A Particle Swarm Optimization Based Verhulst Model for Prognostics

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Abstract

In data-driven prognostic methods, autoregressive moving average (ARMA) model requires stationary time series, and grey model (GM) can achieve high prediction accuracy only for exponential increasingly data sequence. To compensate these shortcomings, a novel prognostic method based on the improved Verhulst model optimized by particle swarm optimization (PSO) is proposed. Firstly, the Verhulst model based on the process that has the saturated condition is presented. Secondly, the traditional Verhulst model’s inaccuracy cause is analyzed. Thirdly, based on the inaccuracy cause, the background value of the Verhulst model is reconstructed by the PSO algorithm. Moreover, to improve prediction accuracy, at the prediction stage, the information contained in the data is updated through metabolism. Finally, to validate our proposed approach, two experiments are conducted to compare the improved Verhulst model with ARMA model, GM (1, 1) model and grey relevance vector machine (GRVM), respectively. The experiments results show that: (1) the improved Verhulst model is more suitable to describe the process that has the saturated condition than ARMA model, GM (1, 1) model and GRVM model; (2) the improved Verhulst model has smaller prediction errors evaluated by mean absolute error (MAE), mean square error (MSE), mean absolute percentage error (MAPE) and root mean square error (RMSE); (3) the improved Verhulst model has a high efficiency.

Keywords: Prognosis, Verhulst Model, Background Value Reconstruction, Particle Swarm Optimization, Metabolism

1. Introduction

Prognostics and health management (PHM) is an enabling discipline consisting of technologies and methods to assess the reliability of a product in its actual life cycle conditions to determine the advent of failure and mitigate system risk [1]. Assessing the extent of deviation or degradation from an expected normal condition for system or component can contribute to: (1) advance warning of failures; (2) minimizing unscheduled maintenance, extending maintenance cycles, and maintaining effectiveness through timely repair actions; (3) reducing the life-cycle cost of equipment by decreasing inspection costs, downtime, and inventory; (4) improving qualification and assisting in the design and logistical support of fielded and future systems [2]. Therefore, PHM is widely used in all kinds of fields nowadays. Miao et al. [3-4] used wavelets and hidden Markov models to monitor the condition of rotating machinery. Dai et al. [5-6] proposed prognostic approach based on risk mitigation for telecom equipment under free air cooling conditions. Long et al. [7-8] proposed diagnostics of filtered analog circuits with tolerance based on LS-SVM using frequency features. Chen et al. [9-10] used neuro-fuzzy and Bayesian algorithms to predict the machine health condition. He et al. [11-12] proposed a method to estimate the remaining useful life of lithium-ion batteries based on Dempster-Shafer theory and the Bayesian Monte Carlo method.

There are mainly two prognostic approaches: physics of failure (PoF) approach and data-driven approach. PoF prognostic methods rely on knowledge of system or component loading condition, material property, and failure mechanism, and tend to be computationally complex. This shortcoming confines its application [13]. For data-driven approaches, the main advantage is that it doesn’t require extensive knowledge on failure mechanism. Prognostic data is derived from measurable parameters such as voltage, current, and temperature [14]. The data-driven prognostic techniques can be classified

