

COVID-19 Epidemic Trend Forecast Research

Xiao Shiyang

Zhang Hongli

Cheng Hongyuan

Wang Yu

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This article uses SEIR Model and LSTM Model pair 6 High-risk country COVID-19. The epidemic forecast is simulated and evaluated and analyzed SEIR Model and LSTM. The accuracy of the model's predictions, and COVID-19. The peak of the epidemic and the future 5. The cumulative number of confirmed diagnoses for the day is estimated. The purpose of this article is to help understand COVID-19. To understand the current development trend of the epidemic. If you want to know the relevant data of this article And program code, please visit [project-stat223](https://github.com/project-stat223).

Key words: COVID-19, SEIR, LSTM, Predictive analysis

1

introduction

COVID-19 It is a major public health event. Although governments have adopted various measures to protect cities or countries, such as Through restrictions, traveller isolation requirements, contact tracing, etc., the large-scale global population movement has caused the rapid spread of the disease and spread it all over the world. While the epidemic is under control in China, COVID-19. The global spread of has caused a surge in Asia, Europe, the Middle East and North America. As of 2020 year 5 month twenty four Day, as the global epidemic risk continues to increase, the 215. There are already more than 5,103,006 Cases with 333,401 People lost their lives.

COVID-19 It has constituted a global pandemic and has spread to most countries and regions in the world. By understanding the development trend of confirmed cases in a certain area, the government can adopt corresponding policies to control and respond to the epidemic. However, in the face of this new infectious disease and its complex features with many unknown factors, a single model estimate may yield biased results, and the prediction results produced by different mathematical models are inconsistent. Therefore, in order to achieve objective estimation, we have studied and implemented the two most commonly used methods: SEIR Model and LSTM Model, forecast Up COVID-19. The spread of the spread.

2 Related research

Many scholars use SEIR. The model predicts the epidemic situation in Hubei and the whole country. Yang et al. (2020) Think the scale of the epidemic is 2. Reached its peak in the second half of the month, to 4. Decrease gradually at the end of the month. If the lockdown of Wuhan is postponed by five days, the scale of the epidemic in mainland China will triple. Wang Siyuan et al. (2020) The peak of the predicted epidemic situation in Hubei Province is at 2 month twenty one day, 5 month 10. Around the end of the epidemic, the cumulative number of deaths is 6471 example. Qing Dengli et al. (2020) According to the effective regeneration number, it is reduced to 1. It can be seen that the "turning point" of the epidemic situation in Hubei and the whole country is at 3. Has appeared at the beginning of the month. Sun Deshun et al. (2020) Select 2020 year 1 month 10 To 2 month 28. Related data of the day, established SEIR. The results of the model suggest that strict isolation of the incubation period and the infected population, while continuously increasing the removal rate of patients, can effectively control the epidemic of the infectious disease. Liu et al. (2020) Use four stages SEIR Model captured COVID-19. The evolution trajectory, effective prediction COVID-19. The peak value, scale and duration. As the UK is in COVID-19. The initial response was incorrect, so it will become another epicenter. Marimuthu et al. (2020) The study found that the implementation of public health interventions will delay the peak period and cause the epidemic curve to flatten. In the absence of public health interventions, the peak period will be in the first 94 Day; if there are effective interventions, such as lock-in 42 Days, social distancing, contact tracing and case isolation, the peak period will be delayed 44 Days, and In the first 138 Day happens. Tomar et al. (2020), Yan et al. (2020) research shows LSTM. The fit of the neural network is closer to the actual value, The prediction accuracy is high. yud Use long-term short-term memory LSTM Method to understand covid-19. The increasing correlation over time has found that it is difficult to obtain exactly the same number of confirmed cases over time, but LSTM Can provide similar patterns between actual and forecast. the result shows, LSTM Is a promising predictive tool by learning from big data and potentially disseminating covid-19. A pandemic can predict future outbreaks.



