and 2 show comparisons of the water quality parameter values for the three different approaches.

It can be observed that, for both RMSE and *MAPE*, RGA–SVR exhibits better generalization and prediction ability in the validation process than the traditional SVR and BP neural network methods. In terms of the two water quality indicators, the better prediction is water temperature, and then dissolved oxygen. This may be because the water temperature is less affected by external environmental factors, while the dissolved oxygen content is the result of a series of physical chemistry interaction processes, so the effects of other factors change over time.

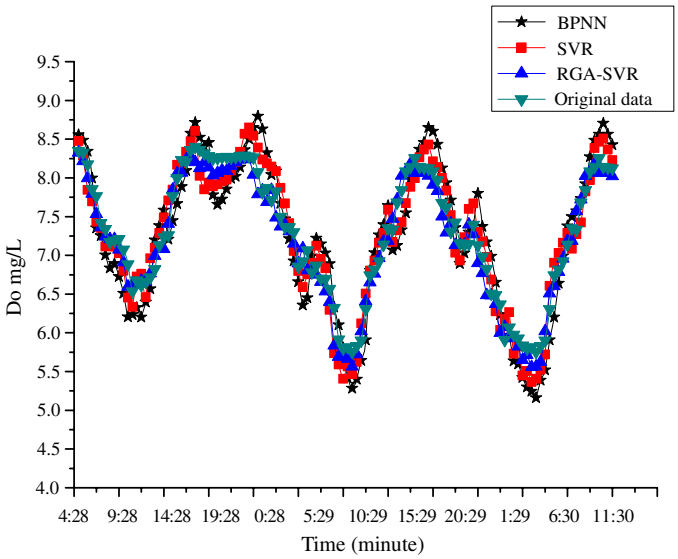

Fig. 4. DO content prediction.

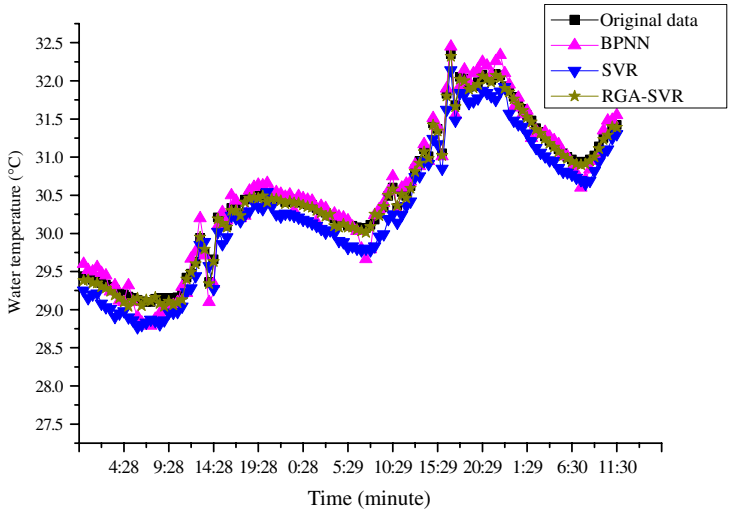

Fig. 5. Water temperature prediction.

Generally, the RGA–SVR forecast model has excellent performance. This is because RGA–SVR implements the principle of structural risk minimization in place of experiential risk minimization, which gives it excellent generalization ability for small sample sizes. And it has no requirement in data series distribution, also can be in the wake of changing disciplinarian of data. Thus, the prediction error of RGA–SVR is also small when the data exhibit great fluctuation. Through the above study, we can conclude from the results that the RGA–SVR algorithm is more suitable for the prediction of water quality than the BP neural network and traditional SVR methods.

5. Conclusion

Water quality prediction is very important for intensive aquaculture. It can help provide early warnings of the change of water quality and reduce the loss of aquaculture. The method introduced here employs a hybrid RGA–SVR approach for the forecasting of aquaculture water quality, in which a real-value genetic algorithm is used to select suitable parameters for SVR. The genetic algorithm consists in maintaining a population of chromosomes, which represent potential solutions to the problem to be solved. From actual experiments using monitored aquaculture water quality data from aquatic factories of YiXing in China, the hybrid approach of support vector regression with genetic algorithm optimization is able to provide reliable data on the water quality prediction of large-scale intensive aquaculture. The experimental results also suggest that the application of an artificial intelligence technique is perfectly suitable for the forecasting operation of nonlinear time

series problems. The RGA–SVR forecasting method can help avoid economic losses caused by water quality problems to a certain extent. However, in the training process of the RGA–SVR model, operation of the genetic algorithm is difficult: different types and rates of crossover and mutation need to be set for different problems. So, how to use advanced techniques to update the appropriate features and parameters of the proposed model will be an important direction for future development.

Acknowledgments

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