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COVID-19 Epidemic Prediction Based on Deep Learning

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Abstract In this paper, a multi-layer gated recurrent unit neural network (multi-head GRU) model is proposed to predict the confirmed cases of the new crown epidemic (COVID-19). We extract the time series relationship in the data, and the rolling prediction method is adopted to ensure the simple structure of the model and achieve higher precision and interpretability. The prediction results of this model are compared with the LSTM model, the Transformer model and the infectious disease model (SIR). The results show that the proposed model has higher prediction accuracy. The mean absolute error (MAE) of epidemic prediction in most countries (the United States, Brazil, India, the United Kingdom and Russia) is respectively 197.52, 68.02, 200.67, 24.78 and 123.50, which is much smaller than the prediction error of the SIR model, LSTM model and Transformer model. For the spread of the COVID-19 epidemic, traditional infectious disease models and machine learning models cannot achieve more accurate predictions. In this paper, we use a GRU model to predict the real-time spread of COVID-19, which has fewer parameters so that it can reduce the risk of overfitting to train faster. Meanwhile, it can compensate for the transformer model's shortcomings to capture local features.

Keywords COVID-19, deep learning, time series forecasting, gated recurrent unit neural network

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1. Introduction

In December 2019, many patients with "pneumonia of unknown cause" appeared in Wuhan, Hubei Province, China. Through the monitoring of related diseases, a series of infection cases of new atypical viral pneumonia were successively discovered. Since the population in China was at the peak of returning to their hometown during the Spring Festival, the new type of viral pneumonia quickly spread to other regions of China and even neighboring countries in a very short period. On 11 February, 2020, the increasingly severe pneumonia epidemic caused concerns in many countries. The World Health Organization named the pneumonia epidemic caused by a new type of coronavirus "COVID-19", or the COVID-19 epidemic for

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short.

At the early stage of the outbreak of COVID-19 pneumonia, the Chinese government took many intervention measures, including isolating suspected and confirmed patients, closing many transportation channels in Wuhan and timely lengthening the Spring Festival holiday time to avoid population shift, the epidemic had been effectively controlled.

Since March 2020, the epidemic spread rapidly in the United States, the United Kingdom, India and other countries. Up to 5 March, 2022, a total of 443,450,514 COVID-19 cases had been confirmed worldwide with a total of 6,008,173 deaths. Globally, there were 1,724,651 new confirmed cases and 8,889 new deaths in a single day. To prevent and control the global pandemic effectively, it is necessary to understand the dynamics of COVID-19 and predict the infection mode.

Basing and Tay [1], as well as Chitnis, Cushing and Hyman [7], established infectious disease models to understand the infection mechanism and propose corresponding control measures. Sharomi et al. [25] studied transmission and established models to analyze the dynamics of infectious disease. Jajarmi et al. [15] successfully controlled the transmission rate of infectious disease in infants using an improved SIRS model. A similar mathematical model proposed by Baleanu et al. [2, 13] successfully helped clinicians better understand the characteristics of the human liver and the transmission of dengue outbreaks. Most of the data-driven methods used in the previous studies [19] are linear methods, and they have ignored the time series in the data, and do not capture the transmission dynamics of novel coronavirus. Statistical models, such as autoregressive moving average (ARIMA), moving average (MA) and autoregressive methods (ARs), mainly rely on assumptions, but it is difficult for these models to predict real-time transmission rates. Benvenuto et al. [8, 28] established various statistical and mathematical models to simulate the spread of the current COVID-19 outbreak. However, these models do not fit the given data perfectly in many cases, and have low accuracy in predicting the growth of COVID-19 transmission. James and Tripathi [16] used the concept of derivative to calculate the acceleration of confirmed infection and death cases, and then applied the multivariate linear function and the calculus chain rule of the composite function of the confirmed infection to determine the acceleration of the death function. They fit different ARIMA models for the acceleration of each death function, and found that seasonal changes affect the transmission of the virus. Jia [17] et al. proposed two impulsive systems to describe the impact of multilateral imported cases of COVID-19. Based on the published data, they simulated and analyzed the epidemic trends under different control strategies. R_0 is commonly used to measure i to predict how many people will be infected by an infected person where additional weights are placed on people who have never been infected with the current disease or who have not been vaccinated. If a disease has an R_0 value of 10, an infected person will spread the disease to 10 persons around. Zhang et al., [28] used the R_0 method to determine the infection rate of the new virus on the Diamond Prince cruise ship. However, it is difficult to find the origin of the infectious disease by identifying the patient zero and the people whom they interacted with during the incubation period by using this method. Baleanu et al. [3, 14, 27] proposed complex nonlinear models to address infectious diseases. While these epidemiological models are good at capturing important components of infectious diseases, some assumptions are needed to make on the parameters. In addition, if these hypothetical parameters do not fit the data perfectly, the accuracy of the models is low.