Figure 1: SEIRmodel

Reddy et al. (2020) Based on the epidemic data, evaluate key characteristics to predict current Canadian and global COVID-19. The trend of the outbreak and the possible end time, using LSTM Network, the results show that the possible end of the outbreak is 2020 year 6 Around the month. In addition, we also compared the spread rate of the epidemic in Canada, Italy and the United States, and found that the United States has the highest transmission rate and Canada has the lowest transmission rate.

3 research method

3.1 SEIRmodel

based on COVID-19 Epidemiological characteristics of infection, usually adopted SEIR Model to study the dynamics of this disease. SEIR The model is a deterministic population spread model. It assumes that the total population remains unchanged and that each individual in the same "bin" has the same characteristics. It classifies the population, and each type exists as a "bin". SEIR The model divides the research objects into S, E, I, R Four types: 1) S is susceptible (susceptible), indicating a potentially infectious population. The individual is susceptible before infection, that is, the individual may be infected by neighboring individuals. 2) E Latent state (exposed), which means a group that has been infected but did not show symptoms of infection. 3) I is infected (infected), which means that a person showing symptoms of infection will also infect susceptible individuals that they can come into contact with with a certain probability. 4) R is removed state (removed) Means people who are out of the system and are no longer affected by infectious diseases.

Remember $S(t), E(t), I(t), R(t)$ Respectively time t The number of susceptible persons, the number of latent persons, the number of infected persons, and the number of evacuated persons obviously have $S(t) + E(t) + I(t) + R(t) = N$, among them N is the total population. Suppose a susceptible person τ The probability of being in contact with an infected individual and being infected is β . Since the proportion of susceptible individuals is S/N , At the moment t There are a total of $I(t)$ Infected individuals, so susceptible The number of individuals changes according to the following rate of change:

$$\frac{dS}{dt} = -\beta \frac{SI}{N} \quad (1)$$

Correspondingly, the number of latent individuals increases according to the following rate of change, and the overall probability per unit time σ Transformed into an infected individual:

$$\frac{dE}{dt} = \beta \frac{SI}{N} - \sigma E \quad (2)$$

The number of infected persons is provided by the latent group, and individuals are at the same time with a unit time probability γ Converted to removal status:

$$\frac{dI}{dt} = \sigma E - \gamma I \quad (3)$$

Correspondingly, those who move out with probability γ Conversion from the infected group to the remover group:

$$\frac{dR}{dt} = \gamma I \quad (4)$$

SEIR The essence of the model is a system of ordinary differential equations about time. The disease trend it predicts depends only on the parameters and start time.

3.2 LSTMmodel

LSTM model (Long Short-Term Memory) Is a recurrent neural network used in the field of deep learning (RNN) Architecture is passing Systematic RNN In the model, the training algorithm used is the time-series back-propagation algorithm (Back Propagation Through Time, which is BPTT). BPTT It is an extension of the cyclic network that relies on backpropagation, expressing time through a series of well-defined and orderly calculations that connect one time step to the next. When the calculation time of the model is long, the residual error that needs to be returned will show an exponential drop, resulting in slow update of network weights, and RNN The long-term memory effect of the model cannot be reflected, so LSTM The model came into being. LSTM Model by Hochreiter et al. (1997) It is proposed that a memory unit is added between the neuron units of each hidden layer, which can learn long-term dependence on information and avoid RNN Long-term dependence that cannot be solved. Since then, many scholars have improved it, making LSTM Got on many issues

Widely used and achieved considerable success (Gers et al., 2000; Graves et al., 2005b,a; Schmidhuber et al., 2007; Bayer et al., 2009; Schaul et al., 2010; Graves et al., 2013; Bayer et al., 2014).

