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A novel prediction model based on decomposition-integration and error correction for COVID-19 daily confirmed and death cases

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ABSTRACT

Coronavirus disease (COVID-19) has infected billion people around the world and affected the economy, but most countries are considering reopening, so the COVID-19 daily confirmed and death cases have increased greatly. It is very necessary to predict the COVID-19 daily confirmed and death cases in order to help every country formulate prevention policies. To enhance the prediction performance, this paper proposes a prediction model based on improved variational mode decomposition by sparrow search algorithm (SVMD), improved kernel extreme learning machine by Aquila optimizer algorithm (AO-KELM) and error correction idea, named SVMD-AO-KELM-error for short-term prediction of COVID-19 cases. Firstly, to solve mode number and penalty factor selection of variational mode decomposition (VMD), an improved VMD based on sparrow search algorithm (SSA), named SVMD, is proposed. SVMD decomposes the COVID-19 case data into some intrinsic mode function (IMF) components and residual is considered. Secondly, to properly selected regularization coefficients and kernel parameters of kernel extreme learning machine (KELM) and improve the prediction performance of KELM, an improved KELM by Aquila optimizer (AO) algorithm, named AO-KELM, is proposed. Each component is predicted by AO-KELM. Then, the prediction error of IMF and residual are predicted by AO-KELM to correct prediction results, which is error correction idea. Finally, prediction results of each component and error prediction results are reconstructed to get final prediction results. Through the simulation experiment of the COVID-19 daily confirmed and death cases in Brazil, Mexico, and Russia and comparison with twelve comparative models, simulation experiment gives that SVMD-AO-KELM-error has best prediction accuracy. It also proves that the proposed model can be used to predict the pandemic COVID-19 cases and offers a novel approach for COVID-19 cases prediction.

1. Introduction

1.1. Research backward

In mid-December 2019, a number of patients with "unexplained pneumonia" began to appear in Wuhan, China. Through related disease tests, some experts have discovered a series of new SARS infection in succession. On January 12, 2020, the World Health Organization (WHO) named the new type of coronavirus as 2019-nCov. The increasingly severe epidemic gradually attracted the attention of countries around the world [1–3]. On February 11th, 2020, the pneumonia infected in novel coronavirus was named "COVID-19" (corona virus disease 2019), which is called COVID-19 for short. 2019 new coronavirus (2019-nCOV) is a new strain of coronavirus, which is mainly transmitted through respiratory droplets and is highly infectious [4,5], resulting in a rapid rise in the number of confirmed cases and deaths in the epidemic.

The epidemic caused by the outbreak of coronavirus not only threatens people's lives in a country or region, but also greatly reduces people's demand for going out, so tourism, catering, transportation and other industries have been affected to varying degrees, which resulting in huge economic losses. Due to the great impact of the epidemic on the global economy, society and people's daily life, as well as the rapid increase of infection cases in COVID-19, short-term prediction of infection cases is needed. It is particularly important that the accurate prediction results can be used to judge the development trend of epidemic situation. It can provide a reasonable and effective basis for the department to formulate better and more scientific epidemic prevention [6,7], thus indirectly ensuring people's life health and safety. At the same time, it

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also provides reference for various countries and regions to jointly carry out efficient joint prevention and control.

1.2. Literature review

In recent years, many scholars have done more and more research on the accurate prediction models of COVID-19 case. At present, the prediction models of COVID-19 case are mainly divided into three categories. The first category is the theoretical model, the second category is the single artificial intelligence model, and the third category is the decomposition-integration model.

(1) Theoretical model for prediction of COVID-19 cases mainly includes autoregressive integrated moving average (ARIMA) [8–10], seasonal autoregressive integrated moving average (SARIMA) [8] and so on. ArunKumar et al. [8] used auto-regressive integrated moving average (ARIMA) and seasonal auto-regressive integrated moving average (SARIMA) to forecast the cumulative COVID-19 cases in the top 16 countries. Through comparative model experiments, Guleryuz [9] proposed ARIMA model that can be applied in predicting fresh outbreak situations. Comparing exponential, logistic and Gompertz growth, Mangla et al. [11] used ARIMA model to predict COVID-19 cases in India and the result shows that ARIMA model has the best fitting effect. In the case study of COVID-19, most methods based on theory are adopted. Theoretical models are widely used in the prediction of COVID-19 cases because of their convenience and small amount of calculation. Influenced by actual environment, the obtained data of COVID-19 cases have nonlinear and non-stationary characteristics. However, these models ignore the inherent characteristics of data and are mostly suitable for linear data. Therefore, the theoretical model can't fully capture the development trend of the COVID-19 epidemic.

(2) Different from theoretical model, single artificial intelligence model, hereinafter referred to as single model, can usually deal with nonlinear data better. With the deepening of research, some scholars have proposed to use single model to predict COVID-19 cases, such as support vector machine (SVM) [1], long short-term memory (LSTM) network [12–14], and recurrent neural network (RNN) [15]. The convergence time of SVM algorithm is too long, which is not conducive to the rapid determination of COVID-19 cases prediction. Subsequently, the least square support vector machine (LSSVM) based on SVM has attracted much attention. Singh et al. [16] studied the COVID-19 case prediction model based on LSSVM and ARIMA, respectively, and the results show that the prediction accuracy of LSSVM is higher than that of ARIMA model, and also demonstrate the deficiency problems of ARIMA model. Luo et al. [17] used LSTM and extreme gradient boosting (XGBOOST) algorithms to predict the spread of COVID-19 in America. The result shows that LSTM has better COVID-19 cases prediction ability compared with the XGBOOST. Although these single artificial intelligence models have achieved good prediction result, they still face challenges. For example, LSTM model has poor prediction effect on small sample data and takes a long time [18], and the RNN also has some limitations in dependency and handling non-smooth continuous data. Neural networks generally have the disadvantage of over-fitting and long training time. In order to improve the prediction accuracy of COVID-19 cases, Li et al. [19] used extreme learning machine (ELM) to predict COVID-19 cases, and compared the prediction effects of ELM and LSTM. The experimental results show that ELM has a better prediction effect than LSTM. Some scholars tried to apply ELM to the field of prediction in COVID-19 cases. Chakraborty et al. [20] used ELM to predict COVID-19 cases, and achieved good prediction results. Due to the characteristics of ELM's random input weight and biases, the stability of prediction is poor. Thus, these shortcomings of the above model will affect the accuracy of prediction.

(3) The decomposition technology has started to receive attention from researchers in data preprocessing recently. The decomposition-integration model based on the idea of "first decomposition and then integration" has great advantages in dealing with non-stationary and nonlinear data, and its forecasting effect is better [21–24]. In order to further improve the prediction accuracy, some scholars have introduced the decomposition-integration model into the case prediction of COVID-19. The idea of this model is to firstly decompose COVID-19 cases data into several components, then predict each component with selected model, and finally reconstruct the prediction results of each component, which will achieve higher prediction accuracy. In the field of COVID-19 case prediction, decomposition-integration models mainly include models based on ensemble empirical mode decomposition (EEMD) [25–27]. For example, Qiang et al. [25] proposed a decomposition-integration model based on EEMD combined with ARIMA, and applied it to COVID-19 cases prediction in Pakistan. The decomposition-integration model in other literature [26,27] are similar to those in literature [25]. The research and experimental results of the above literature all show that the prediction accuracy of the decomposition-integration model is higher than that of the single model. However, EEMD has two faults such as the lack of strict mathematical theoretical basis [28–30] and the existence of mode mixing [31]. These two points will affect the prediction effect of COVID-19 cases. In addition, this paper summarizes the research status of COVID-19 cases prediction as shown in Table 1.

Table 1
The research status of COVID-19 cases prediction.

Models	References	Advantages	Disadvantages
Statistical models		Statistical models are accurate in predicting linear data, simple in structure and easy to implement.	Statistical models ignore the inherent characteristics of data and are mostly suitable for linear data.
ARIMA SARIMA	ArunKumar et al. [8]		
ARIMA	Guleryuz [9] Katris [10] Mangla et al. [11]		
Single artificial intelligence models		Intelligent models do not need to consider complex mathematical knowledge and have strong robustness.	Intelligent models may fail to achieve the best prediction results due to improper parameter setting.
SVM	Zagrouba et al. [1]		
LSTM	Chimmula et al. [12] Elsheikh et al. [13] Prasanth et al. [14]		
RNN	Li et al. [15]		
LSSVM	Singh et al. [16]		
XGBOOST	Luo et al. [17]		
ELM	Li et al. [19] Chakraborty et al. [20]		
Decomposition-integration models		The decomposition-integration model has great advantages in dealing with non-stationary and nonlinear data, and its forecasting effect is better.	EEMD has two faults such as the lack of strict mathematical theoretical basis and the existence of mode mixing.
EEMD-ARIMA	Qiang et al. [25]		
EEMD-ARIMAX	Da Silva et al. [26]		
EEMD-ANN	Hasan [27]		

1.3. Motivation

In recent years, machine learning has attracted the attention of researchers. ELM has the merit of strong universality and fast speed [32,33] and it has achieved good prediction results by applying different fields of prediction. Due to the characteristics [34,35] of ELM's random input weight and biases, the stability of ELM prediction is poor. However, kernel extreme learning machine (KELM) overcomes the shortcoming of poor stability of ELM prediction and improves the prediction accuracy of the algorithm [36,37]. KELM have been widely confirmed and applied to various fields of forecasting. For example, KELM has achieved good prediction results in predicting carbon prices [38], crude oil price [39], and oil production [40] so on. Therefore, KELM is adopted as the prediction method in this paper, which makes up for the lack of this technology in COVID-19 field. But, KELM needs to properly selected regularization coefficients and kernel parameters, which affected performance of KELM. Zhang et al. [39] used particle swarm optimization (PSO) to optimize the parameters of KELM model, which effectively improved the prediction accuracy. Aquila optimizer (AO) is a new optimization algorithm based on population. AlRassas et al. [40] proposed to improve adaptive neuro-fuzzy inference system (ANIFS) with AO algorithm and compared traditional optimization algorithms such as gray wolf optimizer (GWO), PSO and other improved ANIFS. The experimental results show that AO algorithm can best improve the prediction accuracy of ANIFS, which shows good optimization ability of AO. Therefore, this paper uses AO algorithm to adaptive choice the parameters of KELM, named AO-KELM.

Inspired by the recent literature based on decomposition-integration model in COVID-19 case prediction, decomposition technology is introduced into this paper. Comparing the disadvantages of EEMD, variational mode decomposition (VMD) [41] has higher decomposition resolution and solved the mode aliasing problem. So VMD can better capture the inherent characteristics of data [42,43] and has been widely used in various time sequence prediction [44–47]. The research on the case prediction in COVID-19 by using the idea of decomposition-integration has just started. VMD is applied to this paper, which further upgrade the prediction performance of COVID-19 cases. But, VMD needs to be preset the mode number K and penalty factor α. Unfortunately, these two parameters are usually set artificially. In recent years, many scholars have improved VMD by algorithm. Li et al. [48] used GA (genetic algorithm) to optimize the combination of VMD parameters in the aspect of fault diagnosis, which obviously improves the decomposition accuracy of VMD. Therefore, the selection of mode number and penalty factor plays an important role in VMD. However, GA algorithms are easy to fall into local optimum, and their convergence speed is slow. SSA is a new swarm intelligence optimization algorithm, which has strong optimization ability and fast convergence speed. Based on this, this paper will propose an adaptive decomposition method, which uses sparrow search algorithm (SSA) to adaptively select the number of modes and penalty factors for VMD, named SVMD, so as to avoid the blindness of VMD when setting parameters.

When VMD decomposes the original data, each intrinsic mode function (IMF) component is directly established after decomposition, ignoring the rich information contained in the residual. This will greatly affect the prediction effect. Therefore, the residual component is obtained by subtracting the decomposed integrated sequence from the original sequence, and the residual component is further predicted to obtain better prediction accuracy. Although decomposition greatly improves the prediction accuracy, the prediction error of each component will be superposed and the final error will increase. With the deepening of research, in order to obtain better prediction performance, some scholars introduced error correction [49,50] into time series prediction, which achieved good effect. So error correction is innovatively introduced into COVID-19 cases prediction.

1.4. Contributions & innovations

According to the above literature research and motivation analysis in COVID-19 case prediction, the mainstream prediction method is EEMD combined with single artificial intelligence model. Although these forecasting methods have achieved good results, most of them have the following problems:

➢ EEMD is easy to produce modal mixing and poor decomposition effect.
➢ The influence of the error after decomposition prediction on the accuracy is not considered.
➢ A single artificial intelligence model is easily influenced by its own parameter setting, ignoring the parameter optimization, which leads to poor and unstable prediction effect.