The above research has not considered that the spread of COVID-19 is dynamic, and the dataset of COVID-19 contains time series, so it is logical to use a sequence of networks to extract patterns. The data processed are inherently dynamic, and deep learning models can capture the dynamic changes between data well, such as recurrent neural networks, which are well suited for modeling spatiotemporal sequences. Long short-term memory (LSTM) is a novel recurrent network architecture in combination with a proper gradient-based learning algorithm. Ghany, Zawbaa and Sabri [11] predicted the confirmed and death cases of COVID-19 based on LSTM with ten hidden units (neurons). Chandra, Jain and Chauhan [5] applied recurrent neural networks such as LSTM, bidirectional LSTM and encoder-decoder LSTM models in multi-step (short-term) COVID-19 infection forecasting. Based on the results of the LSTM network, Vinay and Zhang [6] predicted the possible ending point of the outbreak would appear around June 2020.

Polyzos, Samitas and Spyridou [23] proposed a Transformer model that is used to perform language translation. The transformer is a model architecture that entirely relies on attention mechanisms to draw global dependencies between input and output. Fitra, Yudistira and Mahmudy [9] used Transformer to find the best hyperparameters to model the growth of COVID-19 cases. Jin, Wang and Yan [18] developed a new neural forecasting model based on the idea of transformer, which is called attention crossing time series (ACTS), and that makes forecasts via comparing patterns across time series obtained from multiple regions.

The large number of parameters and slow training speed of LSTM, as well as the inherent shortcomings of transformers in local feature capture, have prompted us to look for other deep learning methods. Compared with LSTM and transformer, GRU has fewer parameters so that it reduces the risk of overfitting to train faster. Meanwhile, it can compensate for the transformer model's shortcomings to capture local features. In this paper, we use a GRU model to predict the real-time spread of COVID-19, which can help public healthcare providers and policymakers make the necessary arrangements to deal with a potential surge in COVID-19 patients.

2. Data processing

The COVID-19 epidemic data studied in this paper come from the daily data on epidemics provided by Johns Hopkins University in the United States (https://github.com/CSSEGISandData/COVID19/tree/master/csse_covid_19_data/csse_covid_19_time_series). We used daily series data on the new confirmed cases and deaths of the five countries (the United States, the United Kingdom, Russia, India and Brazil) from 22 January, 2020 to 20 September, 2021. At data preprocessing stage, we first remove the invalid recorded data in the sequence data and missing values which are linearly interpolated.

2.1. Data Differentiation

In the time series data of source datasets, the daily data represent the cumulative number of confirmed and death cases. Therefore, the first-order difference is performed on the confirmed and death data to obtain daily new confirmed and death cases for five countries. We select the new diagnosed cases and new deaths during the first 7 days before prediction as the time lag features.

2.2. Data smoothing and structure processing

According to the records of the official documents in the data, due to the influence of the recording time and other factors, the data fluctuate greatly, and there are many abnormal values. This paper adopts the moving average method with the three-time step (7 days, 14 days and 21 days). By comparing the final prediction performance, we find that the prediction performance of the model is the best when the time step size is 7. Therefore, subsequent smoothing operations use +7 as the step size. At the same time, considering the influence of the week on the prediction, we have added the week as additional variables. We turn the week of the predicted day into the form of one-hot vector as the week features. Our input features are shown in Table 1.