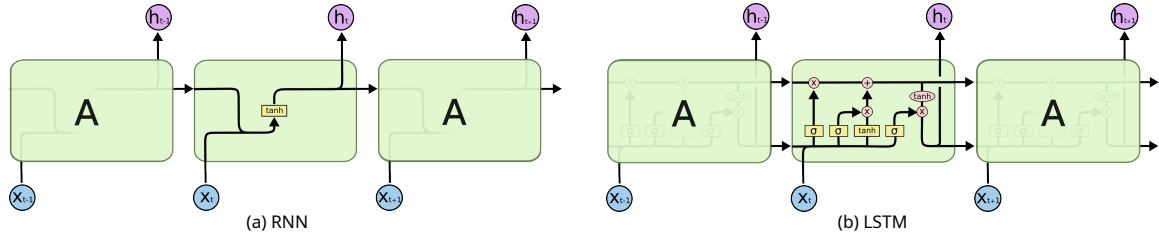


Figure 2: RNN Model and LSTM The structure of the model

Figure 2 shows RNN Model and LSTM The structure of the model, where the blue circle x indicates input information, purple circle h indicates the output information, the yellow box represents the neural network layer, and the pink circle represents point-by-point operations, such as vector addition. Each line carries from a node the vector of the input that is output to another node. The merged line represents the connection of the vector, while the separated line represents that its content is copied and then distributed to different locations. From the picture 2 visible, RNN versus LSTM The biggest difference is -LSTM There is an additional information conveyor belt at the top level, namely Cell state C_t , which is where the information is remembered, and this is also LSTM Core.

LSTM Pass is called the gate (gate) Structure regulation, with the ability to delete or add information to the cell state. The door is a selective The way information passes is determined by σ (sigmoid) Composed of neural network layers and point-by-point multiplication operations. σ Layer output 0 To 1 The value between describes how much each amount of information can pass. 0 It means "no amount is allowed to pass", 1 It stands for "Allow any amount to pass." Common LSTM The unit consists of a cell and an input gate (input gate), an output gate (output gate) And a forgotten door (forget gate) composition. The cell remembers the value at any time interval, and three gates control the flow of information in and out of the cell.

LSTM In the model, the first step is to decide what information to discard from the cell state. This decision was made through a process called the "forgotten door layer" σ Layer decision. The gate will read h_{t-1} with x_t As input, for cell state C_t Each number in the output is one in 0 To 1 The value between, denoted as f_t , Indicates how much information is retained, 1 Means "full retention of information", 0 Means "discard information completely."

$$f_t = \sigma(W_f \cdot [h_{t-1}, x_t] + b_f) \quad (5)$$

The second step is what information is stored in the cell state. The first is called "input gate layer" σ The layer decides which information needs to be updated, the The probability is expressed as i_t ; Then enter in the door layer \tanh Layer to create a new candidate value vector C_t , Add it to the cell state.

$$i_t = \sigma(W_i \cdot [h_{t-1}, x_t] + b_i) \quad (6)$$

$$C_t = \tanh(W_c \cdot [h_{t-1}, x_t] + b_c) \quad (7)$$

The third step is to update the old cell state. f_t Indicates that the last information has been forgotten C_t Degree, i_t Indicates that the candidate value C_t . The degree of joining, through the combination of the two information in the second step, it is truly realized which old information is removed, which new information is added, and finally the cell's information is obtained. status C_t .

$$C_t = f_t * C_{t-1} + i_t * C_t \quad (8)$$

The final step is to determine what to output, that is, to decide what kind of prediction to make. First, by running the "output gate layer" σ Layer to determine the output cell state C_t Which parts of the cell; then, pass the cell state through \tanh Layer to process so that the value is in -1 versus 1 Between and then versus σ The output of the layer is multiplied, and the final output determines the part of the output.

$$o_t = \sigma(W_o \cdot [h_{t-1}, x_t] + b_o) \quad (9)$$

$$h_t = o_t * \tanh(C_t) \quad (10)$$

4 Current status of the epidemic

This article selects six countries with more severe epidemics other than China as the research objects, namely the United States, Russia, Brazil,