To avoid the above problems as much as possible, a novel prediction model based on SVMD, AO-KELM and error correction idea, named SVMD-AO-KELM-error, is proposed for COVID-19 daily confirmed and death cases. The innovative work and contributions in this paper is:

(1) The decomposition-integration model based on EEMD has the shortcomings of modal mixing and lack of theoretical basis. In order to avoid these shortcomings, this paper applies VMD to the prediction of COVID-19 daily cases and deaths, which improves the prediction accuracy.
(2) In order to solve the shortcoming of selecting the mode number K and penalty factor α of VMD, SVMD algorithm is proposed, which uses sparrow search algorithm to adaptively select K and α, so as to avoid the blindness of VMD when presetting parameters.
(3) In this paper, KELM is applied to COVID-19 prediction for the first time. But, KELM needs to properly selected regularization coefficients and the kernel parameters, which affected performance of KELM. Therefore, this paper uses AO algorithm to adaptive choice the parameters of KELM.
(4) Although decomposition-integration model has realized good prediction results, there are still some errors. To reduce the influence of errors on the prediction results, this paper uses the idea of error correction to deal with errors, which further improves the prediction effect.
(5) SVMD-AO-KELM-error is proposed. First of all, SVMD decomposes the COVID-19 cases data into some IMF and residual components. Secondly, each component is predicted by AO-KELM. Then, the prediction error of IMF and residual are predicted by using the idea of error correction. Finally, the prediction results of each component and error prediction results are reconstructed to complete the final prediction results. Through the simulation experiment of COVID-19 daily confirmed and death cases in Brazil, Mexico and Russia, and comparison with twelve comparative models, simulation experiment gives that SVMD-AO-KELM-error has higher prediction effect.

For convenience, the full name of the abbreviation used in this paper is shown in Appendix A.

2. Basic theory

2.1. Variational mode decomposition

VMD (variational mode decomposition) proposed in 2014 [41] is a completely non-recursive modal variation and signal processing method. According to the number of decomposition modes, VMD can adaptively search for the best center frequency and limited bandwidth of each mode, and realize effective separation of intrinsic mode function (IMF) and frequency domain division of signals. The core idea of VMD is to construct and solve variational problems. The specific steps are as follows:

Step 1. Construct a variational problem

Firstly, VMD decomposes the original signal $f(t)$ into mode functions $\{x_k(t)\}$. Next, the resolved signal of each mode function is obtained by Hilbert, and the corresponding one-sided spectrum is calculated. Then, the spectrum is multiplied with the exponential term $e^{-j\omega_k t}$ of the center frequency ω_k to transfer the spectrum of each modal function to the base band. Finally, the bandwidth is estimated by the Gaussian smoothness of the demodulated signal, and the sum of IMF bandwidths is minimized by a constraint equation [51]:

$$\begin{cases} \min\limits_{\{x_k\},\{\omega_k\}} \left\{ \sum_{k=1}^{K} \left\| \partial_t \left[\left(\delta(t) + \frac{j}{\pi t} \right) * x_k(t) \right] e^{-j\omega_k t} \right\|_2^2 \right\} \\ \text{s.t.} \sum_{k=1}^{K} x_k(t) = f(t) \end{cases} \tag{1}$$

where, $f(t)$ is the original signal, k is the mode number, $\{x_k\}$ *and* $\{w_k\}$ are the kth modal component and the center frequency after decomposition, $\sigma(t)$ is the unit impulse signal, and $*$ is the convolution symbol.

Step 2. Solve the variational problem

Firstly, the Lagrange equation with penalty factor α and Lagrange multiplier λ is added, which transforms Equation (1) into an unconstrained variational problem:

$$\begin{aligned} L(\{x_k\},\{\omega_k\},\theta) = {} & \alpha \sum_{k=1}^{K} \left\| \partial_t \left[\left(\delta(t) + \frac{j}{\pi t} \right) x_k(t) \right] e^{-j\omega_k t} \right\|_2^2 \\ & + \left\| f(t) - \sum_{k=1}^{K} x_k(t) \right\|_2^2 + \left\langle \theta(t), f(t) - \sum_{k=1}^{K} x_k(t) \right\rangle \end{aligned} \tag{2}$$

Then, the alternating direction multiplier iterative algorithm combined with the Fourier isometric transform is used to optimally obtain each modal component and central frequency. Search for the saddle point of the extended Lagrangian function by continuously updating $\widehat{x}_k^{n+1}(\omega), \omega_k^{n+1}$ *and* $\widehat{\theta}^{n+1}(\omega)$:

$$\widehat{x}_k^{n+1}(\omega) = \frac{\widehat{f}(\omega) - \sum_{k=1}^{K} \widehat{x}_k(\omega) + \frac{\widehat{\theta(\omega)}}{2}}{1 + 2C(\omega - \omega_k)^2} \tag{3}$$

$$\omega_k^{n+1} = \frac{\int_0^\infty \omega |\widehat{u}_k(\omega)|^2 d\omega}{\int_0^\infty |\widehat{u}_k(\omega)|^2 d\omega} \tag{4}$$

$$\widehat{\theta}^{n+1}(\omega) = \widehat{\theta}^{n}(\omega) + \gamma \left[\widehat{f}(\omega) - \sum_{k=1}^{K} \widehat{x}_k^{n+1}(\omega) \right] \tag{5}$$

where, $\widehat{x}_k^{n+1}(\omega)$ and w_k^{n+1} represent wiener filtering and center frequency of modes, respectively, and $\widehat{\theta}^{n+1}(\omega)$ represents Lagrange factor. When η satisfies Equation (6), the iteration is stopped.

$$\sum_{k=1}^{K} \frac{\|\widehat{x}_k^{n+1} - \widehat{x}_k^{n}\|_2^2}{\|\widehat{x}_k^{n}\|_2^2} < \eta \tag{6}$$

Finally, the original signal is decomposed into k modal components according to the optimal solution. Refer to Reference [41] for detailed steps of VMD.

2.2. Improved variational mode decomposition based on sparrow search algorithm

Sparrow search algorithm (SSA) is proposed in 2020 [52]. Its background is to imitate the foraging behavior of sparrows. In sparrow population, there are two behavior patterns such as discoverers and followers. Discoverers actively search for abundant food sources, provide foraging directions and areas, and followers get food through discoverers. During each iteration, the positions of discoverers and followers are updated respectively according to Equation (7) and Equation (8).

$$X_{j,i}^{t+1} = \begin{cases} X_{j,i}^{t+1} \exp\left(\frac{-j}{\alpha . iter_{\max}} \right), R_2 < S_{ST} \\ X_{j,i}^{t} + QL, R_2 \geq S_{ST} \end{cases} \tag{7}$$

$$X_{j,i}^{t+1} = \begin{cases} Q \exp\left(\frac{X_b - X_{j,i}^t}{i^2} \right), j > n/2 \\ X_p^{t+1} + \left| X_{j,i} - X_p^{t+1} \right| B^{+} L, j \leq n/2 \end{cases} \tag{8}$$

where, t indicates the iteration times of foraging process, $i = 1, 2, ..., m$, $iter_{\max}$ is the maximum number of iteration, $X_{j,i}^t$ is the jth dimensional position of the ith individual in the tth iteration; α is a random number between [0,1]; R_2 is the warning value, and the value is [0,1]; S_{ST} is a safe value, and the value is [0.5,1]; L is the n-dimensional unit column vector, Q is a random matrix with normal distribution. In Equation (8), X_p is that the optimal location searched by the current discoverer, X_b is the worst position in the current global situation; B is a row matrix of m columns, each element in B is assigned 1 or -1 and $B^{+} = B^T(BB^T)^{-1}$..

For convenience of description, making up 10%–20% in the population, this part of sparrows is called watchmen and Scout. The following is a description of its position update.

$$X_{j,i}^{t+1} = \begin{cases} X_c^t + \beta \left| X_{j,i}^t - X_c^t \right|, f_j > f_c \\ X_{j,i}^t + K \left(\frac{X_{j,i}^t - X_{Worst}^t}{(f_j - f_b) + \varepsilon} \right), f_j \leq f_c \end{cases} \tag{9}$$

where, K and β is the step control parameter, X_c represents the global optimal position, K represents the movement direction of sparrows and takes random numbers from -1 to 1, β obeys a normal distribution with a variance of 1 and a mean of 0; f_j is the fitness value of the jth current sparrow; To avoid zero error, ε is a minimal constant; f_c and f_b are the optimal and worst fitness values of current sparrow population, respectively.

VMD is adopted to decompose signals, and the decomposition level K of IMF should be preset according to experience. It will easily lead to information loss or over-decomposition. Through experiments, it is found that the penalty factor α that affect the decomposition effect. Due to the larger the magnitude of the penalty factor α, the lower the bandwidth of the IMF, and vice versa. Therefore, an improved VMD based on SSA is proposed, named SVMD. SSA optimizes the combination of K and α of VMD to avoid uncertainty of artificial setting and the flow chart of SVMD is given in Fig. 1. The following are the detailed steps of SVMD.

Step 1. Input the original sequence.

Step 2. Initialize the following parameters. Set the sparrow population size to 20 and the number of iterations to 10. Set the range of K of VMD to Refs. [3,9] and the range of α of VMD to [500,2000], and define [K, α] as the individual location of the sparrow search.

Step 3. Take multiscale multivariate fuzzy entropy (MMFE) as fitness function. The mean value of the MMFE of each IMF component after calculating the VMD decomposition is defined as the fitness value.

Step 4. If $t < G$, calculate the fitness value of the current individual, where t is the iteration number and G is the maximum iteration number. Sort fitness value out to seek out the current optimal f_c and f_b.

Step 5. Update the position of the sparrow (discoverer) of the previous fitness value by Equation (7). Use Equation (8) to update the position of the sparrow (follower) of the last fitness value. Use Equation (9) to

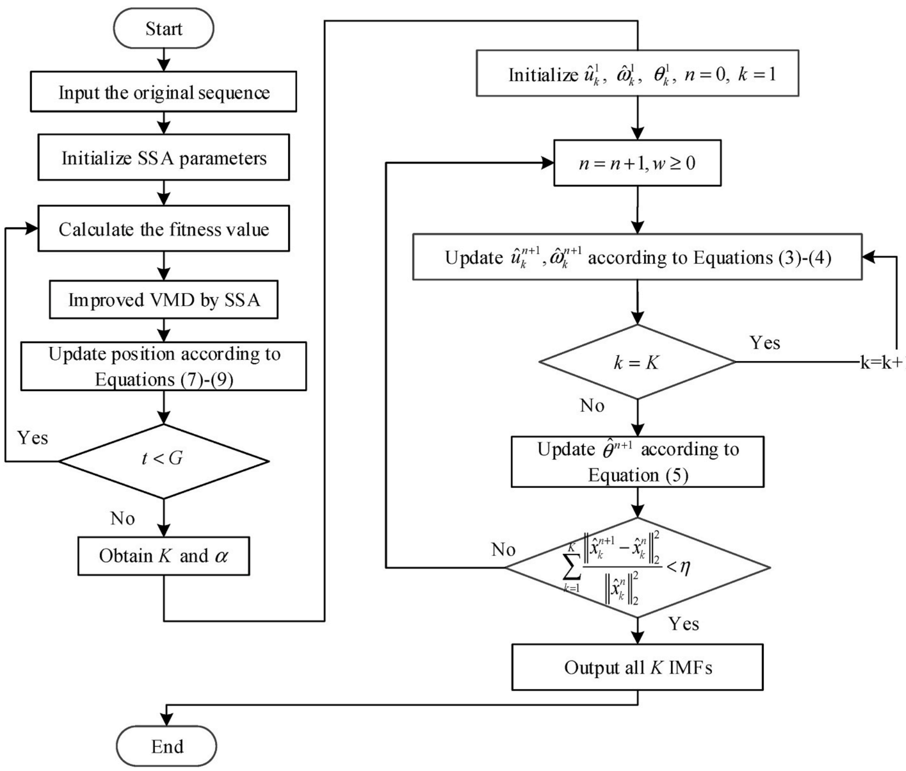


Fig. 1. Flow chart of SVMD.

randomly update the position of some sparrows (watchmen).

Step 6. Discoverer, follower and watchmen reaches the updated individual position by step 5. The current individual is computationally compared with the updated individual fitness value, and if the fitness value of the updated individual is smaller than that of the current individual, the updated individual position will be defined as the new sparrow position.

Step 7. Repeat steps 5 and 6.

Step 8. Else, output VMD optimal parameters $[K, \alpha]$.

Step 9. Set the decomposition level and penalty factor of VMD using the selected K and α respectively. By using VMD to decompose the original sequence, K IMFs were obtained.

Step 10. End.

2.3. Kernel extreme learning machine

Kernel extreme learning machine (KELM) is a single hidden layer forward network. Through the introduction of kernel function, KELM gets a modification based on ELM [53]. KELM has the merits such as better fast learning speed and generalization ability. So KELM has better performance and more stable, and been used in regression fitting problems [54–56].

For N different sets of samples of $\{(x_i, t_i)\}_{i=1}^{N}$, when the number of ELM implicit layer nodes is M and the excitation function is $g(\cdot)$, output function of ELM is as follows:

$$f_{\mathrm{ELM}}(x) = h(x)\beta = H\beta \tag{10}$$

where, β represents output weight vector between hidden layer and output layer. H is output matrix of corresponding hidden layer. The Equation of β and H is as follows:

$$H = \begin{bmatrix} h(x_1) \\ \vdots \\ h(x_N) \end{bmatrix} = \begin{bmatrix} g(\omega_1 x_1 + b_1)\cdots & g(\omega_M x_1 + b_M) \\ \vdots & \vdots \\ g(\omega_1 x_N + b_1)\cdots & g(\omega_M x_N + b_M) \end{bmatrix}_{N\times M} \tag{11}$$

$$\beta = \begin{bmatrix} \beta_1 \\ \vdots \\ \beta_M \end{bmatrix} \tag{12}$$

where, b is the bias of the hidden layer, ω is the weight between the input layer and the hidden layer.

