

# The Prediction of Apple Pests Based on CEEMD-GWO-GRU

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Received 1 March 2023; Revised 1 April 2023; Accepted 17 May 2023

**Abstract.** The study aimed to address the harm caused by frequent occurrence of *Carposina sasakii* by proposing a predictive model (GEEMD-GWO-GRU) and a warning mechanism. This model combined Complementary Ensemble Empirical Mode Decomposition (CEEMD) and Grey Wolf Optimization Algorithm (GWO) with Gated Recurrent Unit (GRU). The historical data on *Carposina sasakii* was first decomposed using CEEMD, then each eigenfunction modeled through GWO-GRU. Finally, the prediction of each eigenfunction was integrated to develop an apple and peach microcephalus prediction and early warning model based on GRU. Results indicated that the CEEMD-GWO-GRU model was more accurate in predicting apple *Carposina sasakii* disease compared to other methods, displaying an average absolute percentage error of 0.823% and a coefficient of determination of 0.961. This method has potential as a new strategy for agricultural pest and disease prediction.

**Keywords:** gated recurrent unit, Grey Wolf Optimisation, complementary integrated empirical mode decomposition, *Carposina sasakii*

## 1 Introduction

As the most grown fruit in China, apples cover an area of over 30 million acres and account for about 50% of the world's total fruit production [1]. *Carposina sasakii* Matsumura is one of the more frequent pests and diseases in apple growing. The *Carposina sasakii* eats fruit with its young, causing the fruit to fall off, resulting in fruit deformity, edible value reduction, loss of commodity value, the harm seriously affects the fruit yield and quality, and brings huge economic losses to the fruit industry every year [2]. It is found in China, as well as in Japan and Russia, and mainly affects apple, pear and peach fruits [3-4]. The disease occurs mostly from June to September [5], and its severity varies regularly with the season [2]. If we can predict the occurrence and severity of pests and diseases and take timely control measures, we can reduce apple yield to a certain extent.

Agricultural pest prediction models are divided into three main categories: static models, time-series dynamic models and spatial propagation models [6]. The following are examples of each of the three types of models in turn: M. Li et al [7]. used LVQ neural network, BP neural network and decision tree C4.5 algorithm proposed by J. Y. Su et al [8] performed spatio-temporal monitoring of wheat yellow rust based on temporal multispectral images, which provided important guidance for early monitoring of yellow rust at farm scale. Y. S. Kim et al [9] combined environmental conditions and long short term memory recurrent neural networks for early prediction of rice blast, the accuracy reached 67.4%. Y. F. Cao et al [10] studied rice disease early prediction based on temporal hyperspectral and multi-task learning focusing on the disease incubation period of the crop, which can guide the development of crop disease control strategies in a timely manner. In view of the difficulty in accurately predicting and simulating plant phenotypes, C. Y. Wang et al [11] took advantage of the spatial and temporal dependence of plant growth and development and proposed a plant growth and development prediction model based on ST-LSTM. X. Y. Peng et al [12] proposed an integrated prediction model based on EMD (empirical mode decomposition) and PSO-LSTM (particle swarm optimized long-and short-term memory neural network) to predict the ship's motion attitude. Ji et al [13] respectively to build a static early warning model for vegetable disease in facilities, and predicted the possibility of disease occurrence in predicted years according to climate conditions and soil environment. All the three models could accurately predict cucumber black star disease with an accuracy of ninety per cent. Q. Shen et al [16] proposed the temperature vegetation dryness index (TVDI) as a method of predicting the damage caused by bark beetles. Using Landsat8 data. W. Z. Tan [17] introduced

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Richard's function to describe the temporal dynamics of disease prevalence and constructed the EpiSimulator disease prediction model, which was highly accurate in predicting the timing and severity of the occurrence of rice blight and maize blotch in the short term. Kim et al [18] combined long time series meteorological data and the disease epidemiological model *epirice* to develop a model for predicting the temporal dynamics of rice leaf blight and blast.

In recent years, deep learning algorithms, represented by Long short term memory structure (LSTM) networks, have been widely used for the analysis of time-series data. Studies have shown that LSTM outperforms deep feedforward neural networks for time-series data [15]. LSTM can effectively learn sequential patterns from data containing temporal information by capturing long-term dependencies through memory units and gating mechanisms [14]. GRU simplifies its structure compared to LSTM. The calculation method of GRU's gate is similar to LSTM, so the parameters are much less than LSTM, resulting in less training time. Moreover, its performance in multiple datasets proves that GRU has accuracy performance no less than LSTM. Zhao et al [19] proposed a multi-point mushroom room temperature and humidity prediction method based on the combination of convolutional neural network (CNN) and gated recurrent unit neural network (GRU) for the characteristics of temporal, nonlinear, and spatial distribution variability in the mushroom room. In order to improve the prediction accuracy of daily average water demand of green pepper during the growing season, X. H. Lian et al [20] proposed a PSO-GRU (particle swarm algorithm-gated recurrent unit) model.

The above studies demonstrate the feasibility of the GRU algorithm for crop disease prediction, but the hyperspectral data and multi-species meteorological factor data used in the above studies are difficult for farmers to obtain, and there is a lot of noise interference in the acquired data. To address both of these issues, a grey complementary ensemble empirical pattern decomposition (CEEMD) and wolf optimisation algorithm (GWO) coupled with a long and short-term memory neural network (GRU) are proposed to build an *Carposina sasakii* insect disease prediction model (CEEMD-GWO-GRU). The original time series of *Carposina sasakii* numbers was simple for the farmer to obtain. Firstly, the data decomposed into a series of eigenfunctions using CEEMD, in this process the noise is eliminated, then the individual eigenfunctions were modelled using GWO-GRU, and finally the predictions of each eigenfunction were integrated to obtain the final results.

## 2. Pest's Prediction Models Based on CEEMD-GWO-GRU

### 2.1. Empirical Mode Decomposition

Empirical Mode Decomposition was proposed by Huang et al [21] and is applicable to non-linear, non-stationary signal processing. EMD can decompose signals of arbitrarily different scales based on local features of the signal to produce relatively smooth and characteristic scales of intrinsic mode function (IMF). The original sequence is therefore decomposed into an intrinsic mode function and residual components as in equation (1).

$$x(t) = \sum_{i=1}^m c_i(t) + r_m(t). \quad (1)$$

In the equation:  $m$  indicates the number of IMF,  $c_i(t)$  indicates the order of IMF,  $r_m(t)$  indicates residual component.