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into four categories [15]. The first category is time series prediction method, for example autoregressive moving average (ARMA) model, which can have a better prediction accuracy only if dynamic process is linear or stationary. The ARMA model is applied to forecast soft fault of analog filter circuit in literature [16]. Regression analysis prediction method is the second category, such as support vector machine (SVM), relevance vector machine (RVM) and so on. Although its advantage is good fitting performance for nonlinear sequence, it has a high demand on historical data. The grey relevance vector machine (GRVM) is employed to predict the ripple voltage of radar transmitter high voltage power supply in literature [17]. Neural network is the third category. Although we don't need to establish the mathematical model of the system based on neural network, it is known that the neural network prediction method has some shortcomings, such as a large number of samples, slow convergence rate and local extremum. A degradation model based on neural network for computing and updating residual life distributions is proposed in literature [18]. The last category is grey prediction method. Grey prediction methods have many advantages, such as small samples, simple implementation and being suitable for uncertain system. The properties of GM (1, 1) model and direct GM (1, 1) model are presented in literature [19]. High prediction accuracy can be obtained by using GM (1, 1) model or ARMA model when the data sequence has an exponential form. However, in practice, the data sequence often has the saturated condition, namely, increase slowly at initial stage, then speed up, finally, grow slowly or stop growing. Therefore, high prediction accuracy can not be obtained based on GM (1, 1) model or ARMA model. To solve this problem, the Verhulst model which is mainly used to describe the process that has the saturated condition is applied in this paper. However, the traditional Verhulst model can not predict with a high accuracy due to the background value construction. The particle swarm optimization (PSO) algorithm, therefore, is employed to reconstruct the background value of the Verhulst model. Moreover, to improve prediction accuracy, at the prediction stage, the information contained in the data is updated through metabolism.

This paper is organized as follows. In Section 2, the Verhulst model based on the process that has the saturated condition is presented. The construction steps of the Verhulst model is illustrated in detail. And the traditional Verhulst model inaccuracy cause is also explained explicitly in this Section. In Section 3, background value reconstruction of the Verhulst model based on the PSO algorithm is expounded. In Section 4, the prediction procedure of the improved Verhulst model is described. In Section 5, two experiments are conducted to compare the improved Verhulst model with ARMA model, GM (1, 1) model and GRVM model, respectively. Finally, some concluding remarks are given in Section 6.

2. Verhulst model

2.1. Verhulst model definition

Verhulst model derives from Malthusian model which is used to predict the biological reproduction [20-22]. The biological reproduction, Malthusian thought, increases in exponential form and it can be described as

\[ \frac{dp(t)}{dt} = ap(t) \]  
\[ p(t) = e^{at} \]  

where \( p(t) \) is the amount of biological reproduction, \( a \) is the constant.

The Malthusian model is suitably used to predict biological reproduction at the initial stage. However, it can not be suitably applied when the growth rate of biological reproduction gradually turns slowly influenced by a variety of factors. To solve this problem, a German biologist, Verhulst, came up with an approach to modify the Malthusian model in 1837. Therefore, the Verhulst model was obtained as the following [23-24]

\[ \frac{dp(t)}{dt} = ap(t) - b(p(t))^2, \quad p(0) = p_0 \]

where \( b \) is the constant, \((p(t))^2\) is the damping term which represents various adverse effects for biological reproduction. The solution of the equation (3) is
\[ p(t) = \frac{a/b}{1 + (a/b \frac{1}{p_0}) - 1}e^{-a(t-t_0)} \] (4)

where \( t_0 \) is the starting time, \( p_0 \) is the initial value of \( p(t) \).

As shown in Fig.1, the Verhulst model describes the trend that grow, roughly speaking, following the exponential law until a stability level is reached; in particular, the growth rate is initially increasing, then decreasing (in Fig.1, the model parameters are \( a = 4, b = 1 \) and \( p_0 = 0.5 \)) [25].

Hence, the Verhulst model can be mainly used to describe the process that has the saturated condition, namely, increase slowly at initial stage, then speed up, finally, grow slowly or stop growing. In real applications, the Verhulst model is often used to population projection, propagation prediction and economic life prediction of product, etc [26-29].