ELM learning process can be equivalent to finding the optimal solution by using the least square method. In order to improve the stability and generalization ability of the model, the regularization coefficient C is introduced to obtain the least square solution, namely

$$\widehat{\beta} = H^T\left(\frac{I}{C} + HH^T\right)^{-1} T \tag{13}$$

where, I represents unit matri, T represents the target vector of the training sample. Then ELM's network output is as follows:

$$f_{\mathrm{ELM}}\left(x\right) = H\left(H^T\left(HH^T + \frac{I}{C}\right)^{-1} T\right) \tag{14}$$

When the specific form of feature map $h(x)$ of hidden layer is undiscovered, it will introduce kernel function to measure the similarity between samples. KELM kernel matrix can be defined according to Mercer condition, and then its network output is:

$$f_{\mathrm{KELM}}\left(x\right) = H\left(H^T\left(HH^T + \frac{I}{C}\right)^{-1} T\right) = \begin{bmatrix} K(x, x_1) \\ \vdots \\ K(x, x_N) \end{bmatrix} (I/C + \Omega_{\mathrm{KELM}})^{-1} T \tag{15}$$

It can be seen from Equation (15) that the kernel matrix $\Omega_{\mathrm{KELM}} = HH^T$ only depends on the input data and training samples number. In

KELM, the data (x_j, x_i) in the low-dimensional input space is transformed into the inner product $h(x_j)\cdot h(x_i)$ in the high-dimensional feature space by kernel function $K(x_j, x_i)$, which has nothing to do with the dimension of the feature space, thus effectively avoiding the dimension disaster problem.

Because the parameters and constraints of radial basis function are relatively few, this paper chooses radial basis function as the kernel function. Radial basis function $K(x_j, x_i) = \exp\left(-\frac{1}{\lambda^2}\|x_j - x_i\|^2\right)$ as the kernel function of KELM is used in this paper, where λ is the kernel parameter.

This radial basis function is also called Gaussian function. It can be seen from equation of radial basis function and Equation (15) that there are two adjustable parameters in KELM, namely, the kernel parameter λ and regularization coefficient C, which have great influence on improving the prediction performance of KELM.

2.4. Aquila optimizer algorithm

The Aquila optimizer (AO) was proposed in 2021 [57]. The AO algorithm steps for establishing are as follows:

The first kind of vertical dive:

When the Aquila identifies the prey area, it preliminarily selects the best hunting area in the whole world by soaring at high altitude to determine the search space where the best solution is located. This method is shown in Equation (16).

$$\begin{cases} Z_1(t+1) = (Z_H(t) - rZ_{best}(t)) + \left(1 - \frac{t}{K}\right)Z_{best}(t) \\ Z_H(t) = \frac{1}{N}\sum_{i=1}^{N} Z_i(t), i \in [1, n] \end{cases} \tag{16}$$

where, generated by search method Z_1, $Z_1(t+1)$ represents the solution of $(t+1)$th iteration; $Z_{best}(t)$ is the best solution, representing the nearest position of the target prey; K and t are the maximum number of iteration and the current iteration, respectively; $Z_H(t)$ is the position average of the current solution at the tth iteration, and r is a random value between 0 and 1; n represents the dimension of the given problem.

The second kind of short gliding attack:

When the prey area is found in the soaring from high altitude, the Aquila hovers over the target prey to narrow the hunting area, that is, to reduce the search space for the optimal solution. This method is shown in Equation (17).

$$\begin{cases} Z_2(t+1) = L(D)Z_{best}(t) + Z_R(t) + r(y - z) \\ L(D) = b \times \frac{\sigma\mu}{|p|^{\frac{1}{\beta}}} \end{cases} \tag{17}$$

where, $Z_R(t)$ is the random solution between 1 and N, D is the dimensional space, and $L(D)$ is the hunting flight distribution function; b and β are fixed values of 0.01 and 1.5, respectively; μ and p are random numbers from 0 to 1 respectively, σ is the intermediate variable.

The third kind of low-altitude flight:

When the prey area is accurately determined and the Aquila is ready to land and attack, it will test the prey's reaction in the selected target area by low-altitude and slow-descent attack, and slowly approach the target. This method is shown in Equation (18).

$$Z_3(t+1) = \alpha(Z_{best}(t) - Z_H(t)) - r + \delta(r(U_B - L_B) + L_B) \tag{18}$$

where, α and δ is an adjustment parameter, which is fixed at a smaller value of 0.1. L_B and U_B represent the lower and upper bounds of the given problem, respectively.

The fourth kind of walking capture:

When the Aquila approaches the target on the same day, it attacks the prey from above the land according to its movement and converges quickly. This method is shown in Equation (19).

$$\begin{cases} Z_4(t+1) = C_F Z_{best}(t) - P_1 Z(t) r - P_2 L(D) + rP_1 \\ C_F(t) = \frac{2r-1}{t^{(1-K)^2}} \\ P_1 = 2r - 1 \\ P_2 = 2\left(1 - \frac{t}{K}\right) \end{cases} \tag{19}$$

where, C_F is the quality function used to balance the search strategy, P_1 represents the various movements of the Aquila in hunting prey, P_2 represents the flight slope of the Aquila in hunting, and $Z(t)$ is the current solution of the tth iteration.

2.5. Improved kernel extreme learning machine by Aquila optimizer algorithm

Due to the direct use of KELM model, its kernel parameters and regularization coefficients are randomly assigned, which can seriously affect the prediction performance of the model. To improve the prediction performance of KELM, KELM improved by Aquila optimizer (AO) algorithm, named AO-KELM, is proposed. AO's parameter settings are given in Table 2.

In the implementation of AO-KELM model, this paper sets the predicted fitness function which is the root mean square error, namely

$$fitness = \sqrt{\frac{1}{N}\sum_{i=1}^{N}[h(i) - h_d(i)]^2} \tag{20}$$

where, $h(i)$ is the predicted output, $h_d(i)$ is the expected output. Flow chart of AO-KELM is shown in Fig. 2.

2.6. Error correction idea

Considering that there is a certain error between the prediction results of each component after VMD decomposition and each component before prediction, and the prediction errors of each component will be superimposed, which will have a large impact on the final prediction results. In order to further improve the prediction accuracy, we adopt the idea of error correction to solve this problem [58]. Therefore, the AO-KELM model is proposed to correct the prediction error sequence. The process of error correction is shown in Fig. 3.

The error correction idea is specified as follows:

Step 1. Divide the original sequence into training set and test set. Assume that the length of the original sequence is n, the length of the training sequence is k, and the length of the test sequence is n-k.

Step 2. Establish AO-KELM model for the original sequence $[x_1 x_2 \cdots x_n]$ to obtain the initial predicted sequence $[y_6 y_7 \cdots y_n]$. However, after the AO-KELM model is trained, the training set will generate an error sequence $[e_6 e_7 \cdots e_k]$. The test set uses the trained model to obtain the prediction sequence. This process generates an error sequence $[e_{k+1} e_{k+2} \cdots e_n]$ for the test set. The final error sequence $[e_6 e_7 \cdots e_n]$ is obtained by integrating the error sequence of the training set and test set.

Step 3. Establish AO-KELM model for the prediction error sequence $[e_6 e_7 \cdots e_n]$ and the error prediction sequence $[e'_{k+1} e'_{k+2} \cdots e'_n]$ is obtained by the trained model. Finally, the initial prediction sequence and error

Table 2
AO parameter setting.

Parameter	Value
Population size	10
Max-iteration	50
Kernel function width optimization range	[1,100]
Regularization parameter optimization range	[1,500]

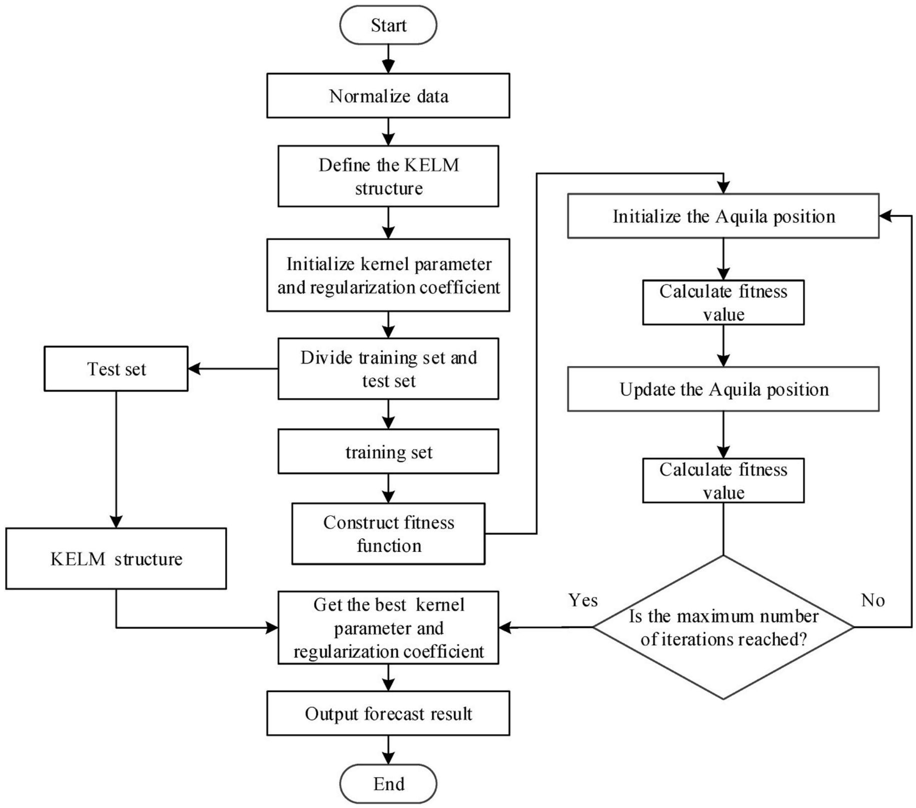


Fig. 2. Flow chart of AO-KELM.

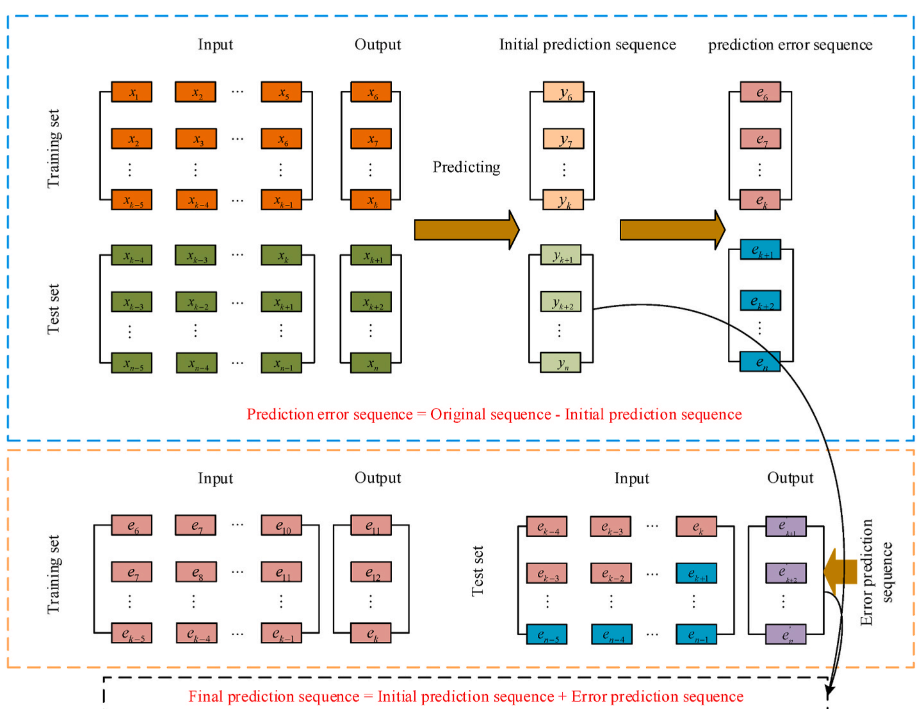


Fig. 3. The process of error correction.

prediction sequence are superimposed to get the final prediction sequence.

3. The proposed model

To enhance prediction performance, this section proposes a COVID-19 cases prediction model combined with SVMD, AO-KELM, and error correction idea, named SVMD-AO-KELM-error. Firstly, SVMD decomposes the COVID-19 case data into some IMF components and residual is considered. Secondly, each component is predicted by AO-KELM. Then, the prediction error of IMF and residual are predicted by using the idea of error correction. Finally, error prediction results and prediction results of each component are reconstructed to get final prediction results. Flow chart of the SVMD-AO-KELM-error prediction model is given in Fig. 4.