### 2.2. EEMD

The EEMD method was proposed by Wu and Huang et al [22] to improve the modal aliasing phenomenon. The method adds Gaussian white noise to EMD to give continuity to the signal at different scales, effectively avoiding the signal aliasing phenomenon caused by the discontinuity of IMF during EMD decomposition. The specific steps are as follows [23].

(1) Gaussian white noise  $n_i(t)$  with a mean of 0 and a constant standard deviation is added several times to the original signal  $s(t)$ .

$$x_i(t) = s(t) + n_i(t). \quad (2)$$

(2) EEMD decomposition of the signal  $x_i(t)$ . The result of the decomposition is expressed as:

$$x(t) = \sum_j IMF_j + residual. \quad (3)$$

$$IMF_j = \frac{1}{N} \sum_{i=1}^N IMF_{ij}. \quad (4)$$

In the equation:  $IMF_{ij}$  is the  $j$  th  $IMF$  component obtained by adding the white noise signal decomposition for the  $i$  th time.

### 2.3. CEEMD

Yeh et al [24] improved EEMD by adding random Gaussian white noise in positive and negative pairs, which empirically proved to be very effective in removing residual auxiliary noise from the reconstructed signal. The method is called Complementary Ensemble Empirical Mode Decomposition. CEEMD is divided into three main steps:

(1) Add  $n$  sets of positive and negative paired auxiliary white noise to the original signal, resulting in a set of  $2n$  signals.

$$\begin{bmatrix} M_1 \\ M_2 \end{bmatrix} = \begin{bmatrix} 1 & 1 \\ 1 & -1 \end{bmatrix} \begin{bmatrix} S \\ N \end{bmatrix}. \quad (5)$$

In the equation:  $S$  is the original signal;  $N$  is the auxiliary white noise;  $M_1, M_2$  is the signal after adding positive and negative paired white noise

(2) The EMD decomposition is performed on each signal in the set, and each signal is obtained as a set of IMF components, where the  $i$  IMF component of the  $j$  component is denoted as  $c_{ij}$ .

(3) Multi-component quantities are averaged to obtain decomposition results

$$c_j = \frac{1}{2n} \sum_{i=1}^{2n} c_{ij}. \quad (6)$$

In the equation:  $c_j$  denotes the  $j$  th IMF component obtained after decomposition.

### 2.4. Grey Wolf Optimizer

Based on a novel intelligent algorithm, Mirjalili et al [25] proposed the Grey Wolf Optimizer (GWO). The algorithm simulates the hierarchy and hunting behaviour of grey wolves in nature. The Grey Wolf Optimizer, a swarm intelligence optimisation algorithm that simulates the predatory behaviour of grey wolves, has the advantages of strong convergence, fewer parameters and easy implementation, and has stronger convergence speed and search capability than particle swarm algorithms (PSO) and bat algorithms (BA), and is therefore widely used for the adjustment and optimisation of model parameters [26-27]. The Grey Wolf Optimizer proposed by Mirjalili et al is shown in Fig. 1.

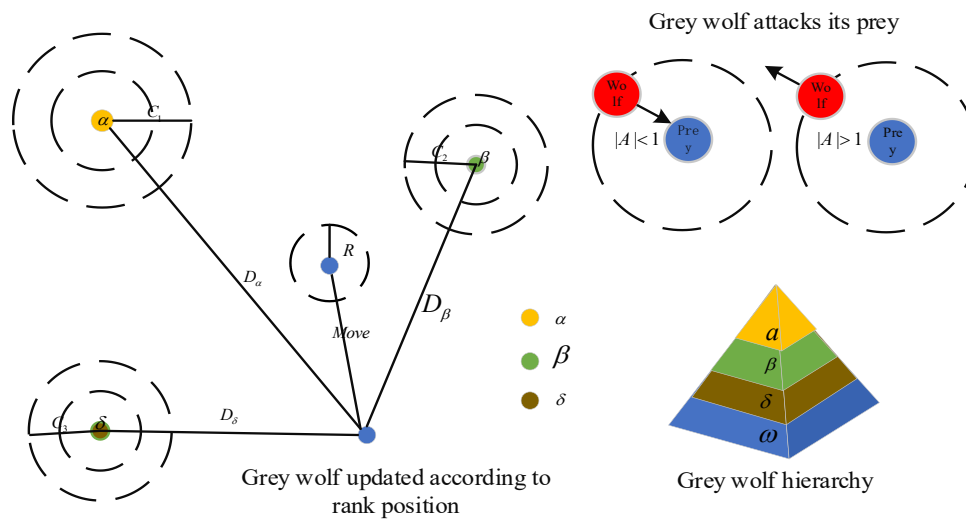


Fig. 1. Grey Wolf Optimisation Process

(1) Social Classes

There is generally a strict hierarchy within the grey wolf pack, with the whole pack being divided into four groups. The head wolf at the top of the pyramid is  $\alpha$ , whose role is mainly to make decisions about hunting behaviour. The second tier is  $\beta$ , which is the successor to  $\alpha$  when the pack is missing. The third tier is  $\delta$ , which follows the instructions of  $\alpha$  and  $\beta$ . At the bottom,  $\omega$  is the general member. The first three layers are, in order, the three best adapted groups and guide wolf  $\omega$  in its search towards the target.

(2) Surrounding the prey

During optimisation, location updates are made between individuals of the wolf pack, equation (7) represents the inter-individual distance and equation 2.8 represents the grey wolf update method.

$$\bar{D} = |\bar{C} \cdot \bar{X}_p(t) - \bar{X}(t)| \tag{7}$$

$$\bar{X}(t+1) = \bar{X}_p(t) - \bar{A} \cdot \bar{D} \tag{8}$$

In the equation:  $\bar{D}$  denotes the distance between the individual and the prey;  $t$  denotes the number of current iterations;  $\bar{X}$  denotes the position of the grey wolf;  $\bar{X}_p$  denotes the position of the food.