2.2. Verhulst model construction

In real applications, how to construct the Verhulst model based on specific data sequence is a significant problem. The steps of constructing Verhulst model are as follows:

1) Suppose a non-negative data sequence
\[ X^{(0)} = (x^{(0)}(1), x^{(0)}(2), \cdots, x^{(0)}(n)) \]

2) Apply accumulating generation operation (AGO) on the raw sequence
\[ X^{(1)} = (x^{(1)}(1), x^{(1)}(2), \cdots, x^{(1)}(n)) \]
where
\[ x^{(1)}(k) = \sum_{i=1}^{k} x^{(0)}(i), k = 1, 2, \cdots, n \]

3) Calculate the mean sequence \( Z^{(1)} \)
\[ Z^{(1)} = (z^{(1)}(2), z^{(1)}(3), \cdots, z^{(1)}(n)) \]
here,
\[ z^{(1)}(k) = \lambda x^{(1)}(k) + (1 - \lambda)x^{(1)}(k - 1) \] (5)
where generally \( \lambda = 0.5, k = 2, 3, \cdots n. \)

Then, the Verhulst model is defined as the following [20-21]
\[ x^{(0)}(k) + az^{(1)}(k) = b(z^{(1)}(k))^2 \] (6)
And the whitenization equation is be defined as [20-21]
\[
\frac{dx^{(1)}}{dt} + ax^{(1)} = b(x^{(1)})^2
\]  
(7)

4) Solve the parameter column \( \hat{a} = [a, b]^T \) of the equation (7) based on least square (LS) estimation
\[
\hat{a} = [a, b]^T = (B^T B)^{-1} B^T Y
\]  
(8)

where
\[
B = \begin{bmatrix}
-z^{(1)}(2) & (z^{(1)}(2))^2 \\
-z^{(1)}(3) & (z^{(1)}(3))^2 \\
& \vdots \\
-z^{(1)}(n) & (z^{(1)}(n))^2
\end{bmatrix},
Y = \begin{bmatrix}
x^{(0)}(2) \\
x^{(0)}(3) \\
\vdots \\
x^{(0)}(n)
\end{bmatrix}.
\]  
(9)

5) Obtain time response function of the Verhulst model
\[
x^{(1)}(k + 1) = \frac{ax^{(1)}(1)}{bx^{(1)}(1) + (a - bx^{(1)}(1))e^{-st}}, k = 0, 1, \ldots
\]  
(10)

where
\[
x^{(1)}(t)|_{t=1} = x^{(0)}(1)
\]

6) Acquire the Verhulst model of raw data sequence
\[
\hat{x}^{(0)}(k + 1) = \hat{x}^{(1)}(k + 1) - x^{(1)}(k), k = 1, 2, \ldots, n-1
\]  
(11)

where \( \hat{x}^{(0)}(k + 1) \) is the prediction value of original data sequence.

Note that, in practice, the saturated sequence already has some degree of exponential form, so the original sequence can be regarded as \( X^{(1)}(i) \) directly, this means that we need not apply AGO on \( X^{(0)}(i) \) to obtain \( X^{(1)}(i) \). And \( X^{(1)}(i) \) in (9) should be the inverse accumulated generating operation (IAGO) sequence of the original sequence.

2.3. Verhulst model inaccuracy cause

From equation (10)-(11), it can be seen that the prediction accuracy depends upon the parameters \( a \) and \( b \). And the parameters \( a \) and \( b \) rest on \( z^{(1)}(k) \) based on equation (8)-(9). Moreover, the value of \( z^{(1)}(k) \) lies on the \( \lambda \) based on equation (5). That is to say that the construction of background value \( z^{(1)}(k) \) is one of the key factors which lead to the prediction error. The background value error is shown in Fig.2.

![Figure 2. Error of background value](image)

Solve the integral between the intervals \([k - 1, k]\) for the equation (7) based on Fig.2, and then we can get the following
\[
\int_{k-1}^{k} \frac{dx^{(1)}}{dt} dt + a \int_{k-1}^{k} x^{(1)} dt = b \int_{k-1}^{k} (x^{(1)})^2 dt
\]

(12)

Namely

\[
x^{(0)}(k) + a \int_{k-1}^{k} x^{(1)} dt = b \int_{k-1}^{k} (x^{(1)})^2 dt
\]

(13)

(14)

Comparing the left side of equation (6) with (14), it can be seen that the actual background value is \( \int_{k-1}^{k} x^{(1)} dt \). From Fig.2, \( \int_{k-1}^{k} x^{(1)} dt \) stands for the area of curved edge shape ABCED. Obviously, the area of ABCD is always greater or equal to the area of ABCED. Therefore, this phenomenon results in the prediction error. To solve this problem and improve prediction accuracy, the PSO algorithm is employed to reconstruct the background value of the Verhulst model in this paper.