The concrete step of the flow chart in Fig. 4 is:

Step 1. Normalize the original data of confirmed and death cases by Equation (21).

$$x_{normal} = \frac{x_{orgin} - x_{\min}}{x_{\max} - x_{\min}} \tag{21}$$

Step 2. Use SVMD to decompose the original data of confirmed and death cases, and get components $\{IMF1, IMF2, \cdots, IMFn\}$.

Step 3. Calculate the residual component as Res by Equation (22).

$$\mathrm{Res} = x_{normal} - \sum_{i=1}^{n} IMFi \tag{22}$$

Step 4. Establish AO-KELM prediction model for each component $\{IMF1, IMF2, \cdots, IMFn, \mathrm{Res}\}$. Firstly, each component is divided into training set and test set. The training set is used to train the model, and the test set is used to verify. The multi-input single-output strategy is used to divide the data set, that is, the historical data of a certain period of time is used as the input of the AO-KELM model to predict the development trend of COVID-19 data in the next day. Assume that the total length of the data is n, the length of the training set is k, and the length of the input sample is 5. The specific method of dividing the data set is shown in Fig. 5. Then, the first 5 data are used to predict the 6th data, which is a rolling forecast with a period of 5. That is, the first 5 data $(x_{n-5}, x_{n-4}, x_{n-3}, x_{n-2}, x_{n-1})$ are used as input variables of the model, and the output variables are x_n. Finally, each component prediction result is $\{IMF1', IMF2', \cdots, IMFn', \mathrm{Res}'\}$ by the trained model.

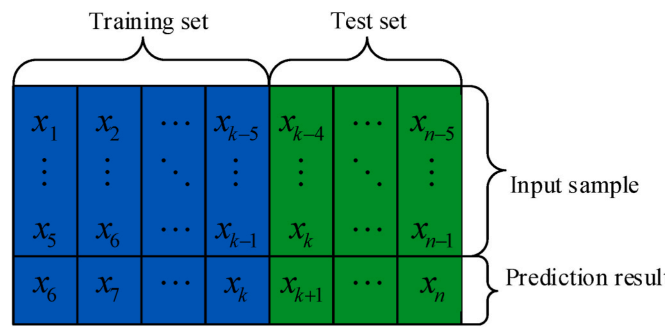


Fig. 5. The specific method of dividing the data set.

Step 5. Calculate each component prediction error in Step 4 as $\{e_1, e_2, \ldots, e_{n+1}\}$ by Equation (23). Then each component prediction error is predicted by AO-KELM and the error prediction result is $\{e_1', e_2', \ldots, e_{n+1}'\}$.

$$\begin{cases} e_i = IMFi - IMFi', i = 1, \ldots, n \\ e_i = \mathrm{Res} - \mathrm{Res}', i = n+1 \end{cases} \tag{23}$$

Step 6. Get the final prediction results by reconstructing each component prediction result $\{IMF1', IMF2', \cdots, IMFn', \mathrm{Res}'\}$ and error prediction result $\{e_1', e_2', \ldots, e_{n+1}'\}$ by Equation (24):

$$Y = \mathrm{Res}' + \sum_{i=1}^{n} IMFi' + \sum_{i=1}^{n+1} e_i' \tag{24}$$

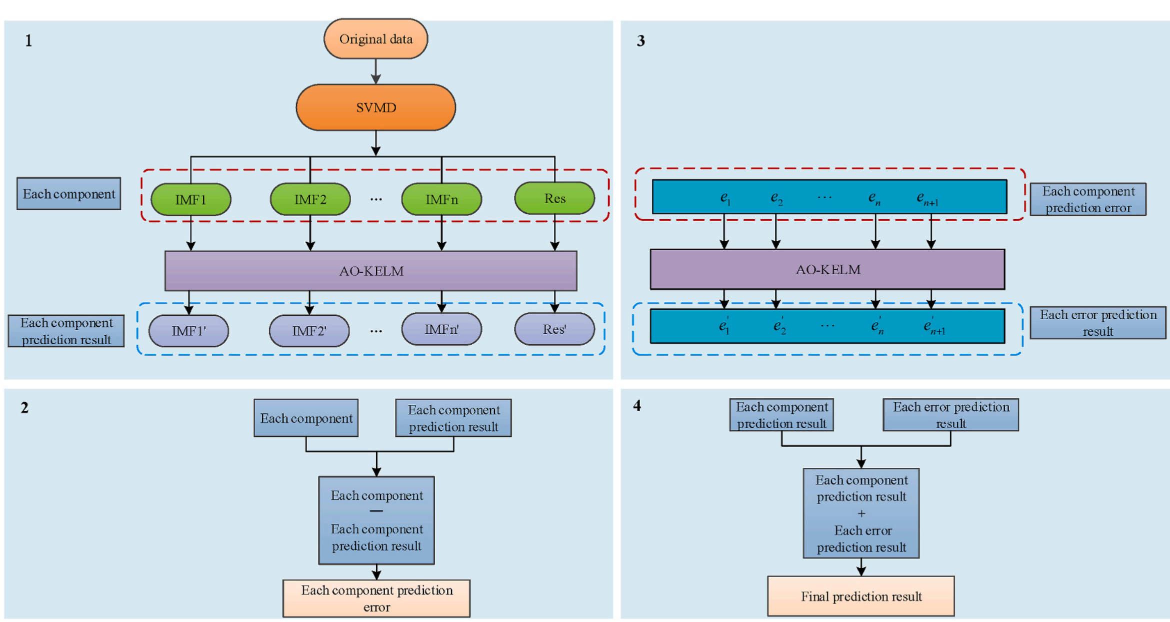


Fig. 4. SVMD-AO-KELM-error prediction model.

Step 7. Error analysis of prediction results.

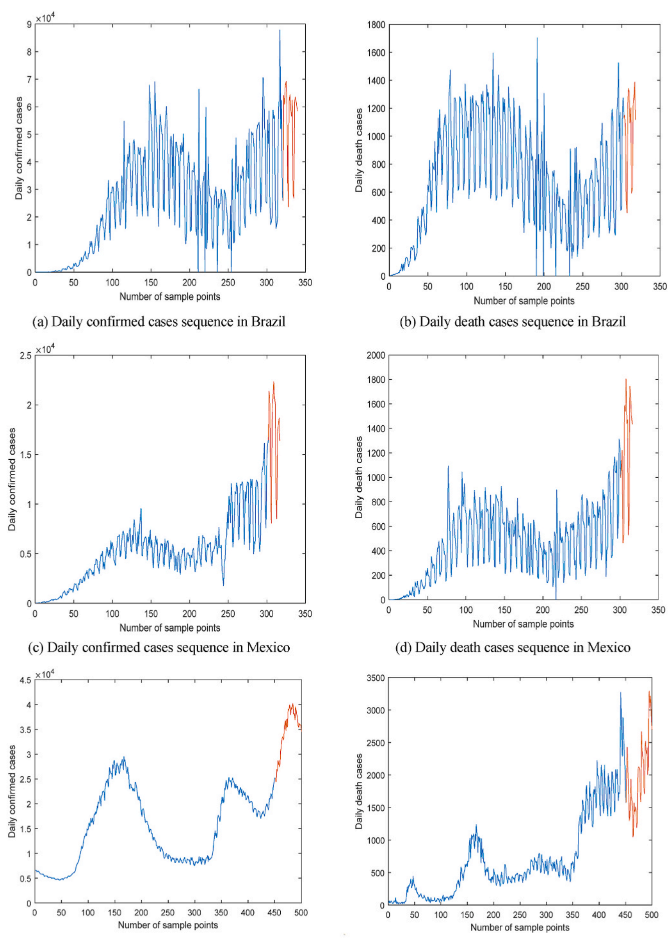
4. Simulation experiment

Section 4.1 is the experimental data source. Section 4.2 is comparison model description. Section 4.3 is prediction model evaluation indexes. Section 4.4 is simulation experiment in Brazil. Section 4.5 is simulation experiment in Mexico and Russia.

4.1. Data source

The COVID-19 dataset is got from https://data.humdata.org/dataset/novel-coronavirus-2019-ncov-cases Csv files of cases, death cases and recovered cases in all countries are provided in columns. From January 22, 2020 to November 22, 2021, there are three categories of separate documents created, and COVID- 19 data set contains death cases, confirmed cases, and recovery cases.

In this paper, three data sets named case 1, case 2 and case 3 are selected for simulation experiments to verify the validity of the proposed model. Case 1 and case 2 are respectively that a total of 340 COVID-19 cases and deaths in Brazil from February 25, 2020 to January 30, 2021 and a total of 318 COVID-19 cases and deaths in Mexico from March 17, 2020 to January 29, 2021 are selected, among which the last 20 data are predicted. Case 3 is that a total of 500 COVID-19 cases and deaths were selected from July 11, 2020 to November 22, 2021 in Russia, of which the last 50 data were predicted. After preprocessing the data, daily confirmed and death cases sequence in Brazil, Mexico and Russia are shown in Fig. 6. Blue represents training set and red represents test set in



(a) Daily confirmed cases sequence in Brazil (b) Daily death cases sequence in Brazil

(c) Daily confirmed cases sequence in Mexico (d) Daily death cases sequence in Mexico

(e) Daily confirmed cases sequence in Russia (d) Daily death cases sequence in Russia

Fig. 6. Daily confirmed and death cases sequence in Brazil, Mexico and Russia.

Table 3
A visual presentation of three data sets.

COVID-19 data		Country	Size	Training Set	Test Set	Date
case 1	daily confirmed cases daily death cases	Brazil	340	320	20	2020/02/25–2021/01/30
case 2	daily confirmed cases daily death cases	Mexico	318	298	20	2020/03/17–2021/01/29
case 3	daily confirmed cases daily death cases	Russia	500	450	50	2020/07/11/-2021/11/22

Fig. 6. A visual presentation of three data sets is given in Table 3. The simulation environment is MATLAB 2016b, the operating system is Windows 10 64-bit, the processor is Intel Core i5-4210U, and the memory (RAM) is 8 GB.

4.2. Comparison model description

To compare SVMD-AO-KELM-error performance, a total of twelve comparison models are selected. There are both decomposition-integration model and single model. The single model includes RBFNN (radial basis function neural network), LSSVM, ELM, KELM and AO-KELM where LSSVM comes from Reference [16] and ELM comes from Reference [20]. The purpose of choosing this kind of model is to prove the superiority of AO-KLEM. The decomposition-integration model includes EEMD-ARIMA, EEMD-ANN, EEMD-KELM, SVMD-ELM, SVMD-KELM, SVMD-LSSVM and SVMD-AO-KELM.

The model introduction and selection meaning of decomposition-integration is as follows:

The EEMD-ARIMA comes from Reference [25]. The implementation steps of this model are as follows: Firstly, COVID-19 data is decomposed into several IMF components by EEMD, and then ARIMA prediction model is established for each IMF component. Finally, the final prediction result is obtained by reconstructing the prediction results of each component. The EEMD-ANN comes from Reference [27]. The implementation steps of EEMD-ANN and EEMD-KELM are similar to those of EEMD-ARIMA, only the prediction method is different. These models are introduced to illustrate the shortcomings of EEMD and the superiority of SVMD model. The implementation steps of the SVMD-AO-KELM model are as follows: Firstly, COVID-19 data is decomposed into several IMF components by SVMD, and then IMF components is predicted by AO-KELM. Finally, the prediction results of each component are reconstructed to obtain the final prediction results. The implementation steps of SVMD-ELM, SVMD-KELM, and SVMD-LSSVM are similar to those of SVMD-AO-KELM, only the prediction method is different. The purpose of choosing this model is to illustrate the advancement and performance superiority of the decomposition-integration model based on SVMD. The implementation steps of the SVMD-AO-KELM is similar to SVMD-AO-KELM-error, but error is not corrected. The purpose of joining this model is to indicate the effectiveness of the error correction strategy.

In order to better illustrate the fairness and meaningfulness of all comparison models, Table 4 shows the parameter settings of the approach in each model. For the parameter settings in the proposed SVMD-AO-KELM-error, the optimization algorithm is adopted to determine them.

Table 4
Parameter settings of the approach in each model.

Approach	Parameter	parameter value
RBFNN	Number of neurons in input layer	5
	Number of neurons in hidden layer	50
	Number of neurons in output layer	1
	Radial base expansion parameters	0.08
	Function	newrb
ELM	Number of hidden layers	20
	Activation function	Sigmoid
LSSVM	Regularization parameter	400
	Kernel function	RBF
ANN	Number of hidden layers	6
	Number of iterations	100
KELM	Regularization parameter	400
	Kernel parameter	30
ARIMA	Order of AR	4
	Differential order	1
	Order of MA	4
EEMD	Ratio of the standard deviation of the added noise and that of signal	0.2
	Ensemble number	200

4.3. Evaluation index

To evaluate the decomposition-integration model scientifically and comprehensively, root mean square error (RMSE), mean absolute error (MAE), mean absolute percentage error (MAPE) are selected. Their equations are [59]:

$$RMSE = \sqrt{\frac{1}{m}\sum_{p=1}^{m}\left|\hat{x}_p - x_p\right|^2} \tag{25}$$

$$MAE = \frac{1}{m}\sum_{p=1}^{m}\left|\hat{x}_p - x_p\right| \tag{26}$$

$$MAPE = \frac{1}{m}\sum_{p=1}^{m}\left|\frac{\hat{x}_p - x_p}{x_p}\right| \tag{27}$$

where, $\hat{x}_p$ is predictive data, x_p is original data, m is total sample number.