(3) Hunting attacks on prey

In order to mathematically model the hunting behaviour of the grey wolf, it is assumed that the grey wolf  $\alpha$  knows some information about the potential prey. On this basis, the top three best positions obtained so far are saved and the search agent must be updated according to the current three best positions, with the following update process.

$$\begin{cases} \bar{D}_\alpha = |\bar{C}_\alpha \cdot \bar{X}_\alpha - \bar{X}| \\ \bar{D}_\beta = |\bar{C}_\beta \cdot \bar{X}_\beta - \bar{X}| \\ \bar{D}_\delta = |\bar{C}_\delta \cdot \bar{X}_\delta - \bar{X}| \end{cases} \tag{9}$$

$$\begin{cases} \bar{X}_1 = \bar{X}_\alpha - \bar{A}_\alpha \cdot (\bar{D}_\alpha) \\ \bar{X}_2 = \bar{X}_\beta - \bar{A}_\beta \cdot (\bar{D}_\beta) \\ \bar{X}_3 = \bar{X}_\delta - \bar{A}_\delta \cdot (\bar{D}_\delta) \end{cases} \quad (10)$$

The completion of the hunt is marked by the prey stopping moving, a process that can be achieved by lowering  $\bar{a}$ . When the random value  $\bar{A}$  is at  $[-1,1]$ , the position between the next position of the search agent and the position of the prey is updated. In the algorithm, when  $|\bar{A}| < 1$  indicates a forced wolf attack on the prey.

### 2.5. Gated Recurrent Unit

Gated Recurrent Unit (GRU) is a neural network model proposed by Kyunghyun Cho et al. in 2014, which improves upon the Long Short-Term Memory (LSTM) model. GRU neural networks are a type of recurrent neural network (RNN). Traditional RNNs suffer from the problem of gradient disappearance and cannot efficiently process data with long-term dependencies. As a variant of RNN, LSTM neural network can learn long-term dependent information is shown in Fig. 2. Similar to LSTM neural network, GRU neural network is also a type of RNN that is capable of effectively retaining long-term dependence in time series data.

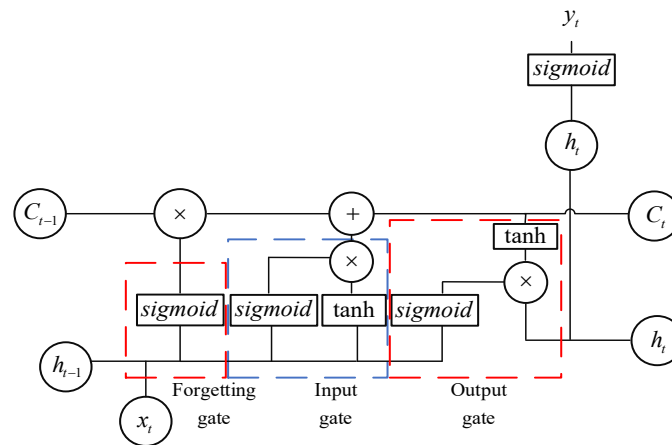


Fig. 2. Long short term memory structure

The structure of GRU neural network is shown in Fig. 3. In the picture,  $r_t$  is the resetting gates,  $u_t$  is the update gate,  $x_t$  is the input value at time  $t$ ,  $h_t$  is the output value at time  $t$ ,  $h_{t-1}$  is the hidden state of the previous moment.

As shown in Fig. 3 the working principle of GRU neural network is as follows:

(1) Resetting Gate

The gate gets a gated signal between 0 and 1

$$r_1 = \sigma(W_r h_{t-1} + W_r x_t). \quad (11)$$

In the equation:  $h_{t-1}$  is the hidden state of the previous moment,  $x_t$  is the input of the current time,  $W_r$  is their respective weight,  $\sigma$  is the Sigmoid function.

$$h_t = \tanh[(r_t \odot W'_h h_{t-1}) + W'_x x_t]. \tag{12}$$

In the equation:  $W'_h$ ,  $W'_x$  is respective weight of  $h_{t-1}$  and  $x_t$ ,  $\odot$  is multiplication of Hadamard;  $\tanh$  is Nonlinear activation function.

(2) Update Gate

The update and reset gates are computed in the same form, but for each gate, the result of multiplying the weight matrix with the input and hidden states is unique, which indicates that the final vector is different for each gate. The formula is as follow.

$$u_t = \sigma(W_z h_{t-1} + W_z x_t). \tag{13}$$

In the equation:  $W_z$  is the weight matrix corresponding to the Update gate output.

$$h_t = u_t \odot h_{t-1} + (1 - u_t) \odot \tilde{h}_t. \tag{14}$$

In the equation:  $u_t$  indicates selective memory,  $(1 - u_t)$  indicates selective forgetting

The GRU neural network has an advantage over the LSTM neural network because it can perform both selective memory and forgetting simultaneously using only one gate  $u_t$ , whereas LSTM requires multiple gates. Although the input/output structure of a GRU is similar to that of a standard RNN, its internal architecture is similar to that of an LSTM. The GRU has one fewer internal “gating” and fewer parameters than the LSTM, but it can achieve the same effect as the LSTM. Therefore, we have chosen the GRU neural network, which has high computing power and low time cost, as the neural network component for our fusion method.

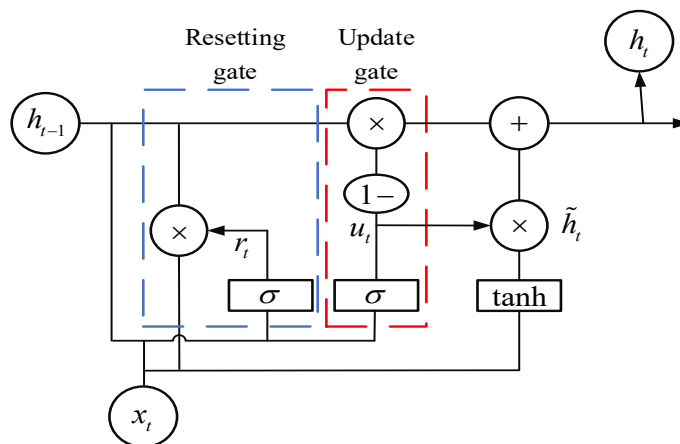


Fig. 3. Gated recurrent unit

### 3. Predictive Model Design for Pest in Apples

#### 3.1. Experimental Scheme

In this study, the main objective is to address the technical challenges associated with predicting and providing early warning for fruit diseases and pests. These challenges include low accuracy of traditional disease prediction methods, complex factors that contribute to the occurrence of agricultural diseases, and difficulties in obtaining

and processing data from farmers based on remote sensing and spectral data analysis. To overcome these limitations, a deep learning model was utilized to design an experimental scheme that focused on three specific areas: pest data collection and preprocessing, model training and evaluation, and fruit tree disease early warning. A flowchart of the overall test approach depicted in Fig. 4 was used.