3. Background value reconstruction of Verhulst model

In Section 2.3, the cause of the traditional Verhulst model's inaccuracy is illustrated clearly due to \( \lambda = 0.5 \). To improve the prediction accuracy of the Verhulst model, the PSO algorithm is applied to optimize the parameter \( \lambda \) in equation (5) to reconstruct the background value of the Verhulst model.

3.1. PSO principle

In 1995, Kennedy and Eberhart proposed PSO algorithm inspired by the foraging behavior of birds [30-31]. The PSO algorithm has many advantages, such as simple concept, easy implementation, and quick convergence [31]. And it has been widely used in many fields such as function optimization, neural network training, data mining and fuzzy systems etc.

Its basic idea is that each solution of an optimization problem is called a particle and a fitness function is defined to measure the degree of superiority of every particle [32]. In a PSO system, it starts with the random initialization of a population of particles in the search space and works on the social behavior in the swarm. The position and the velocity of the \( i \)th particle in the \( d \)-dimensional search space can be represented as \( X_i = [x_{i,1}, x_{i,2}, \ldots, x_{i,d}] \) and \( V_i = [v_{i,1}, v_{i,2}, \ldots, v_{i,d}] \), respectively. Every particle has its own best position (pbest) \( P_i = [p_{i,1}, p_{i,2}, \ldots, p_{i,d}] \) corresponding to the personal best objective value obtained at time \( t \). The global best particle (gbest) is denoted by \( P_g = [p_{g,1}, p_{g,2}, \ldots, p_{g,d}] \) which represents the best particle found so far in the entire swarm [33-34]. The new velocity and position of every particle are updated based on the following equations [31]

\[
v_{i,j}(t+1) = w \cdot v_{i,j}(t) + c_1 \cdot r_1 \cdot (p_{i,j} - x_{i,j}(t)) + c_2 \cdot r_2 \cdot (p_{g,j} - x_{i,j}(t))
\]

(15)

\[
x_{i,j}(t+1) = x_{i,j}(t) + v_{i,j}(t+1)
\]

where \( c_1 \) and \( c_2 \) are acceleration coefficients, which are often set the random value between [0,2]; \( w \) is inertia weight coefficient; \( r_1 \) and \( r_2 \) are two independent random numbers uniformly distributed in the range of [0,1].

3.2. PSO improvement

The optimization performance of PSO is largely affected by the value of the inertia weight coefficient \( w \). Some studies show that a big weight coefficient is in favor of avoiding local minimum and a small weight coefficient contributes to convergence rate. Generally, to enhance the global
searching capability, a big value is given to the weight coefficient at the initial stage of searching. Then, the weight coefficient is set to a small value to speed up the convergence rate at the later period of searching. Therefore, the adaptive weight method is adopted as the following [35]

\[ w^k = w_{\text{max}} - \frac{(w_{\text{max}} - w_{\text{min}})}{\text{iteor}} k \]

where \( k \) is the times of iteration at present, \( \text{iteor} \) is the total times of iteration, \( w_{\text{max}} = 1.2, w_{\text{min}} = 0.5 \).

3.3. PSO procedure

The choice of fitness function is another primary factor to influence the performance of the PSO algorithm. To improve the prediction accuracy of the Verhulst model, the root mean square error (RMSE) is a better choice. The fitness function is defined as

\[ \text{fit}(x) = \min\left(\sqrt{\frac{1}{N} \sum_{i=1}^{N} (x_i - \hat{x}_i)^2}\right) \]

where \( N \) is the length of raw data sequence, \( x_i \) is the actual value, \( \hat{x}_i \) is the prediction value.