At last, the standard input data form is [1, 20], which involves 14-time lag features, 7-week features and outbreak days' features.

Table 1. Summary of model variables

Dependent variable	Daily new infections
	1 lag in daily new infections
	2 lags in daily new infections
	3 lags in daily new infections
	4 lags in daily new infections
	5 lags in daily new infections
	6 lags in daily new infections
	7 lags in daily new infections
Independent variable	1 lag in daily new deaths
	2 lags in daily new deaths
	3 lags in daily new deaths
	4 lags in daily new deaths
	5 lags in daily new deaths
	6 lags in daily new deaths
	7 lags in daily new deaths
	Week feature in the predicted day

3. Model building

For the US data set, since its epidemic data are recorded at the county level of each state and the statistics are different, it is impossible to train an accurate prediction model. This paper selects Arizona as the representative, and constructs a GRU neural network model to forecast daily new infection cases. Then, we use the national COVID-19 infection and death data for outbreak forecasts of other countries.

3.1. GRU neural network model

In order to make full use of the previous historical data to predict the development trend of the COVID-19 epidemic in the future period, some researchers use LSTM. However, since GRU outperforms LSTM and has a simpler gate structure (Hidasi et al., [12]), we use GRU for sequence recommendation in this paper.

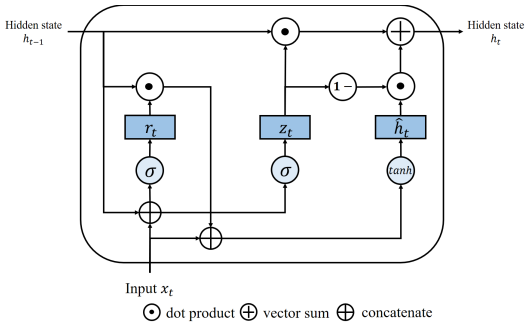

Figure 1. Structural framework of GRU neural network

Figure 1 illustrates the structure of the GRU layer. The hidden state h_t of GRU neural networks module at the $t-th$ interaction x_t is the linear representation of the previous hidden state h_{t-1} with the candidate hidden state $\hat{h}_t$,

$$h_t = z_t \odot h_{t-1} + (1 - z_t) \odot \hat{h}_t, \tag{3.1}$$

where z_t is the update gate, which expresses how much of the hidden state the unit updates from the previous state, and $\odot$ is the element-wise multiplication operator. The z_t can be written as

$$z_t = \sigma(w_z x_t + U_z h_{t-1} + b_z). \tag{3.2}$$

Similar to the update gate, the reset gate r_t can be expressed as

$$r_t = \sigma(w_r x_t + U_r h_{t-1} + b_r), \tag{3.3}$$

where $w_z, w_r \in \mathbb{R}^{1\times d}$ and $U_z, U_r \in \mathbb{R}^{1\times d_h}$ are the weight parameters corresponding to x_t and h_{t-1}, and b_z, b_r are bias. $\sigma(\bullet)$ is a sigmoid function for non-linear projection.

The candidate hidden state $\hat{h}_t$ is computed by

$$\hat{h}_t = tanh(w_h x_t + U_h(r_t \odot h_{t-1}) + b_h, \tag{3.4}$$

where r_t is the reset gate, $w_h \in \mathbb{R}^{1\times d}$ and $U_h \in \mathbb{R}^{1\times d_h}$ are the weight parameters, and b_h is a bias. The last hidden state $h_{|I^u|}$ is used as the input hidden layer for the next prediction based on the current sequence.

Considering the long-time span of the data of the COVID-19 epidemic, to better predict the trend of the novel coronavirus disease in the future, this paper adopts a multi-layer GRU neural network structure to capture the internal connection between the historical epidemic data to achieve better prediction effect. The structure diagram is as shown in Figure 2.