Firstly, collected data on the small carnivores of apple and peach were preprocessed using empirical mode decomposition (EMD) and its derivative method to decompose the time series data of pests and diseases. This resulted in obtaining multi-scale features of the signal and addressing the non-periodic noise inherent in the data.

Secondly, different types of deep learning algorithms were employed to predict each intrinsic mode function, and various optimization algorithms were utilized to optimize the super-parameters in the deep learning algorithm. The accuracy of the prediction model was measured by comparing parameters such as mean absolute error ratio (MAPE), mean absolute error (MAE), root mean square error (RMSE), determination coefficient ( $R^2$ ), running speed, and other indicators.

Finally, the optimal disease and pest prediction model was used to train the test dataset and set a threshold for providing warnings to farmers. The model could forecast the onset of diseases and pests and send appropriate early warnings to farmers about exceeding the threshold.

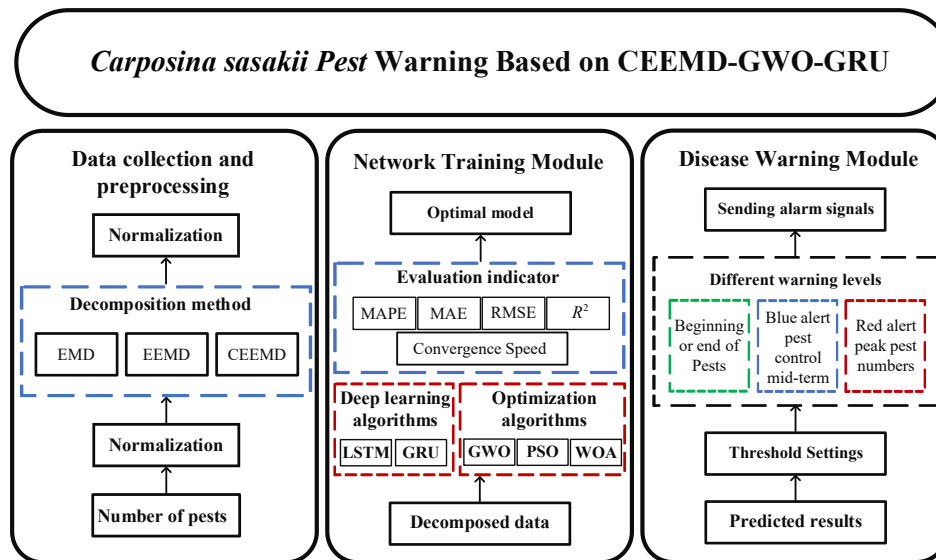


Fig. 4. Experimental scheme

### 3.2. Predictive Model Based on CEEMD-GWO-GRU

In order to improve the prediction accuracy of apple *Carposina sasakii* disease, the original time series of adult *Carposina sasakii* population was firstly processed by CEEMD method to obtain the IMF containing different features of the original data from high frequency to low frequency, and the residual component Residual. The GRU model parameters were optimally adjusted by using GWO, and the number of hidden layer units, learning rate and iteration number in the GRU network were used as wolf position, update the wolf position by calculating the fitness function, obtain the optimal solution of the GRU network model parameters, and use the optimal model parameters to construct the GWO-GRU model for prediction of each IMF component. Finally, the component prediction results are integrated and output as the final prediction results. The flow of the CEEMD-GWO-GRU based apple *Carposina sasakii* disease prediction model proposed in this paper is shown in Fig. 5. According to the flowchart, the specific steps for the construction of the CEEMD-GWO-GRU based apple *Carposina sasakii* disease prediction model are as follows.