These three evaluation indexes respectively represent different meanings. RMSE is a measure of the difference between the predicted data and the original data. The smaller the RMSE value, the higher the prediction accuracy of the model. MAE avoids the offset of positive and negative errors by calculating the absolute average of the errors, and accurately reflects the size of the errors. MAPE is different from the first two, indicating the average relative error, which can reduce the interference of individual discrete points. In short, smaller values of RMSE, MAE and MAPE indexes indicate better forecasting results.

4.4. Simulation experiment of case 1: Daily confirmed and daily death cases in Brazil

4.4.1. SVMD decomposition result

The data of daily confirmed and death cases in Brazil are taken as an example. The parameters of VMD are optimized by SSA, and Fig. 7 is the optimization result of SVMD.

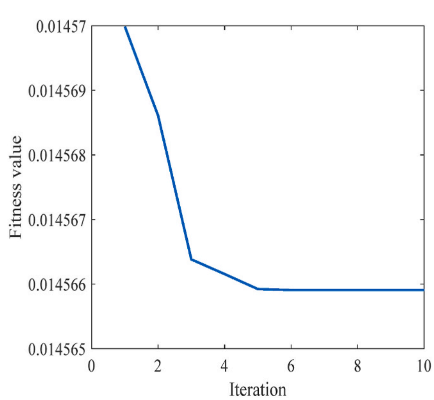
Fig. 7(a) shows that the maximum fitness value of the daily confirmed cases sequence is 0.14566, and the corresponding iteration number is 5. The best parameter combination is $[K, \alpha] = [8{,}1203]$. Fig. 7 (b) shows that the maximum fitness value of the daily death case sequence is 0.0406842, and the corresponding iteration number is 5. The best parameter combination is $[K, \alpha] = [8{,}1433]$. According to the searched optimal parameter combination, decomposition results of COVID-19 confirmed and death cases by SVMD in Brazil are given in Fig. 8(a) and (b). In order to verify the effectiveness and superiority of SVMD, EEMD decomposition result are shown in Fig. 8(c) and (d).

Comparing SVMD and EEMD decomposition results of COVID-19 daily confirmed and death cases in Brazil in Fig. 8, EEMD decomposition results have obvious modal aliasing and many false low-frequency components. Although EEMD can decompose case data adaptively, this will bring great errors to the prediction results of case data. Fig. 8(a) and (b) shows that SVMD effectively decomposes case data into eight components and effectively avoids modal aliasing. The low-frequency component IMF1 decomposed by SVMD clearly expresses the general trend of signal fluctuation.

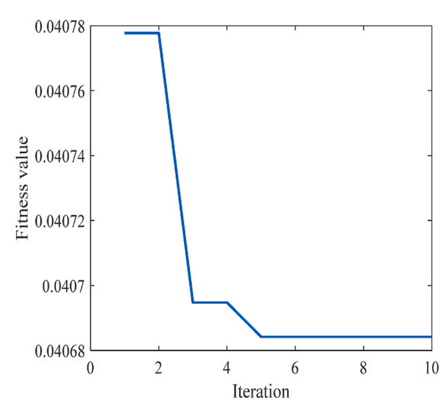
4.4.2. Influence of VMD parameters

Using COVID-19 daily confirmed cases in Brazil as experimental data, the best parameter combination obtained by SSA-VMD search is [8,1203]. In order to explain that the improper combination of K and α parameters will lead to poor parameter selection of VMD, which is equivalent to the effect of prediction accuracy. Different K values and α values are set for VMD respectively, and KELM makes prediction. The evaluation results of different parameter combinations are shown in Table 5. In order to better illustrate the superiority of SSA, we choose PSO and WOA for comparison. According to experience, the parameter settings of WOA is the same as those of SSA algorithm. Parameter settings of PSO are the same as those in section 5.4.3. The evaluation results of VMD improved by different algorithms are shown in Table 6.

It can be seen from Table 5 that the RMSE, MAE and MAPE of [8,1203] have the smallest index values among the different determined parameter combinations, which indicates that the prediction effect is the

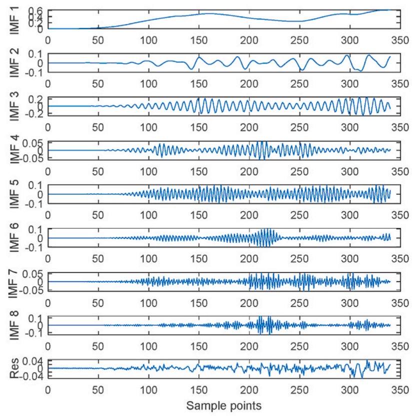


(a) Optimization result of daily confirmed cases

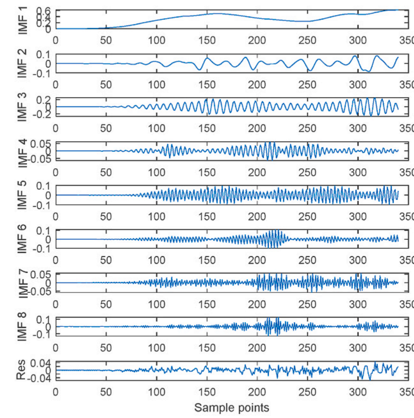


(b) Optimization result of daily death cases

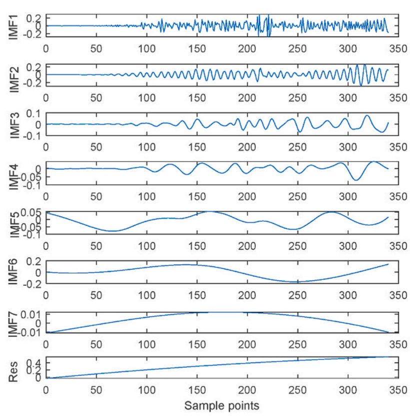
Fig. 7. The optimization result of SVMD.



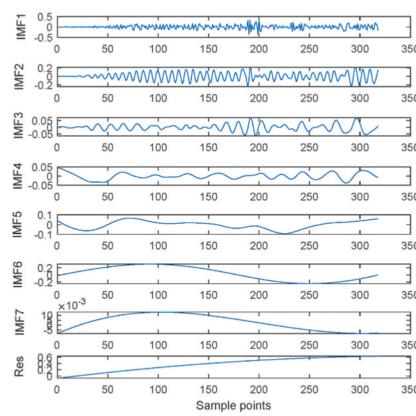
(a) SVMD decomposition results of daily confirmed cases



(b) SVMD decomposition results of daily death cases



(c) EEMD decomposition results of daily confirmed cases



(d) EEMD decomposition results of daily death cases

Fig. 8. SVMD and EEMD decomposition results of COVID-19 daily confirmed and death cases in Brazil.

Table 5
The evaluation results of different parameter combinations.

K	α	RMSE	MAE	MAPE
3	500	2.1E+03	1.57E+03	0.0298
5	650	2.4E+03	1.73E+03	0.0288
6	700	2.07E+03	1.59E+03	0.0295
8	**1203**	**2.04E + 03**	**1.54E + 03**	**0.0292**
10	1500	2.09E+03	1.61E+03	0.0297

Table 6
The evaluation results of VMD improved by different algorithms.

	K	α	RMSE	MAE	MAPE
PSO-VMD	9	1400	2.06E+03	1.563E+03	0.294
SSA-VMD	**8**	**1203**	**2.04E + 03**	**1.54E + 03**	**0.0292**
WOA-VMD	8	1383	2.069E+03	1.569E+03	0.295

best. It can be concluded that the random setting of the combination of *K* and α parameters of VMD has a poor prediction effect on the decomposed prediction. Therefore, it is very important to select the appropriate parameter combination for VMD, which further proves the rationality of improving VMD by SSA. It can be seen from Table 6, compared with PSO-VMD and WOA-VMD, the RMSE, MAE and MAPE index values of SSA-VMD are the smallest. This also proves the superiority of SSA in improving VMD. In order to test the significant difference between SSA-VMD and the two comparison models statistically, this paper uses Diebol-Mariano (DM) statistics [60] to test the comparison model and SSA-VMD. The results of DM test is shown in Table 7.

Table 7
The results of DM test.

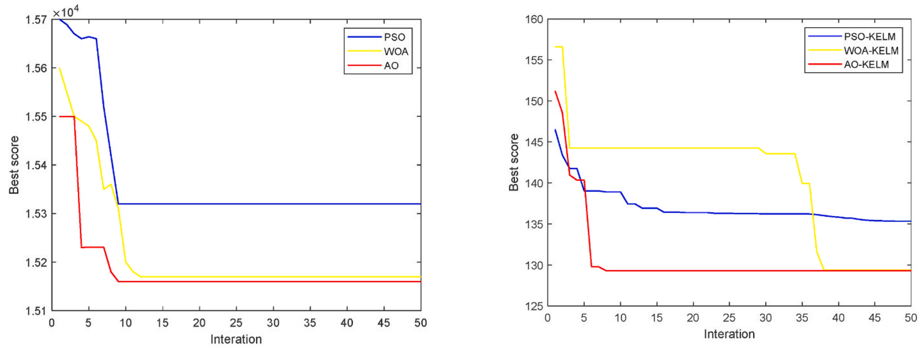
	DM statistics	*P* value
PSO-VMD	4.7534	0.0000
WOA-VMD	3.8346	0.0020

It can be seen from Table 7 that the DM test *P* values of WOA-VMD and PSO-VMD are both less than 0.01. It shows that the comparison model is significantly different from SSA-VMD at the confidence level of 1%. It further shows that SSA-VMD is effective in forecasting.

4.4.3. *Effectiveness of AO algorithm*

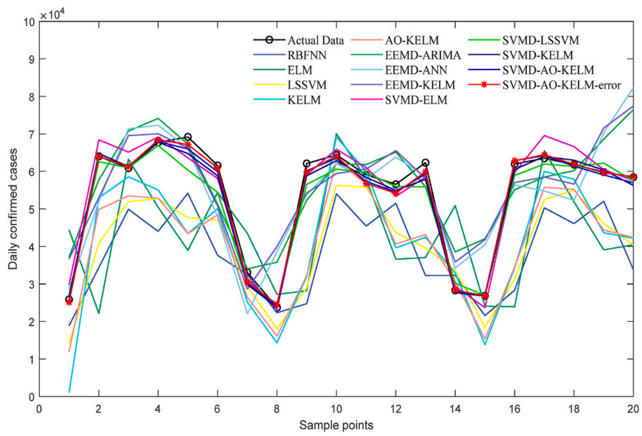
To illustrate the effectiveness of AO algorithm proposed in this paper to improve KELM, we choose PSO and (Whale optimization algorithm) WOA for comparison. For the fairness and persuasiveness of comparison, we set the parameters of the algorithm. The parameters of PSO are set as follows: Population size N is 30. Learning factors c_1 and c_2 are 1.496. We used a ring neighborhood structure in PSO. The maximum iteration number M is 50. The parameter settings of WOA is the same as those of AO algorithm. The daily data of COVID-19 confirmed and death cases in Brazil are used as experimental data, MSE is used as fitness function, and three algorithms are used to optimize KELM. Fig. 9 presents the optimal value iteration curve for improving KELM with three algorithms.

It can be seen from Fig. 9 that, compared with PSO and WOA

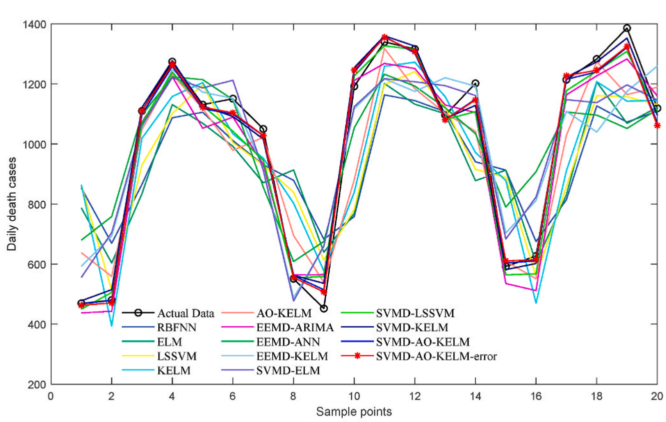


(a) Daily confirmed cases (b) Daily death cases

Fig. 9. The optimal value iteration curve for improving KELM with three algorithms.



(a) Prediction results of daily confirmed cases



(b) Prediction results of daily death cases

Fig. 10. Prediction results of COVID-19 daily confirmed and death cases in Brazil.

algorithms, the fitness value of AO algorithm tends to be stable after the least number of iterations, and the AO algorithm tends to be stable with the minimum fitness value. It can be concluded that KELM improved by AO algorithm has fast convergence speed and strong optimization ability. Therefore, this paper proposes that AO algorithm is more suitable for parameter optimization of KELM, which will have better prediction performance.