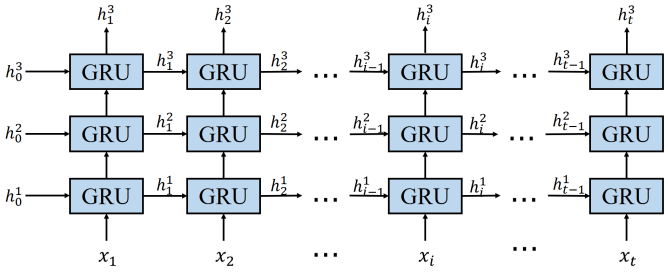

Figure 2. Neural network model structure diagram

A multi-layer gated recurrent unit neural network (multi-head GRU) model is constructed for prediction. The model parameters are the same as the base

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predictor, as shown in Table 2.

Table 2. GRU neural network base predictor parameters

Layers	3
Number of hidden layers	128
Learning rate	0.005
Iterations	500
Dropout	0.1
Batch	10
Training set: Test set	8:2

3.2. Baseline model

In order to verify the effectiveness and performance of the proposed model, we choose and train three baseline models including LSTM deep learning model, Transformer model and the infectious disease dynamics model (SIRS).

LSTM is a recurrent neural network that can learn and predict time series. LSTM is widely used in COVID-19 prediction studies [5, 6, 23]. We build a LSTM deep learning prediction model as a baseline model to predict the number of confirmed COVID-19 cases in the five countries. By inputting the number of COVID-19 confirmed cases and deaths in the previous seven days up to t days, LSTM will output the predicted number of confirmed for $t + 1$ days.

We also use a Transformer model as another baseline model. Transformer model entirely relies on an attention mechanism to draw global dependencies between input and output. Transformer is widely used in NLP and CV fields, and has shown a high performance in sequence models. In this study, we use a Transformer sequence predictor to predict the confirmed number of COVID-19. For specific model parameter settings, see Table 3.

Table 3. LSTM and Transformer predictor parameters

LSTM		Transformer	
Number of hidden layers	128	Length of input window	120
		Length of output window	1
Number of layers	1	Number of layers	1
Learning rate	0.001	Learning rate	0.001
Iterations	500	Iterations	100
Dropout	0.2	Dropout	0.2
Batch size	10	Batch size	10
Training set: Test set	8:2	Training set: Test set	8:2

The third baseline model is the infectious disease dynamics model. This kind of model is based on the survival characteristics of the population. In all the relevant models, the susceptible-infected-recovery base model (SIR model) is a commonly used model due to its simplicity. The SIR infectious disease model divides the population into the following three forms.

(1) Susceptible: S category, which refers to the people who have not been infected by the infectious disease, but are likely to be infected;

(2) Infected: I category, which refers to the people who have been infected and can infect other individuals;

(3) Recovered: R category, which refers to the people who have died, been isolated or recovered and will not be infected again.

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The above three groups of people all change with time t, so we denote the numbers of the three kinds of people as S_t, I_t and R_t respectively.

It can be represented by the following process diagram.

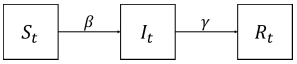

Figure 3. Flow chart of SIR model propagation

The entire system is in a closed state, population flow is not considered, there is no impact from outsiders, and the impact of infectious diseases on the population is far greater than the changes in the population itself. Therefore, if the total amount of the above three populations remain unchanged, it is expressed by the following formula

$$S_t + I_t + R_t = N. \tag{3.5}$$

The SIR infectious disease model can be expressed as the following system of differential equations

$$\begin{cases} \frac{dS(t)}{dt} = -\frac{\beta SI}{N}, \\ \frac{dI(t)}{dt} = \frac{\beta SI}{N} - \gamma I, \\ \frac{dR(t)}{dt} = \gamma I, \end{cases} \tag{3.6}$$

where the the initial numbers S_0, I_0 and R_0 of the three groups of people are all greater than or equal to 0.