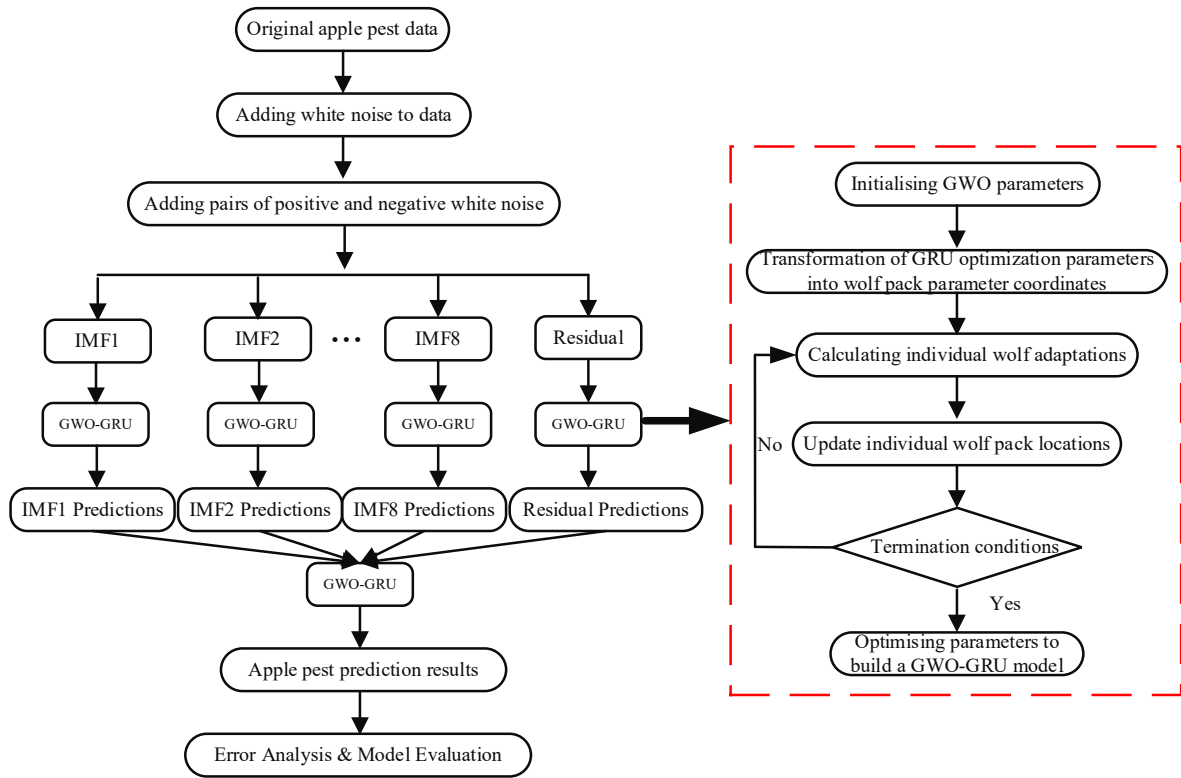


Fig. 5. Apple pest prediction model based on CEEMD-GWO-GRU

Step 1: The raw time series sample data on the dynamics of apple pest incidence are subjected to outlier removal, missing value supplementation and data normalisation, and the processed data are decomposed by CEEMD.

Step 2: The decomposed individual IMF components and residual components are divided into a training set and a test set in the ratio of 3:1 for the processed sample set.

Step 3: Determine the initial data of GWO, including the number of grey wolf populations, initial coordinates and number of iterations. The number of hidden layer units, learning rate and number of iterations of the GRU network are converted into the location coordinates of the wolves, and the training sample set is selected for the GRU to train the model.

Step 4: Calculate individual wolf fitness values, with the grey wolf fitness function set to

$$f = \sum_{i=1}^T (y - y_i)^2. \quad (15)$$

In the equation:  $y$  is the measured value,  $y_i$  is model predictions,  $T$  is length of time series, the smaller fitness function, the better the effect. Individual wolf positions are updated according to the fitness value. When the search reaches the maximum number of iterations or the global optimal position satisfies the minimum bound, the optimal solution is obtained for the three model parameters of the GRU network: number of hidden layer units, learning rate and number of iterations.

Step 5: The GRU network with the above optimised parameters is tested using a test sample set and the component predictions are integrated with the predictions of each modal component from step 2 to obtain the final CEEMD-GWO-GRU prediction results.



### 3.3. Predictive Model Evaluation

As shown in equations (3.2) to (3.4), the mean relative error (MAPE), mean absolute error (MAE), root mean square error (RMSE) and coefficient of determination ( $R^2$ ) of the actual and predicted values are chosen to measure the accuracy of the prediction model. The smaller the MAE and RMSE, the higher the accuracy of the prediction result, and the closer the value of  $R^2$  is to 1, the more accurate the prediction result.

$$MAPE = \frac{1}{N} \sum_{i=1}^N \left| \frac{\hat{y}_i - y_i}{y_i} \right| * 100\%. \quad (16)$$

$$MAE = \frac{1}{m} \sum_{i=1}^m |(y_i - \hat{y}_i)|. \quad (17)$$

$$RMSE = \sqrt{\frac{1}{m} \sum_{i=1}^m (y_i - \hat{y}_i)^2}. \quad (18)$$

$$R^2 = 1 - \frac{\sum_{i=1}^N (\hat{y}_i - y)^2}{\sum_{i=1}^N (y_i - y)^2}. \quad (19)$$

In the equation:  $y_i$  – True values for apple disease data;  $\hat{y}_i$  – Predicted values for apple disease data;  $m$  – Number of test sample sets;  $y$  – Average of true values.

## 4. Experimental Analysis

### 4.1. Experiment Dataset

The data in this paper are the dynamics of the number of adult *Carposina sasakii* insects occurring in the apple-producing region of Liaoning from 2019 to 2021 [28], and the collection sample site belongs to the Hot Spring Experimental Base of the National Plant Protection Xingcheng Observation and Experiment Station, Institute of Fruit Trees, Chinese Academy of Agricultural Sciences, Huludao City, Liaoning Province (N: 40.36'45", E: 120.44'09"), covering an area of 30.67 hectares. Three different golden crown gardens were selected for data collection, and five moth traps were hung randomly in each area, and moth traps were surveyed daily from May each year until September of that year, the range of captured pests is shown in Table 1 and three consecutive years and specific quantity as shown in Fig. 6. Improving the trapping process by using the visual perception-based vegetable pest trap counting method proposed by D. Q. Xiao et al [29] obtain more accurate pest data. The data can be used to support the determination of key control periods for the annual occurrence of regional *Carposina sasakii* moth populations and the prediction of pest occurrence.

**Table 1.** Adult *Carposina sasakii* population range 2019-2021

Parameters	2019 year	2020 year	2021 year
Number of moths caught daily	0~1.79	0~1.90	0~1.26
Maximum number of moths caught daily	10.13	12.67	7.74