4.4.4. Prediction results of each model

This section shows the prediction results and superiority of SVMD-AO-KELM-error in detail. Twelve models in Section 4.2 are compared to demonstrate the superiority of SVMD-AO-KELM-error. So prediction results of COVID-19 daily confirmed and death cases in Brazil are given in Fig. 10, in which red curves represent the proposed model in this paper and black curves represent the original values.

From the prediction result of the single prediction model and decomposed integrated model in Fig. 10, it is shown that the decomposed integrated model is superior to single prediction model, and the fitting degree between the decomposed integrated model and actual signal is evidently better.

In order to further prove that SVMD-AO-KELM-error has a good prediction effect, this section gives the prediction error distribution of daily confirmed and death cases in Brazil are given in Fig. 11.

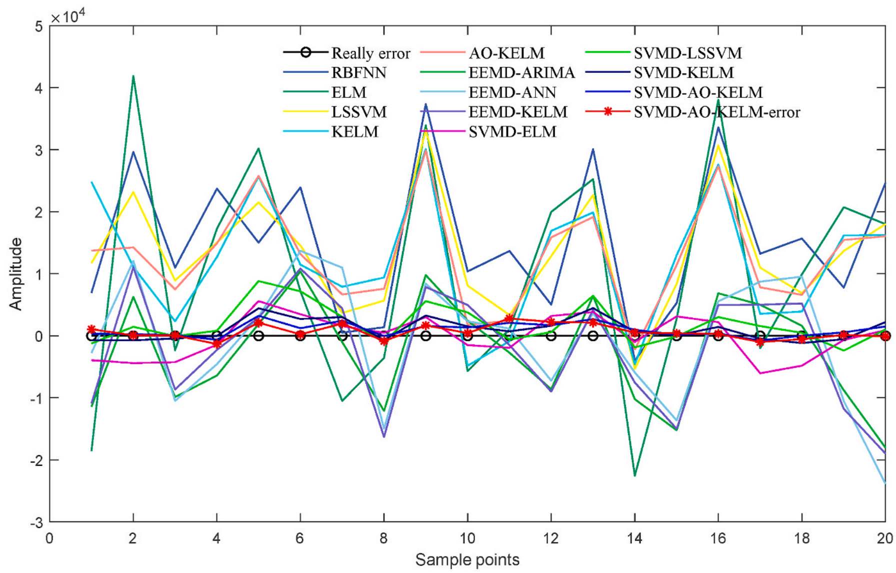
The following conclusion can be drawn from Fig. 11

(1) The prediction error curves of ELM, LSSVM, KELM and AO-KELM fluctuate greatly, and the prediction effect is poor. This is the same as the conclusion that we get in Fig. 10, and the effect of decomposition-integrated model based on SVMD is obviously superior to that of single model.
(2) The error distribution of SVMD-AO-KELM-error and SVMD-AO-KELM is near the base line, and this error range is small.

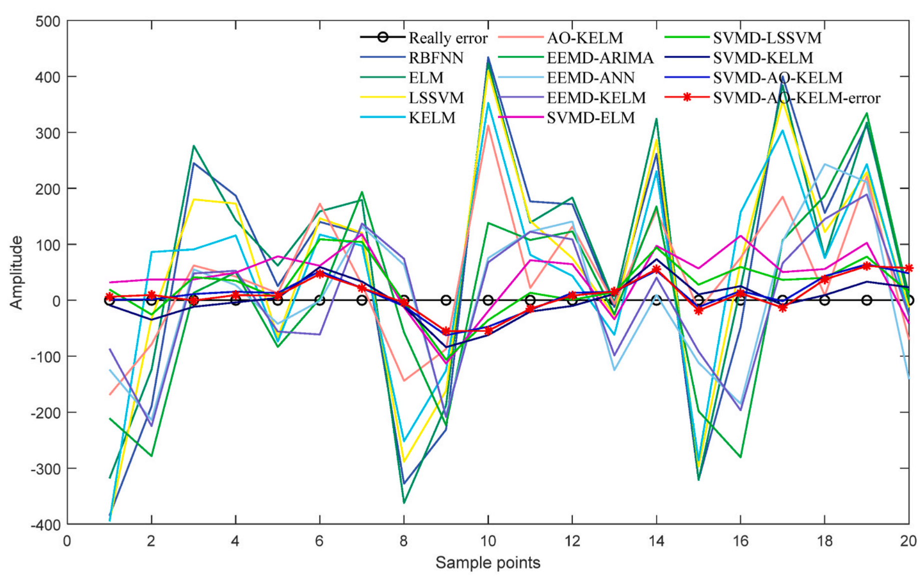
Because the prediction error of SVMD-AO-KELM is very large, adding error correction strategy to this model will further improve the prediction precision. But it is not evident in Figs. 10 and 11. In order to better explain directly that SVMD-AO-KELM-error has higher prediction accuracy, this paper analyzes quantitatively the prediction result of each model by RMSE, MAE and MAPE. Evaluation indexes of different models of Brazil's daily confirmed and death cases are listed in Tables 8 and 9, respectively. In addition, Figs. 12 and 13 clearly show the size of RMSE, MAE, MAPE matching to all models in the form of bar chart. For the convenience of histogram display, all models are numbered as M1, M2, …, M13 in turn according to Table 8. To further reflect the best prediction accuracy of SVMD-AO-KELM-error, box diagram of prediction error sequence of case 1, as shown in Fig. 14.

Figs. 12 and 13 clearly show the size changes of RMSE MAE and MAPE of each model. Fig. 14 shows the smallest fluctuations of M13 (SVMD-AO-KELM-error). These proved that SVMD-AO-KELM-error has the best prediction accuracy. The quantitative analysis results show the prediction results of each model in Tables 8 and 9. By comparing all the models in Table 8, the following analysis is found:

(1) Compared with ELM, LSSVM and RBFNN, the prediction effect of KELM is superior to that of other models. The RMSE, MAE and MAPE values of this model are 1.58E+04, 1.32E+04 and 0.2605 respectively. When the KELM model without optimization is



(a) Distribution chart of prediction error of daily confirmed cases



(b) Distribution chart of prediction error of daily death cases

Fig. 11. Prediction error distribution of daily confirmed and death cases in Brazil.

compared with AO-KELM, the prediction effect of AO-KELM is better and the values of RMSE, MAE, and MAPE are 1.52E+04, 1.30E+04 and 0.2528 respectively. Compared with KELM, the RMSE, MAE and MAPE values of AO-KELM decreased by 3.80%, 1.52% and 8.24% respectively. Thus AO-KELM is able to rise the prediction performance of KELM by effectively selecting the key parameters through AO algorithm.

(2) By comparing the SVMD-based models with the undecomposed models, it is found that the SVMD-based model can better improve the prediction accuracy when the same prediction model is used. Compared with ELM, the RMSE, MAE and MAPE values of SVMD-ELM decreased by 84.06%, 82.71% and 82.53% respectively. Compared with LSSVM, the RMSE, MAE and MAPE values of SVMD-LSSVM decreased by 78.16%, 81.65% and 81.88% respectively. Compared with KELM, the RMSE, MAE and MAPE values of SVMD-KELM decreased by 87.09%, 88.33% and 89.40% respectively. Compared with AO-KELM, the RMSE, MAE and MAPE values of SVMD-AO-KELM decreased by 88.82%, 89.69% and 90.31% respectively.

(3) By comparing the EEMD-based models with the undecomposed models, it is found that the EEMD-based model can better improve the prediction accuracy when the same prediction model is used. The RMSE, MAE and MAPE values of EEMD-KELM were 8.95E+03, 7.75E+03 and 0.1902 respectively. The RMSE, MAE and MAPE values of KELM are 1.58E+04, 1.32E+04 and 0.2755 respectively. When comparing EEMD-KELM and KELM, the values of RMSE, MAE and MAPE for EEMD-KELM were decreased by 43.35%, 41.29% and 30.96% respectively.

(4) Among the EEMD-based models, the EEMD-KELM model has the best prediction results. For example, compared with EEMD-ANN,

Table 8
Evaluation indexes of different models of daily confirmed cases in Brazil.

Model	Model Number	Evaluation index		
		RMSE	MAE	MAPE
RBFNN	M1	1.91E+04	1.57E+04	0.287
ELM	M2	2.07E+04	1.66E+04	0.3229
LSSVM	M3	1.63E+04	1.39E+04	0.2755
KELM	M4	1.58E+04	1.32E+04	0.2605
AO-KELM	M5	1.52E+04	1.30E+04	0.2528
EEMD-ARIMA	M6	9.42E+03	8.16E+03	0.1927
EEMD-ANN	M7	1.02E+04	8.66E+03	0.2001
EEMD-KELM	M8	8.95E+03	7.75E+03	0.1902
SVMD-ELM	M9	3.30E+03	2.87E+03	0.0564
SVMD-LSSVM	M10	3.56E+03	2.55E+03	0.0472
SVMD-KELM	M11	2.04E+03	1.54E+03	0.0292
SVMD-AO-KELM	M12	1.70E+03	1.34E+03	0.0245
SVMD-AO-KELM-error	M13	1.35E+03	9.95E+02	0.02

Table 9
Evaluation indexes of different models of daily death cases in Brazil.

Model	Model Number	Evaluation index		
		RMSE	MAE	MAPE
RBFNN	M1	2.43E+02	2.08E+02	0.2552
ELM	M2	2.38E+02	2.00E+02	0.2396
LSSVM	M3	2.16E+02	1.79E+02	0.2166
KELM	M4	1.93E+02	1.61E+02	0.2034
AO-KELM	M5	1.29E+02	1.00E+02	0.1152
EEMD-ARIMA	M6	1.69E+02	1.39E+02	0.1826
EEMD-ANN	M7	1.36E+02	1.17E+02	0.1468
EEMD-KELM	M8	1.20E+02	1.05E+02	0.1359
SVMD-ELM	M9	6.99E+01	6.24E+01	0.0716
SVMD-LSSVM	M10	5.57E+01	4.30E+01	0.05
SVMD-KELM	M11	3.58E+01	2.69E+01	0.033
SVMD-AO-KELM	M12	3.33E+01	2.60E+01	0.0277
SVMD-AO-KELM-error	M13	3.27E+01	2.53E+01	0.027

the RMSE, MAE and MAPE values of SVMD-KELM decreased by 12.25%, 10.51% and 4.95% respectively. Among the SVMD-based models, SVMD-AO-KELM model has the best prediction results. For example, compared with SVMD-KELM, the RMSE, MAE and MAPE values of SVMD-AO-KELM decreased by 16.67%, 12.99% and 16.10% respectively. These show that when the same decomposition method is used, KELM is better than other prediction methods and KELM before optimization is better than that after optimization.

(5) Comparing KELM, EEMD-KELM and SVMD-KELM, it is found that SVMD-KELM has the best effect. This shows that when using the same prediction method, the prediction effect of the data decomposed by SVMD is significantly better than that of the EEMD method, which can improve the prediction accuracy of COVID-19 daily confirmed in Brazil.

(6) The RMSE, MAE, and MAPE values of SVMD-AO-KELM-error are 1.352E+03, 9.952E+02 and 0.02 respectively. Compared with SVMD-AO-KELM, the RMSE, MAE, and MAPE values of SVMD-AO-KELM-error decreased by 20.59%, 25.75% and 18.37% respectively. This shows that the error correction strategy is able to effectively rise the prediction accuracy. Compared with EEMD-ARIMA, the RMSE, MAE, and MAPE values of SVMD-AO-KELM-error decreased by 85.67%, 87.81% and 89.62% respectively. Compared with EEMD-ANN, the RMSE, MAE, and MAPE values of SVMD-AO-KELM-error decreased by 86.76%, 88.51% and 90.00% respectively. The results give that SVMD-AO-KELM-error has better prediction effect than EEMD-ARIMA and EEMD-ANN. Compared with all models, the three evaluation indexes value of SVMD-AO-KELM-error is the smallest. Thus, SVMD-AO-KELM-error has the best prediction effect.

In short, similar conclusions can be drawn from Table 9. According to the analysis of figures and tables of case 1, it is proved that the proposed SVMD-AO-KELM-error model can improve the prediction accuracy of daily confirmed and death cases in Brazil.

4.5. Simulation experiment of case 2 and case 3: Daily confirmed and daily death cases in Mexico and Russia

To further illustrate the universality and effectiveness of the proposed model in predicting the COVID-19 cases, the proposed method is applied to case 2 and case 3 from Mexico and Russia, respectively, for simulation experiments in this section. The experimental process of

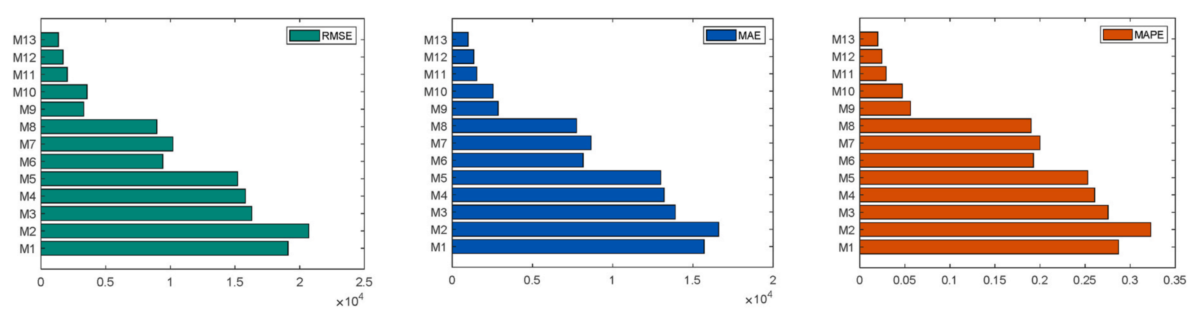


Fig. 12. Bar chart of each model evaluation indexes of daily confirmed cases in Brazil.