The infected person is infectious. First, the contact rate is defined as the number of people who are in contact with an infected person per unit time. Usually, it is set as a function $U(N)$ of the total number of people N. Taking the probability of its infection as b, the number of susceptible people that an infected person can infect in a unit time at time t is $U(N)bS_t/N$, which is called the effective contact rate. There are two assumptions about the contact rate. The first assumption is that the contact rate is a linear function of the total number of people N, that is, $U(N) = rN$. The second assumption is that the contact rate is the constant r, then the disease incidence rate is rbI_tS_t/N, by denoting rb by β, the disease incidence rate is $\beta I_tS_t/N$, called standard incidence, and the SIR model uses standard incidence for modeling.

In the unit time at time t, the infected person is isolated, dead or cured, and will not be infected again, then it is removed from the infected person type, and the number of infected persons is proportional to the number of infected persons I_t. Let the removal intensity be γI_t.

3.3. Model evaluation indicators and result analysis

In this study, MAE is selected as the index to evaluate the performance of the models. It is the average value of the absolute value of the error between the predicted value and the actual value. The smaller the MAE value is, the higher the effectiveness of the model is. The calculation formula is as follows,

$$MAE\,(X,h) = \frac{1}{m}\sum_{i=1}^{m} |h(x^{(i)} - y^{(i)})|. \tag{3.7}$$

We use neural network and SIR models to fit the COVID-19 epidemic in each country, and apply the data of the training set to fit the relationship model between

each feature and the number of new infected persons per day, which finally establishes a COVID-19 epidemic prediction model. By comparing the prediction results of different model methods, the proposed model has better prediction accuracy. The performance of the multi-layer GRU neural network in the five countries is shown in Figures 4-8.

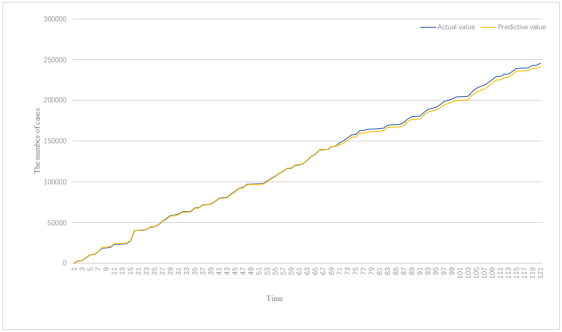

Figure 4. Trends of daily predicted and actual values of COVID-19 in in the United States

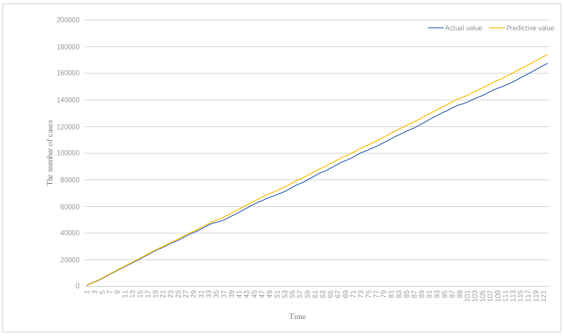

Figure 5. Trends of daily predicted and actual values of COVID-19 in Brazil

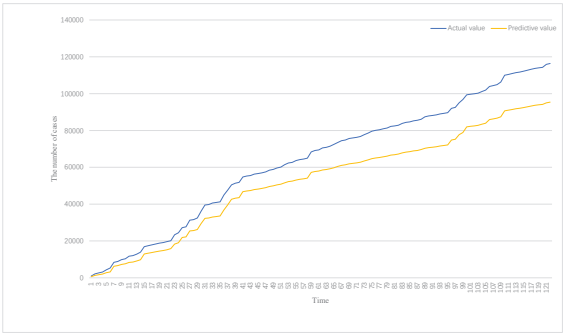

Figure 6. Trends of daily predicted and actual values of COVID-19 in the United Kingdom