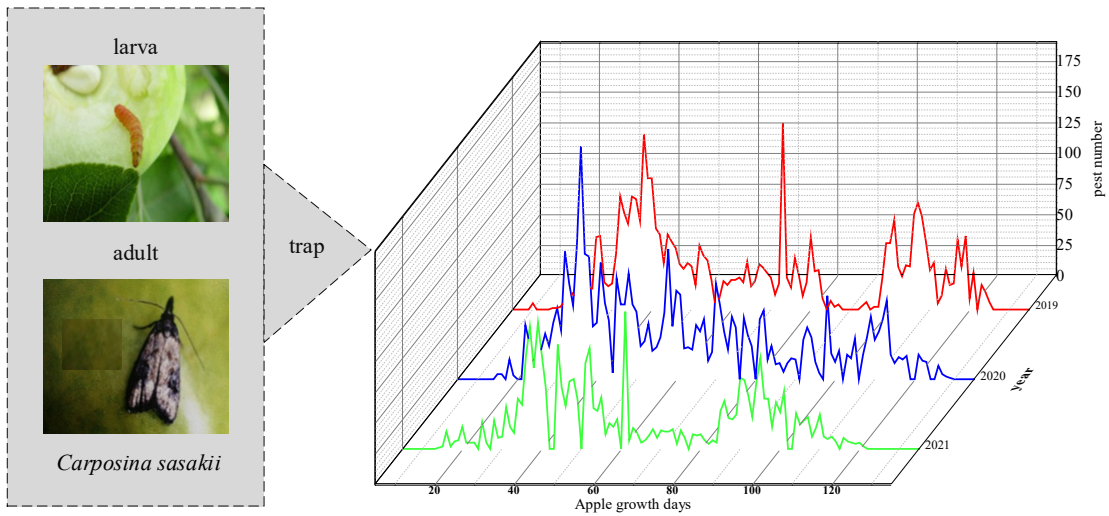


Fig. 6. Count the number of apple *Carposina sasakii* pests

#### 4.2. CEEMD Results

The sample data were divided into two sets: the training set and the test set. The first 360 data were used as the model training set and the last 120 data were used as the model test set. Considering generality, an iterative prediction model was used, with the first 3 points predicting the next point for overall prediction. Firstly, the raw data on the number of captured adult *Carposina sasakii* insects was CEEMD decomposed into IMF1, IMF2, IMF3, IMF4, IMF5, IMF6, IMF7, IMF8 and the residual component Residual. The decomposition of the raw signal is shown in Fig. 7.

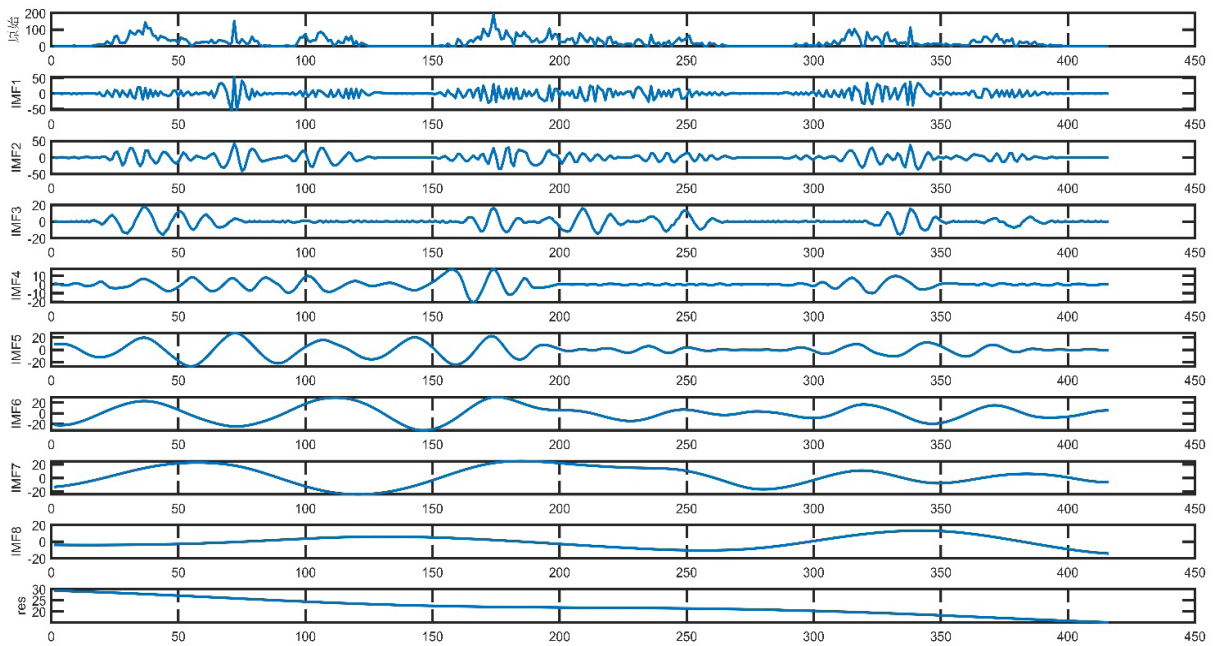


Fig. 7. Raw data decomposition diagram

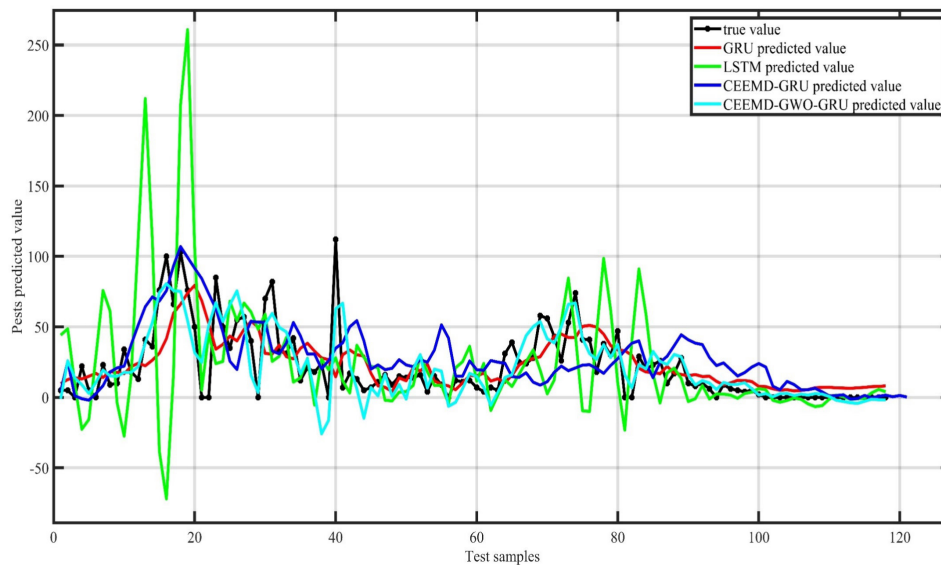
### 4.3. Comparison of Predictive Models

In order to verify the superiority of the proposed models in terms of prediction accuracy, a number of benchmark prediction models are introduced for comparison. Thus, single intelligent prediction models (GWO-GRU), ensemble models with different decomposition methods (EMD-GWO-GRU, CEEMD-GWO-GRU), as well as traditional (GRU, LSTM) with the same decomposition ensemble methods and models with different optimisation algorithms (CEEMD-PSO-GRU, CEEMD-BA-GRU).