The procedure of PSO is summarized as follows:

Step 1: Set the initial parameters of PSO, such as particle number, the largest iteration numbers, maximum velocity, acceleration constant and inertia weight coefficient.

Step 2: Calculate the fitness of every particle.

Step 3: Update the velocity and place of every particle using the adaptive weight coefficient algorithm according to the velocity and place at present.

Step 4: Carry out step 5 if the iteration numbers are less than the total iteration numbers.

Step 5: Compute the fitness of new place for every particle. If the fitness of the particle is smaller than the original individual extremum \( p_{\text{best}} \), update the individual extremum. Otherwise, remain the same value.

Step 6: Get the latest global optimal solution \( g_{\text{best}} \) based on the individual fitness of every particle.

Step 7: Keep the old place, and update the velocity and place of each particle.

Step 8: Compare the fitness of old place with the fitness of new place. If the latter is less than the former, reserve the new place and the fitness of new place. Otherwise, reserve the old place and the fitness of old place.

Step 9: Run the step 4.

Step 10: Acquire the optimal solution.

Based on the procedure of PSO, the flowchart of background value reconstruction of the Verhulst model is shown in Fig. 3.
4. Verhulst model prediction

At the prediction stage, the information contained in the data is updated through metabolism. Its basic idea is that every new prediction value is added to the bottom of the raw data series when we predict backward and the earliest data point is to be removed from the raw data series to keep the dimension of the data sequence all the same. This data processing technology can contribute to improving the forecasting accuracy. The flowchart of the Verhulst model prediction is shown in Fig.4.
5. Experiments

To validate our proposed prognostic approach, we take two experiments to compare our proposed approach with ARMA model, GM (1, 1) model and GRVM model, respectively. In the first experiment, the ARMA model and GM (1, 1) model are used to compare the proposed approach, respectively. In the second experiment, we compare the proposed prognostic approach with GRVM model. In addition, to compare the improved Verhulst model with ARMA model and GM (1, 1) model furthermore, four error evaluation criteria including the mean absolute error (MAE), mean square error (MSE), mean absolute percentage error (MAPE) and root mean square error (RMSE) are adopted.

5.1. Comparing with ARMA model and GM (1, 1) model, respectively

In the first experiment, to compare the prediction accuracy of the improved Verhulst model with ARMA model and GM (1, 1) model, respectively, the original data sequence in literature [16] is used in this paper. The original data sequence and the curve are shown in Table 1 and Fig.5, respectively. In Table 1, there are 46 measurement data points which are the corresponding output voltage with the parameter changes in resistance of the leapfrog filter circuit. From Fig.5, it can be seen that the curve has concave down trend. The procedure of obtaining the data is illustrated clearly in literature [16]. In this experiment, the first 36 measurement data points are used as the training data. Then the improved Verhulst model, ARMA model and GM (1, 1) model are applied to predict the remaining 10 data points, respectively.

The specific prognostic procedure of the improved Verhulst model is as follows:
Step1: Input the 36 data points into PSO algorithm to reconstruct the background value of the Verhulst model, and obtain the optimal parameter \( \lambda \) based on Fig.3.

Step2: Construct the Verhulst model. Predict the value of the next step.

Step3: Based on metabolism data processing technology, update the training data.

Step4: If the backward prediction steps are not reached, run step1. Otherwise, carry out step5.

Step5: Exit the program.

The optimal parameter \( \lambda \) in equation (5) changes at every step based on the prognostic procedure. The parameter \( \lambda \) at the backward prediction 10 steps is shown in Table 2. The ARMA model has been used in literature [16]. Therefore, the GM (1, 1) model is applied to predict the remaining 10 data points. The 37th–46th data points’ prediction results of the proposed approach, ARMA model and GM (1, 1) model are shown in Fig.6.