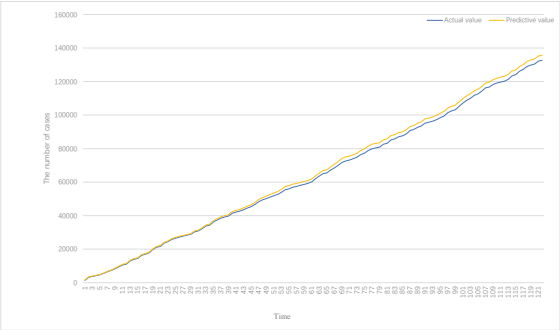

Figure 7. Trends of daily predicted and actual values of COVID-19 in India

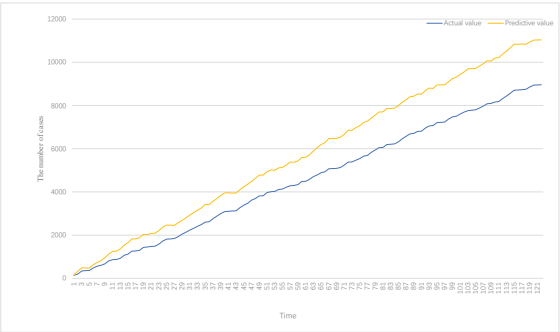

Figure 8. Trends of daily predicted and actual values of COVID-19 in Russia

We also compute the MAE under three baseline models, and the MAE of the four models is shown in Table 4. From Table 4, the MAEs of multi-head GRU neural network are smaller than all of the three baseline models in the five countries except India, which indicate the effectiveness of the proposed model.

Table 4. The MAE of each model in prediction.

Models	*MAE in regions*				
	America	Brazil	India	U. K	Russia
Multi-head GRU neural network	197.52	68.02	200.67	24.78	123.5
LSTM	899.39	174.84	244.58	28.52	142.52
Transformer	997.25	451.41	1012.04	185.05	157.77
SIR Model	552.45	224.72	613.56	134.37	367.49

From the prediction results in Figures 4-8, it can be found that the deep learning prediction model based on the multi-layer GRU neural network proposed in this paper has good prediction performance and can fully capture the before and after dependencies of time series data. At the same time, it can consider a variety of environmental factors as features, and has high accuracy in predicting the epidemic trend of various countries with a good generalization effect. However, since deep learning requires a huge amount of data for training, the requirements for data are relatively high.

It can be seen from this that the traditional infectious disease dynamics model is not particularly effective in the simulation and prediction of the novel coronavirus pneumonia epidemic. This is because the basic assumptions of the model are not met, and the COVID-19 virus has a long incubation period. Therefore, the infected person is not easy to be detected, and there are asymptomatic infections, leading to the incompleteness of the model in considering parameters. Deep learning technology can learn and gain experience from the historical data, improve its performance in tasks and continuously adjust itself to deal with future tasks, and it has strong generalization ability. This can provide accurate prediction guidance for the prediction of epidemic prevention and control, and the effect of the real world needs to be verified in the future.

4. Conclusion

In this paper, we propose the deep learning methods of the multi-head GRU neural work to predict the COVID-19 pneumonia epidemic in five countries. We select the updated daily data of overseas epidemics provided by Johns Hopkins University in the United States, and extract the daily confirmed and death data of the United States, Brazil, the United Kingdom, India and Russia. In terms of variable selection, we take daily new diagnoses and deaths as input variables, and use 7-period lagged data and weeks as independent variables, resulting in a total of 21 independent variables. We find that the multi-head GRU model has a high degree of fit for the epidemic situation in various countries with a good generalization effect.

To examine the effectiveness of the proposed model, we use LSTM, Transformer and SIR models as the baseline models. The results indicate that multi-head GRU neural network has the smallest MAE among the four models in the five countries except India. Although the LSTM prediction model is not as good as the multi-head GRU model, it also shows potential in predicting the novel coronavirus pneumonia epidemic. However, for the dynamic model of traditional infectious diseases, it has been difficult for the SIR model to meet the needs of accurately predicting the development of the epidemic. We also use Transformer, an attention mechanism model that is not commonly used in the novel coronavirus epidemic prediction research, but the prediction results are not good. The role of attention mechanism in the prediction of the novel coronavirus epidemic needs to be further verified.

In conclusion, the improved deep learning model can effectively solve the novel coronavirus epidemic time series forecasting problem and provide good prediction ability.

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