In all of these models, LSTM networks with Sigmoid as the kernel function are employed and different optimisation algorithms are used to optimise the parameters of the GRU. The comparison of evaluation indicators predicted by different algorithms is shown in Table 2. The prediction plots for all models are shown in Fig. 8, where shows the fit of LSTM, GRU, CEEMD-GRU, and CEEMD-GWO-GRU to the measured values of the original sequences.

**Table 2.** Comparative analysis of model prediction accuracy

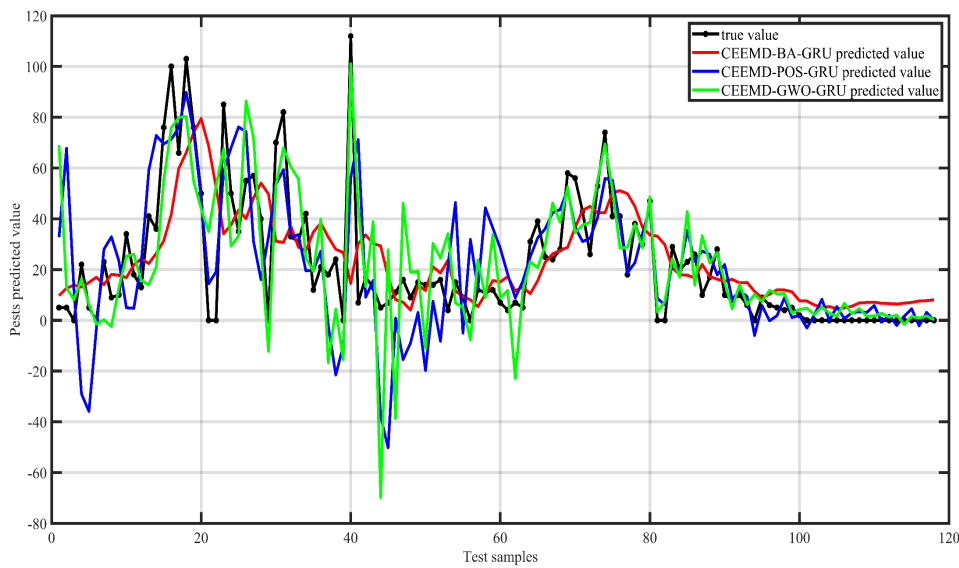
Model	RMSE	MAE	MAPE	$R^2$
GRU	$15.46 \pm 0.04$	$9.98 \pm 0.04$	$28.76 \pm 0.05\%$	$0.926 \pm 0.003$
LSTM	$34.74 \pm 0.05$	$13.08 \pm 0.05$	$37.74 \pm 0.05\%$	$0.841 \pm 0.003$
CEEMD-GRU	$10.11 \pm 0.05$	$6.47 \pm 0.05$	$10.57 \pm 0.03\%$	$0.947 \pm 0.003$
CEEMD-GWO-GRU	$9.72 \pm 0.05$	$5.17 \pm 0.05$	$8.23 \pm 0.03\%$	$0.961 \pm 0.003$



**Fig. 8.** Ablation experiment comparison curves

**Table 3.** Comparison of optimization methods

Model	RMSE	MAE	MAPE	$R^2$
CEEMD-BA-GRU	11.17	7.78	8.76	0.915
CEEMD-PSO-GRU	10.26	6.43	9.27	0.947
CEEMD-GWO-GRU	9.72	5.78	8.23	0.961



**Fig. 9.** Different optimization Model prediction comparison curves

(1) Whichever decomposition and aggregation model, including EMD, EEMD and CEEMD methods (EMD-GWO-GRU, EEMD-GWO-GRU, CEEMD-GWO-GRU) have higher prediction accuracy than the single intelligent model (GWO-LSTM). This result fully demonstrates that the idea of decomposition and aggregation can effectively improve the performance of the models and fully exploit the intrinsic properties of the data.

(2) For the decomposition methods, it is clear that the CEEMD method (CEEMD-GWO-GRU) predicts better than the original data alone using the GRU algorithm, with the three decomposition methods corresponding to MAPE values of 37.6%, 10.5% and 8.2% respectively. This performance is demonstrated by the fact that CEEMD overcomes both the problem of EMD modal confounding and the residual noise generated by EEMD.

(3) For the optimisation algorithm, it can be concluded that the prediction is more accurate after adding the GWO optimisation algorithm (CEEMD-GWO-GRU) than the (CEEMD-GRU) algorithm, due to the fact that the GWO optimisation algorithm can better maintain the balance between exploration and local optimality seeking. The problem of locally optimal solutions with fast convergence is avoided. The promote corresponding MAPE values for the four methods are 20.53%, 29.51%, 2.34% respectively.

(4) The CEEMD-GWO-GRU model has good prediction accuracy compared to the GRU model and GWO-GRU model. Table 3 shows the comparison of evaluation indicators predicted by different optimization algorithms. Compared with the CEEMD-BA-GRU, CEEMD-PSO-GRU, models optimized by different BA, PSO algorithms, the CEEMD-GWO-GRU model also has the best prediction accuracy as in Fig. 9.

#### 4.4. The *Carposina sasakii* Pest Warning

To help farmers estimate the start and end dates of *Carposina sasakii*, a blue warning is triggered when the number of pests caught in traps reaches 15, as indicated by the blue line in Fig. 10. This cue serves to indicate that a mild infestation has occurred in apples and that farmers should take measures such as employing apple fruit sacking to minimize the impact of the disease. The red line in Fig. 10 represents the predicted date for trapping 50 or more *Carposina sasakii*. Upon the appearance of this cue, a red warning message is sent to farmers, indicating that the infestation may be spreading rapidly and urging them to employ measures such as integrated biological control and physical control to contain the spread. In addition, farmers are provided with information on the error between past predictions and actual observations, as depicted in Fig. 11. With this information, they can more accurately determine the ideal timing for implementing pest control measures in accordance with meteorological factors.