In Fig.6, x-axis stands for data points; y-axis is the corresponding output voltage. In Fig.6 (b), to visualize the last three steps prediction results clearly, a small graph is embodied in Fig.6 (b). From Fig.6 (a), it can be seen that the improved Verhulst model prediction results are almost in accordance with the actual value; however, the GM (1, 1) model largely deviates from the actual value. From Fig.6 (b), it can be known that the improved Verhulst model and the ARMA model both have high prediction accuracy. But based on the small graph in Fig.6 (b), the ARMA model gradually deviates from the actual value and the improved Verhulst model still have high prediction accuracy.

Obviously, it can be seen that the prediction error of GM (1, 1) model is significantly larger than the other two models from Fig.6. To have better visual effects, compare the improved Verhulst model with ARMA model, GM (1, 1) model, respectively. The results of comparison are shown in Fig.7 and Fig.8.

### Table 1. The original data sequence

<table>
<thead>
<tr>
<th>S.N.</th>
<th>Output voltage</th>
<th>S.N.</th>
<th>Output voltage</th>
<th>S.N.</th>
<th>Output voltage</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>5.961</td>
<td>19</td>
<td>4.383</td>
<td>37</td>
<td>3.466</td>
</tr>
<tr>
<td>2</td>
<td>5.844</td>
<td>20</td>
<td>4.319</td>
<td>38</td>
<td>3.426</td>
</tr>
<tr>
<td>3</td>
<td>5.732</td>
<td>21</td>
<td>4.258</td>
<td>39</td>
<td>3.387</td>
</tr>
<tr>
<td>4</td>
<td>5.623</td>
<td>22</td>
<td>4.198</td>
<td>40</td>
<td>3.349</td>
</tr>
<tr>
<td>5</td>
<td>5.519</td>
<td>23</td>
<td>4.139</td>
<td>41</td>
<td>3.312</td>
</tr>
<tr>
<td>6</td>
<td>5.419</td>
<td>24</td>
<td>4.083</td>
<td>42</td>
<td>3.275</td>
</tr>
<tr>
<td>7</td>
<td>5.322</td>
<td>25</td>
<td>4.028</td>
<td>43</td>
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</tr>
<tr>
<td>8</td>
<td>5.229</td>
<td>26</td>
<td>3.974</td>
<td>44</td>
<td>3.205</td>
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<tr>
<td>9</td>
<td>5.139</td>
<td>27</td>
<td>3.922</td>
<td>45</td>
<td>3.171</td>
</tr>
<tr>
<td>10</td>
<td>5.052</td>
<td>28</td>
<td>3.871</td>
<td>46</td>
<td>3.137</td>
</tr>
<tr>
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<td>4.967</td>
<td>29</td>
<td>3.821</td>
<td></td>
<td></td>
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<tr>
<td>12</td>
<td>4.886</td>
<td>30</td>
<td>3.773</td>
<td></td>
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<tr>
<td>13</td>
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<td>31</td>
<td>3.725</td>
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<td>14</td>
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<td>3.680</td>
<td></td>
<td></td>
</tr>
<tr>
<td>15</td>
<td>4.657</td>
<td>33</td>
<td>3.635</td>
<td></td>
<td></td>
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<tr>
<td>16</td>
<td>4.585</td>
<td>34</td>
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<tr>
<td>17</td>
<td>4.516</td>
<td>35</td>
<td>3.548</td>
<td></td>
<td></td>
</tr>
<tr>
<td>18</td>
<td>4.448</td>
<td>36</td>
<td>3.506</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

S.N. represents sequence number.