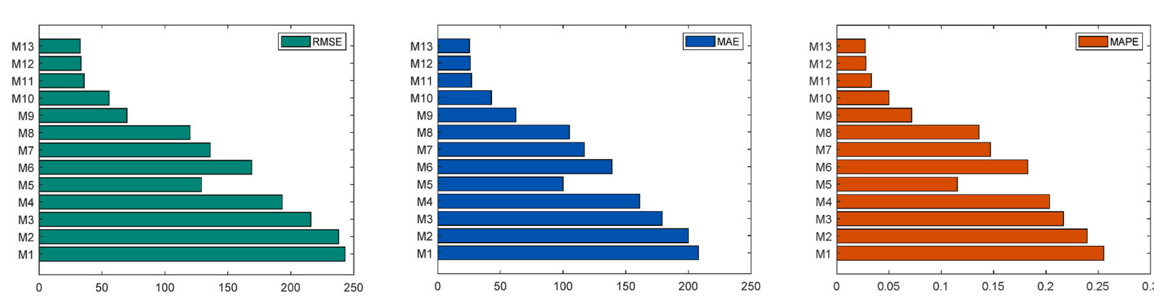
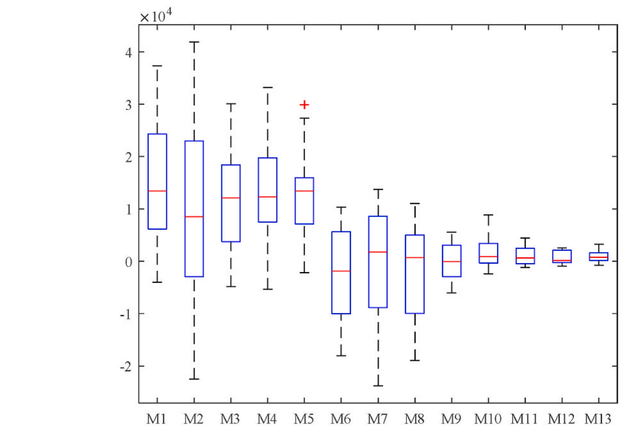
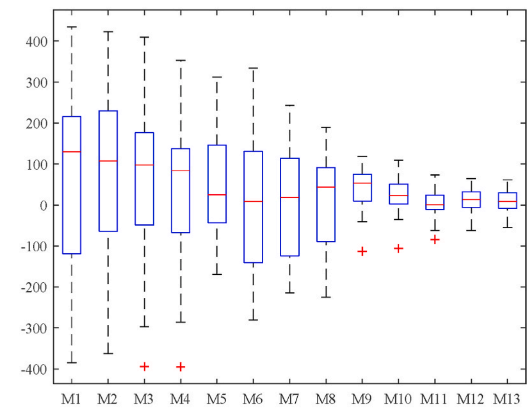


Fig. 13. Bar chart of each model evaluation indexes of daily death cases in Brazil.

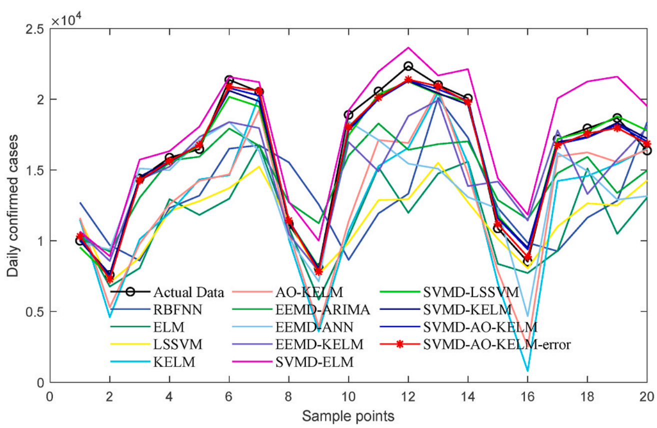


(a) Box diagram of prediction error sequence of daily confirmed cases

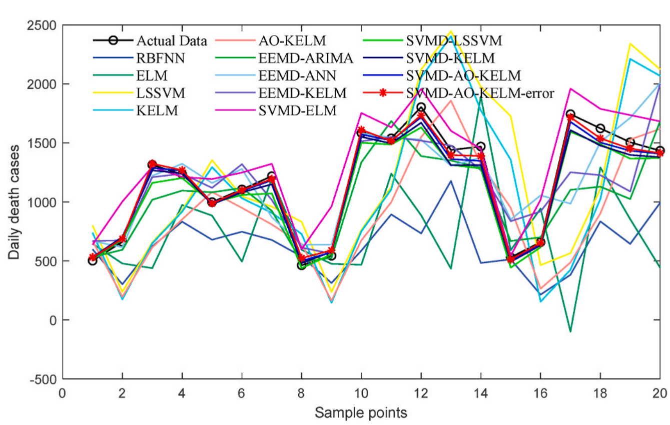


(b) Box diagram of prediction error sequence of daily death cases

Fig. 14. Box diagram of prediction error sequence of case 1.

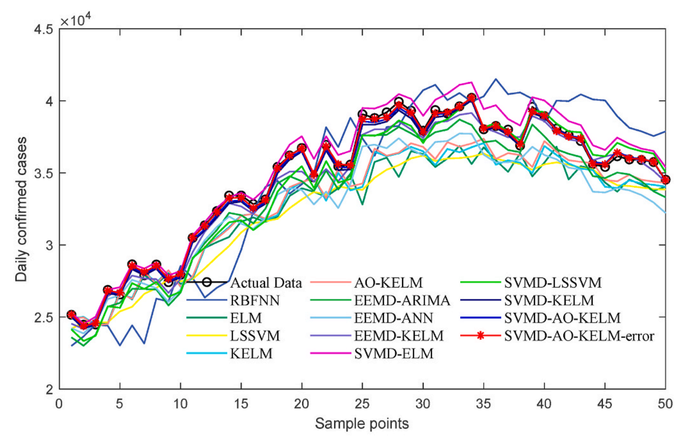


(a) Prediction results of daily confirmed cases

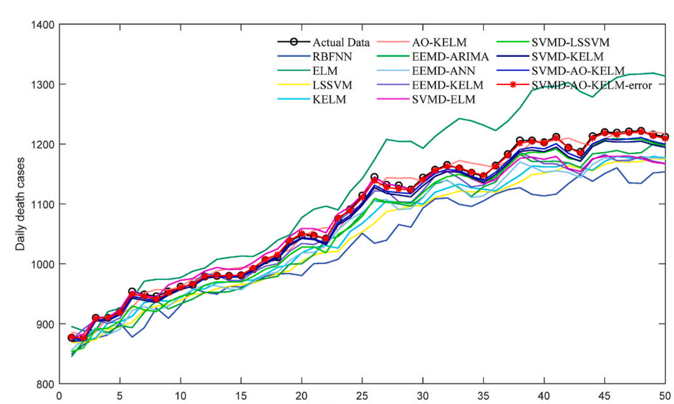


(b) Prediction results of daily death cases

Fig. 15. Prediction results of case 2.



(a) Prediction results of daily confirmed cases



(b) Prediction results of daily death cases

Fig. 16. Prediction results of case 3.

cases 2 and 3 is the same as that of case 1. Therefore, we directly give the following prediction results.

Prediction results of case 2 and case 3 are given in Figs. 15 and 16, in which red curves represent the proposed model and black curves represent the original values. Tables 10 and 11 show the evaluation indexes of different models of case 2 and case 3. Tables 10 and 11 can clearly show the prediction index of SVMD-AO-KELM-error is the lowest. It is proved that SVMD-AO-KELM-error is superior to other benchmark models. In order to further visualize the prediction results, bar chart of each model evaluation indexes case 2 and case 3 are shown in Figs. 17 and 18. Figs. 19 and 20 further show the box diagrams of

Table 10
Evaluation indexes of different models of case 2.

COVID-19 data		Model	Model Number	Evaluation index		
				RMSE	MAE	MAPE
case 2	daily confirmed cases	RBFNN	M1	5.29E+03	4.57E+03	0.2907
		ELM	M2	5.41E+03	4.53E+03	0.262
		LSSVM	M3	5.34E+03	4.42E+03	0.2444
		KELM	M4	4.31E+03	3.65E+03	0.2599
		AO-KELM	M5	3.83E+03	3.19E+03	0.2232
		EEMD-ARIMA	M6	2.98E+03	2.55E+03	0.1649
		EEMD-ANN	M7	3.51E+03	2.75E+03	0.1688
		EEMD-KELM	M8	2.82E+03	2.20E+03	0.1366
		SVMD-ELM	M9	2.04E+03	1.73E+03	0.1288
		SVMD-LSSVM	M10	7.26E+02	5.56E+02	0.0362
		SVMD-KELM	M11	5.87E+02	4.84E+02	0.0305
		SVMD-AO-KELM	M12	5.08E+02	4.31E+02	0.0291
		SVMD-AO-KELM-error	M13	3.13E+02	2.62E+02	0.0175
	daily death cases	RBFNN	M1	6.54E+02	5.48E+02	0.5306
		ELM	M2	6.95E+02	5.16E+02	0.3929
		LSSVM	M3	6.22E+02	5.35E+02	0.5276
		KELM	M4	5.98E+02	5.21E+02	0.5039
		AO-KELM	M5	5.05E+02	4.10E+02	0.3845
		EEMD-ARIMA	M6	2.71E+02	2.05E+02	0.1543
		EEMD-ANN	M7	2.81E+02	2.11E+02	0.2131
		EEMD-KELM	M8	2.59E+02	2.02E+02	0.1905
		SVMD-ELM	M9	2.00E+02	1.67E+02	0.1893
		SVMD-LSSVM	M10	1.03E+02	8.42E+01	0.0683
		SVMD-KELM	M11	8.04E+01	6.44E+01	0.0534
		SVMD-AO-KELM	M12	5.51E+01	4.35E+01	0.0386
		SVMD-AO-KELM-error	M13	4.20E+01	3.49E+01	0.035

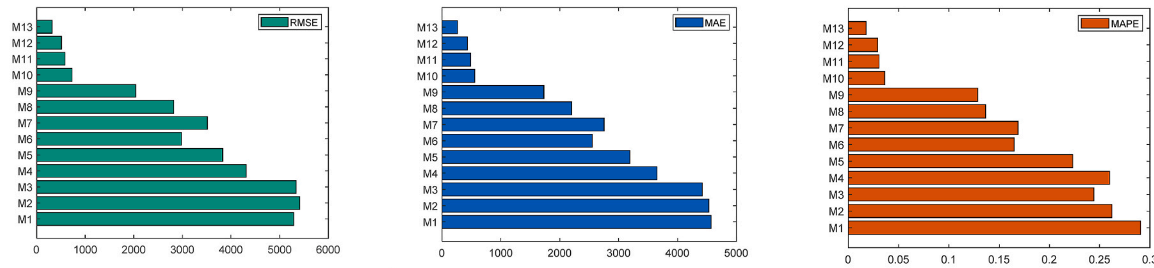
Table 11
Evaluation indexes of different models of case 3.