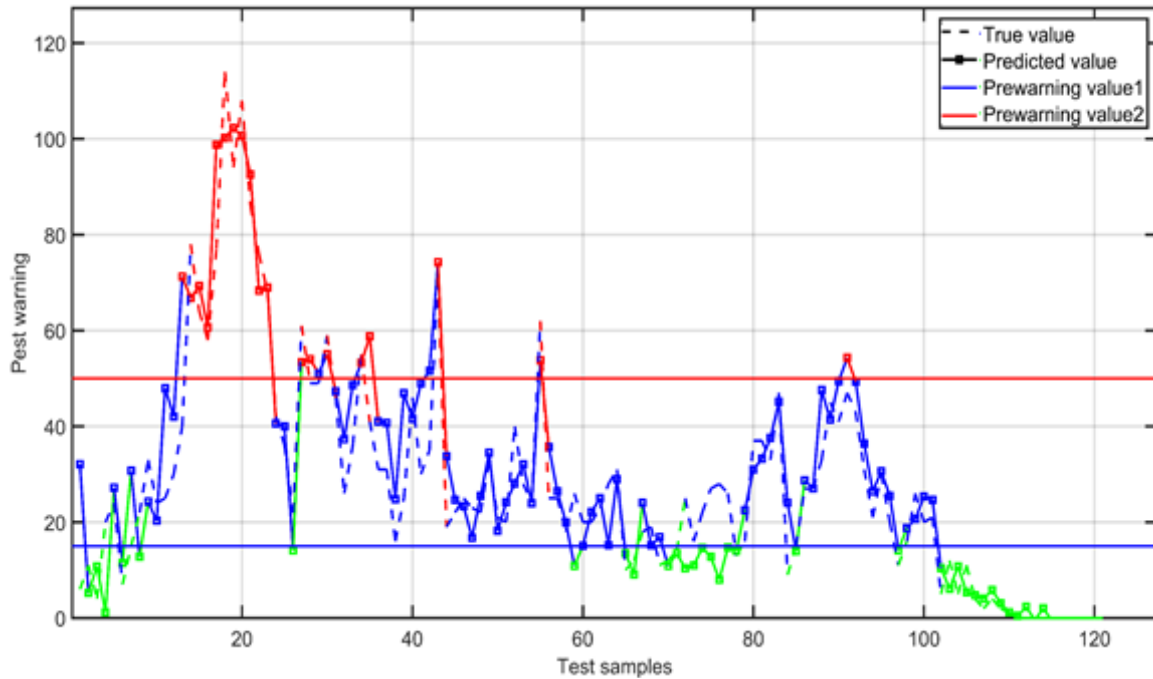


Fig. 10. *Carposina sasakii* pest warning

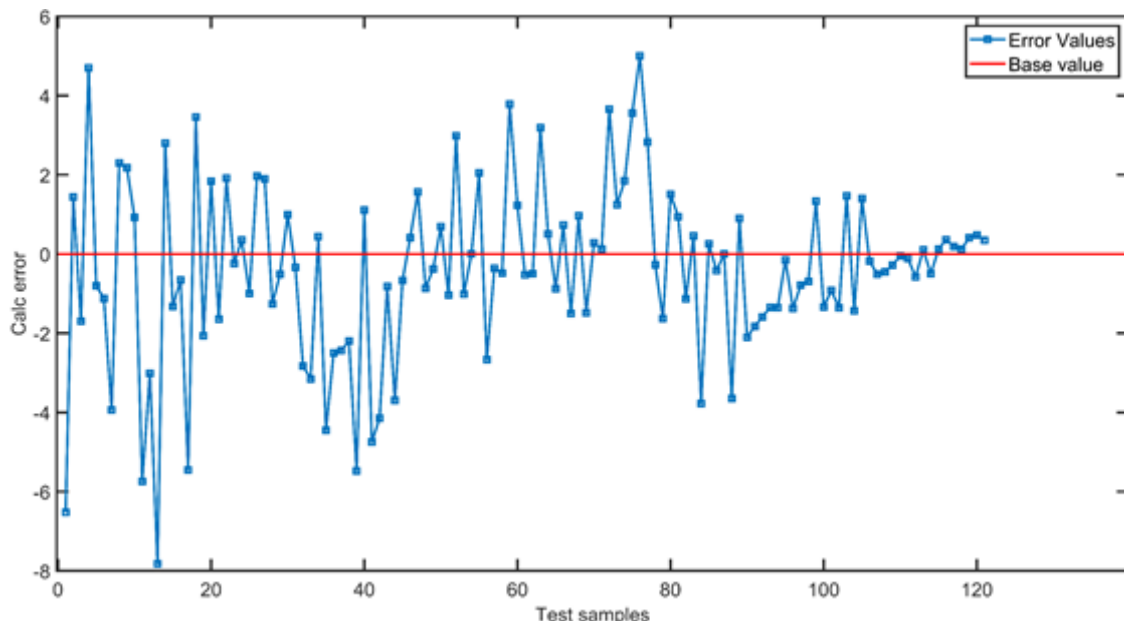


Fig. 11. Prediction errors

## 5. Conclusion

In this paper, a prediction model based on complementary integrated empirical modal decomposition and grey wolf optimisation algorithm to optimize gated recurrent unit neural network parameters is proposed and used for apple's *Carposina sasakii* disease prediction. The model is divided into three steps: firstly, the non-stationary time

series of the number of samples of captured peach *Carposina sasakii* is decomposed into a series of relatively stationary components by CEEMD; then, the GRU network is used to predict each component, and the parameters of the GRU are optimised using the GWO algorithm for the characteristics of each component; finally, the results of all the predicted components are integrated as the final results. In the experiments, the proposed CEEMD-GWO-GRU model was used for apple *Carposina sasakii* prediction, and the model has certain superiority compared with other benchmark models. The experiments demonstrate that relatively smooth components can be obtained by applying the CEEMD method to some highly volatile and irregular sequences, and then using the deep learning method for prediction, the prediction accuracy can be improved to a greater extent, resulting in feasible prediction results.

## Acknowledgement

This research was funded by the Major Project of Scientific and Technological Innovation 2030 (2021ZD0113603) and the Qin Xin Talents Cultivation Program of BISTU (QXTCPA202102).

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