### Table 2. The parameter \( \lambda \) at the backward prediction 10 steps

<table>
<thead>
<tr>
<th>S.N.</th>
<th>Parameter ( \lambda )</th>
<th>S.N.</th>
<th>Parameter ( \lambda )</th>
</tr>
</thead>
<tbody>
<tr>
<td>37</td>
<td>0.501532</td>
<td>42</td>
<td>0.495106</td>
</tr>
<tr>
<td>38</td>
<td>0.502093</td>
<td>43</td>
<td>0.497107</td>
</tr>
<tr>
<td>39</td>
<td>0.506107</td>
<td>44</td>
<td>0.502677</td>
</tr>
<tr>
<td>40</td>
<td>0.494537</td>
<td>45</td>
<td>0.505500</td>
</tr>
<tr>
<td>41</td>
<td>0.494230</td>
<td>46</td>
<td>0.506030</td>
</tr>
</tbody>
</table>

S.N. represents sequence number.
Figure 5. Plot of the original data sequence curve

Figure 6.  
(a) Predict the 37th–46th data points based on GM (1, 1) model and the improved Verhulst model
(b) Predict the 37th–46th data points based on ARMA model and the improved Verhulst model
In Fig.7 and Fig.8, x-axis is the error criteria; y-axis stands for models; z-axis represents the value of errors. From Fig.7 and Fig.8, it can be seen that: (1) the errors of GM (1, 1) model are the largest; (2) the errors of the improved Verhulst model and ARMA model are both quite smaller than GM (1, 1) model; (3) the errors of the improved Verhulst model are the smallest.

Moreover, our proposed prognostic approach also has a high efficiency. The reasons are that: (1) the construction procedure of the Verhulst model is simple; (2) the PSO algorithm has a quick convergence rate. To illustrate the performance of the PSO algorithm with an example, we take the first 36 data points in Table 1 as the training data, and then the PSO algorithm is employed to search the optimal parameter $\lambda$ in equation (5). The varying curve of the optimal individual fitness is shown in Fig.9. From Fig.9, it can be seen that the PSO obtain a high convergence precision after 6 iteration times. In addition, the process of PSO searching only takes 0.531 seconds using a Pentium Core E5800 3GHz processor and 2 GB RAM under a Matlab 2009 environment. However, it is known that the procedure
of the ARMA model order determination is complicated. Because the construction procedure of the GM (1, 1) model is also simple, the efficiency of GM (1, 1) model is also high.

![The optimal individual fitness](image)

**Figure 9.** The varying curve of the optimal individual fitness

From Table2, Fig.5, Fig.6, Fig.7, Fig.8 and Fig.9, it can be concluded that: (1) the Verhulst model is more suitable to describe the concave down trend curve than ARMA model and GM (1, 1) model; (2) the improved Verhulst model is reasonable; (3) the prediction accuracy of the improved Verhulst model is high; (4) the improved Verhulst model has a high efficiency.

### 5.2. Comparing with GRVM model

In the second experiment, to compare the prediction accuracy of the improved Verhulst model with GRVM model, the original data sequence in literature [17] is used in this paper. The curve of the original data sequence is shown in Fig.10. In Fig.10, there are 40 measurement data points which are the ripple voltage of radar transmitter high voltage power supply. Moreover, it can also be seen that the curve has concave up trend. In order to be consistent with literature [17], the 21th–30th measurement data points are used as the training data, then the improved Verhulst model, GRVM model are applied to predict the remaining 10 data points, respectively. The prediction results of the improved Verhulst model and GRVM model are shown in Table 3. The prediction errors of the improved Verhulst model and GRVM model evaluated by MAE, MSE, MAPE and RMSE are shown in Table 4.