COVID-19 data		Model	Model Number	Evaluation index		
				RMSE	MAE	MAPE
case 3	daily confirmed cases	RBFNN	M1	2.71E+03	2.28E+03	0.0679
		ELM	M2	2.52E+03	2.10E+03	0.0583
		LSSVM	M3	2.63E+03	2.31E+03	0.0648
		KELM	M4	2.22E+03	1.88E+03	0.0524
		AO-KELM	M5	2.04E+03	1.69E+03	0.0474
		EEMD-ARIMA	M6	1.33E+03	1.27E+03	0.0373
		EEMD-ANN	M7	1.97E+03	1.83E+03	0.0513
		EEMD-KELM	M8	1.05E+03	9.35E+02	0.0283
		SVMD-ELM	M9	8.39E+02	7.21E+02	0.02
		SVMD-LSSVM	M10	7.40E+02	6.17E+02	0.0178
		SVMD-KELM	M11	3.13E+02	2.54E+02	0.0073
		SVMD-AO-KELM	M12	2.23E+02	1.79E+02	0.0052
		SVMD-AO-KELM-error	M13	1.47E+02	1.14E+02	0.0033
	daily death cases	RBFNN	M1	5.79E+01	5.25E+01	0.0473
		ELM	M2	5.95E+01	5.03E+01	0.0443
		LSSVM	M3	4.10E+01	3.77E+01	0.0341
		KELM	M4	3.34E+01	2.97E+01	0.0266
		AO-KELM	M5	1.19E+01	9.57E+00	0.0089
		EEMD-ARIMA	M6	2.96E+01	2.79E+01	0.0259
		EEMD-ANN	M7	3.22E+01	3.00E+01	0.0271
		EEMD-KELM	M8	2.33E+01	1.86E+01	0.0163
		SVMD-ELM	M9	2.09E+01	1.53E+01	0.0134
		SVMD-LSSVM	M10	1.97E+01	1.87E+01	0.0174
		SVMD-KELM	M11	1.18E+01	1.05E+01	0.0094
		SVMD-AO-KELM	M12	8.39E+00	7.22E+00	0.0064
		SVMD-AO-KELM-error	M13	2.52E+00	2.03E+00	0.0019

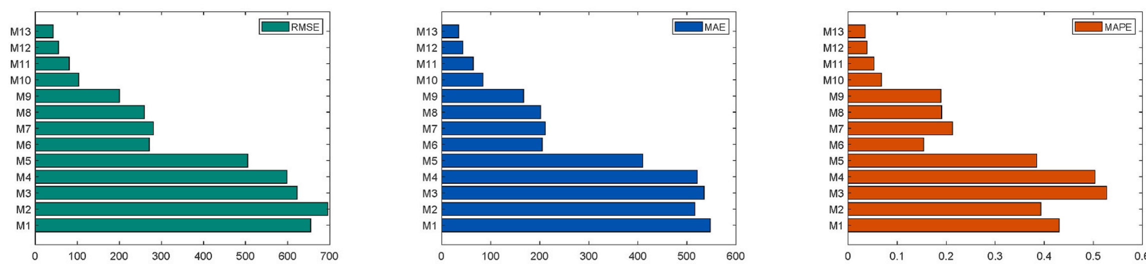
prediction error sequence of case 2 and case 3. Figs. 17 and 18 show that the evaluation index of M13(SVMD-AO-KELM-error) are the smallest. Figs. 19 and 20 show that the error fluctuation of M13(SVMD-AO-KELM-error) are the smallest. Similar to the conclusion of simulation experiment in case 1, the model with the best prediction accuracy is still SVMD-AO-KLEM-error. It is proved that the proposed method is effective and can be used to predict daily confirmed and death cases in COVID-19.

5. Discussion

Some researches on the prediction of COVID-19 daily confirmed and death cases have been carried out. In order to better verify the superiority of the proposed method, a complete discussion is made especially with the latest methods in the literature, such as LSSVM [16], ELM [20], EEMD-ANN [25] and EEMD-ARIMA [27]. Taking Table 8 as an example, RMSE is used as the evaluation index in error. Compared with EEMD-ANN and EEMD-ARIMA, the RMSE of EEMD-KELM decreased by 4.99% and 12.25% respectively. Compared with LSSVM, the RMSE of KELM decreased by 3.07%. All of the above shows that KELM has good prediction performance compared with ANN, ARIMA and LSSVM. Compared with KELM, the RMSE of EEMD-KELM decreased by 43.35%. This shows that after the data is decomposed by EEMD, the intrinsic characteristics of the data can be fully captured, and then the prediction accuracy can be greatly improved. Although EEMD-ANN and EEMD-ARIMA can achieve good prediction results, EEMD has obvious shortcomings. By comparing Fig. 8(a)–(d), it is found that the EEMD deficiency is confirmed due to the appearance of modal aliasing, which affects the prediction accuracy. In the experiment, the prediction effects of EEMD-KELM and SVMD-KELM are further compared, and the RMSE of SVMD-KELM is decreased by 77.21% compared with EEMD-KELM. This shows that SVMD is better than EEMD method with the same prediction method, and the prediction effect is better. It also proves that VMD can improve the prediction accuracy and avoid the shortage of EEMD, but its application is limited by the preset parameter K and α. SVMD, proposed in this paper, uses SSA to adaptively select the K and α

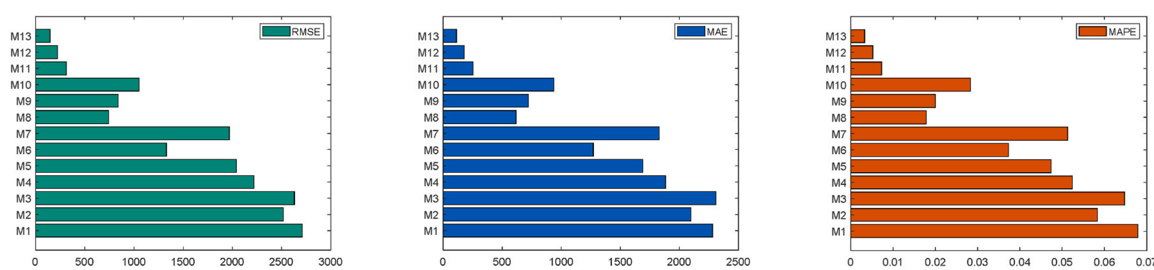


(a) Bar chart of each model evaluation indexes of daily confirmed cases

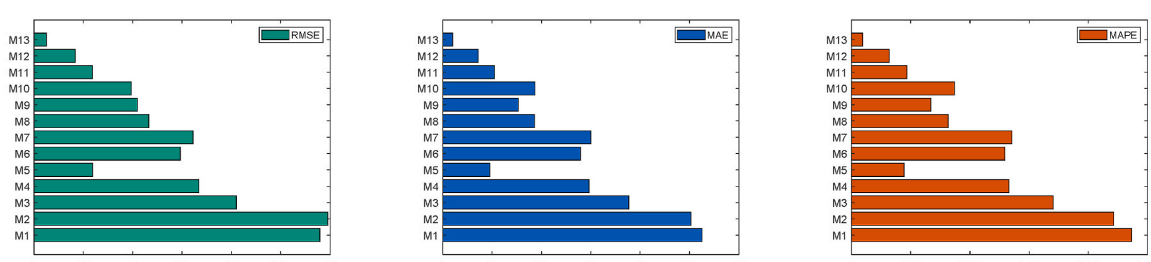


(b) Bar chart of each model evaluation indexes of daily death cases

Fig. 17. Bar chart of each model evaluation indexes of case 2.



(a) Bar chart of each model evaluation indexes of daily confirmed cases



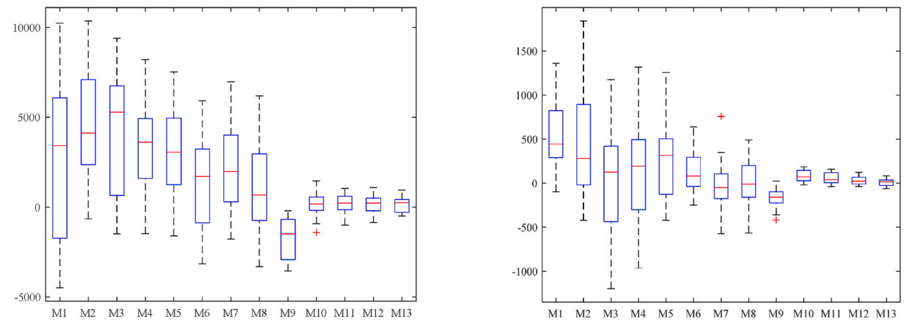
(b) Bar chart of each model evaluation indexes of daily death cases

Fig. 18. Bar chart of each model evaluation indexes of case 3.

of VMD and enhances its adaptability, and is more conducive to its application in prediction of time series.

In this paper, AO is proposed to improve KELM. By observing the convergence curves of the three algorithms in Fig. 9, it can be found that the convergence speed and accuracy of AO algorithm are better than those of PSO and WOA. However, the optimization algorithm has its shortcomings to a certain extent [61–63]. Subsequent research can improve the algorithm, so a better optimization algorithm is developed. Researchers can use better optimization algorithms to improve the prediction model, so as to obtain better optimization results.

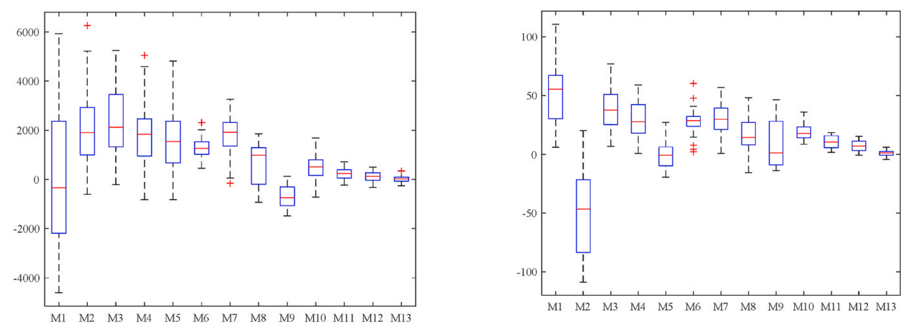
As COVID-19 case data is a nonlinear and non-stationary time series, SVMD is used to decompose COVID-19 case data into a series of stationary time series, which overcomes the shortcomings of EEMD. Comparing the experimental results of models based on SVMD and EEMD, it is concluded that SVMD method has obvious advantages in dealing with COVID-19 case data. The superiority of SVMD method has also been proved in section 4.4.2. The simulation results show that AO-KELM model is used to predict the decomposed sequence, and a good



(a) Box diagram of prediction error sequence of daily confirmed cases

(b) Box diagram of prediction error sequence of daily death cases

Fig. 19. Box diagram of prediction error sequence of case 2.



(a) Box diagram of prediction error sequence of daily confirmed cases

(b) Box diagram of prediction error sequence of daily death cases

Fig. 20. Box diagram of prediction error sequence of case 3.

prediction effect is obtained. By comparing the experimental results, the prediction effect of SVMD-AO-KELM is better than other benchmark models in the model without error correction. When the same forecasting model is used, the model based on SVMD and EEMD is obviously better than the single forecasting model. Although the decomposition-integration model has realized good results, there is still error. To reduce this error, the error correction strategy is used to COVID-19 cases prediction for the first time. Compared with the decomposition-integration model without error correction, SVMD-AO-KELM-error has higher prediction performance. This can be proved in Tables 8–11 So the error correction strategy further rises the prediction accuracy.

The proposed SVMD-AO-KELM-error model is based on decomposition-integration and error correction, which has high prediction accuracy to some extent. However, the proposed model still has limitations. In real life, COVID-19 cases are often affected by temperature, interference of government measures and some other social factors. Therefore, some external factors can be added to the subsequent COVID-19 prediction research to obtain better effect.

6. Conclusion

To promote the prediction performance of COVID-19 cases, avoid the short comings of single model and EEMD-based decomposition-integration model, SVMD-AO-KELM-error is proposed. The innovation is:

(1) This paper proposes a VMD improved by SSA to select the penalty factor and decomposition level of VMD. Compared with EEMD, the original sequence is decomposed by SVMD, which makes the prediction easier and more accurate.

(2) This paper proposes to apply KELM model to predict COVID-19 cases and use AO algorithm to improve KELM. The experimental simulation shows that the prediction performance of KELM is higher than that of single model and the prediction performance of KELM improved by AO is better than that of KELM.

(3) In this paper, the error correction strategy is used to correct COVID-19 cases prediction error for the first time. Experimental result shows the error correction can further improve COVID-19 cases prediction effect.

(4) Twelve comparative models are chosen for experiments to confirm the superiority of SVMD-AO-KELM-error. These experimental results give that SVMD-AO-KELM-error has good prediction accuracy and can effectively predict the COVID-19 daily confirmed and death cases. It also shows the application potential of this proposed model in COVID-19 cases prediction.

Author contributions

Hong Yang: Conceptualization, Methodology. Heng Liu: Data curation, Software, Writing-Original draft preparation. Guohui Li: Supervision, Investigation, Writing- Reviewing and Editing.

Data availability

The data are available at https://data.humdata.org/dataset/novel-coronavirus-2019-ncov-cases.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. The full name of the abbreviation used in this paper

Abbreviation	*Full name*
ARIMA	Auto-regressive integrated moving average
AO	Aquila optimizer
AO-KELM	Improved kernel extreme learning machine by Aquila optimizer algorithm
ANN	Artificial neural network
COVID-19	Corona virus disease 2019
EEMD	Ensemble empirical mode decomposition
ELM	Extreme learning machine
GWO	Gray wolf optimizer
IMF	Intrinsic mode function
KELM	Kernel extreme learning machine
LSTM	Long short-term memory
LSSVM	Least square support vector machine
MMFE	Multiscale multivariate fuzzy entropy
MAE	Mean absolute error
MAPE	Mean absolute percentage error
PSO	Particle swarm optimization
RMSE	Root mean square error
RBFNN	Radial basis function neural network
RNN	Recurrent neural network
SSA	Sparrow search algorithm
SVM	Support vector machine
SVMD	Improved variational mode decomposition by sparrow search algorithm
SLSTM	Stacked long short-term memory
SARIMA	Seasonal autoregressive integrated moving average
USA	The United States of America
UK	United Kingdom
VMD	Variational mode decomposition
WHO	World Health Organization
WOA	Whale optimization algorithm
XGBOOST	Extreme gradient boosting
2019-nCOV	2019 new coronavirus

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