![Plot of the original data sequence curve](image)

**Figure 10.** Plot of the original data sequence curve

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A Particle Swarm Optimization Based Verhulst Model for Prognostics
Weiming Xian, Bing Long, Zhen Liu, Shulin Tian

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246
Table 3. Prediction results of the improved Verhulst model, GRVM model, respectively

<table>
<thead>
<tr>
<th>S.N.</th>
<th>Actual</th>
<th>P-V-I-V</th>
<th>P-V-GRVM</th>
<th>S.N.</th>
<th>Actual</th>
<th>P-V-I-V</th>
<th>P-V-GRVM</th>
</tr>
</thead>
<tbody>
<tr>
<td>31</td>
<td>49.48</td>
<td>49.3972</td>
<td>49.3798</td>
<td>36</td>
<td>66.00</td>
<td>65.4225</td>
<td>65.2664</td>
</tr>
<tr>
<td>32</td>
<td>52.36</td>
<td>51.9634</td>
<td>51.9625</td>
<td>37</td>
<td>70.25</td>
<td>69.9256</td>
<td>69.8157</td>
</tr>
<tr>
<td>33</td>
<td>54.95</td>
<td>54.7938</td>
<td>54.9165</td>
<td>38</td>
<td>76.00</td>
<td>75.0707</td>
<td>74.8151</td>
</tr>
<tr>
<td>34</td>
<td>58.10</td>
<td>57.9380</td>
<td>58.0990</td>
<td>39</td>
<td>82.80</td>
<td>80.9945</td>
<td>80.8560</td>
</tr>
<tr>
<td>35</td>
<td>61.37</td>
<td>61.4599</td>
<td>61.1895</td>
<td>40</td>
<td>89.87</td>
<td>87.8795</td>
<td>88.1805</td>
</tr>
</tbody>
</table>

S.N. represents sequence number.
P-V-I-V represents the prediction value of the improved Verhulst model.
P-V-GRVM represents the prediction value of the GRVM model.

Table 4. Prediction errors of the improved Verhulst model, GRVM model, respectively

<table>
<thead>
<tr>
<th>Error</th>
<th>Improved Verhulst model</th>
<th>GRVM model</th>
</tr>
</thead>
<tbody>
<tr>
<td>MAE</td>
<td>0.651470</td>
<td>0.669901</td>
</tr>
<tr>
<td>MSE</td>
<td>0.874715</td>
<td>0.896609</td>
</tr>
<tr>
<td>MAPE</td>
<td>0.008589</td>
<td>0.008834</td>
</tr>
<tr>
<td>RMSE</td>
<td>0.935262</td>
<td>0.946894</td>
</tr>
</tbody>
</table>

Despite the improved Verhulst model is not always better than the GRVM model from Table 3, the prediction errors evaluated by MAE, MSE, MAPE and RMSE of the improved Verhulst model are all smaller than the GRVM model from Table 4. Moreover, although not all of the prediction values of the improved Verhulst model are better than the GRVM model, the overall prediction accuracy are higher than the GRVM model. In literature [17], the authors pointed out that RVM has many advantages over SVM. However, one shortcoming of RVM is that its training costs a longer period. Therefore, our proposed prognostic approach has a higher efficiency than GRVM model. And it can be concluded that the Verhulst model is more suitable to describe the concave up trend curve than GRVM model.

6. Conclusions

This paper proposes a novel prognostic method by using the improved Verhulst model optimized by PSO algorithm to compensate the drawbacks of the ARMA model and GM (1, 1) model. First, the traditional Verhulst model’s inaccuracy cause is analyzed. Then, based on the inaccuracy cause, the PSO algorithm is applied to reconstruct the background value of the Verhulst model. Moreover, to improve prediction accuracy of the improved Verhulst model, the metabolism data processing technology is employed to update the training set. To validate our proposed prognostic approach, two experiments are conducted to compare the improved Verhulst model with ARMA model, GM (1, 1) model and GRVM model, respectively.

The experiments results show that: (1) the improved Verhulst model is more suitable to describe the process that has the saturated condition than ARMA model, GM (1, 1) model and GRVM model; (2) the improved Verhulst model is more reasonable than the traditional Verhulst model; (3) the prediction accuracy of the improved Verhulst model is high; (4) the improved Verhulst model has a high efficiency.

7. References