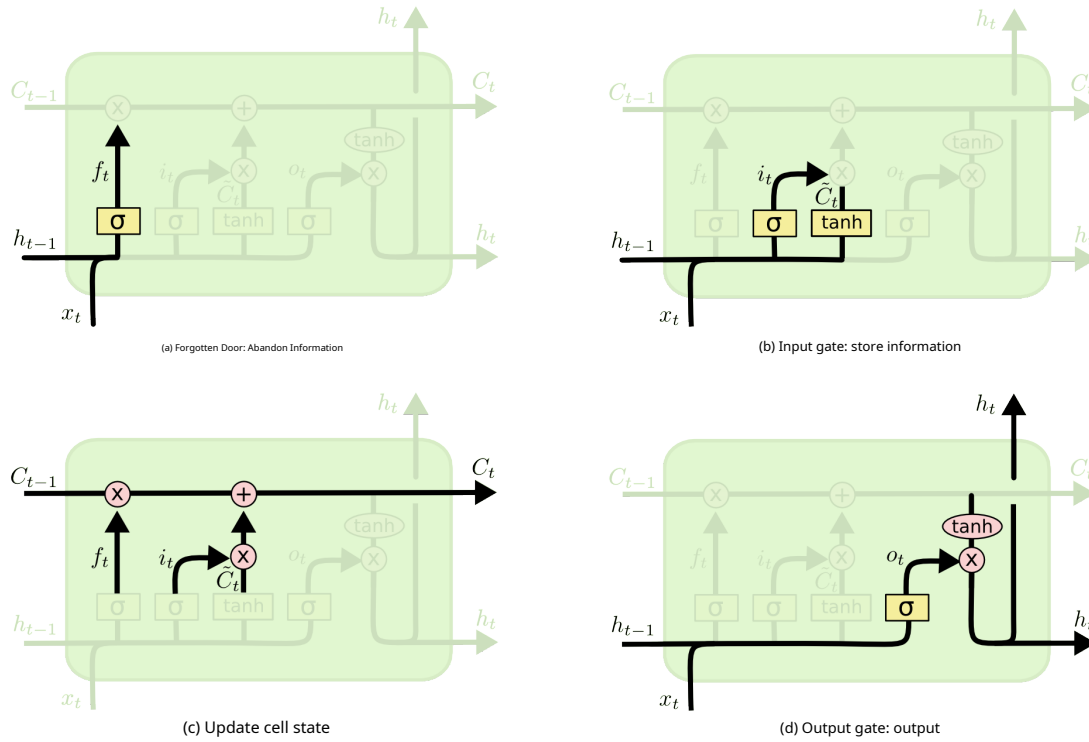


Figure 3: LSTM Information flow

The United Kingdom, Italy, and Germany, represented by these six countries, have a general analysis and processing of the global epidemic data. First, draw a line chart of the cumulative number of confirmed diagnoses in six countries to get a general understanding of the stage of the outbreak in each country.

It can be seen that the number of confirmed diagnoses in the United States has grown much faster than the other five countries. In contrast to the rapid growth of the United States, the number of confirmed cases in the remaining five countries has grown relatively flat. The following will temporarily remove the United States from the line chart. The current situation of the epidemic situation in five countries To exhibit, and the first of the five countries to appear 100. The date of the confirmed case is set as the start date, namely 2020 year 2 month twenty three day.

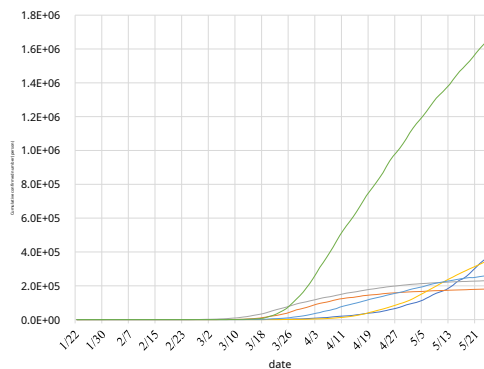


Figure 4: Cumulative number of confirmed cases in six countries

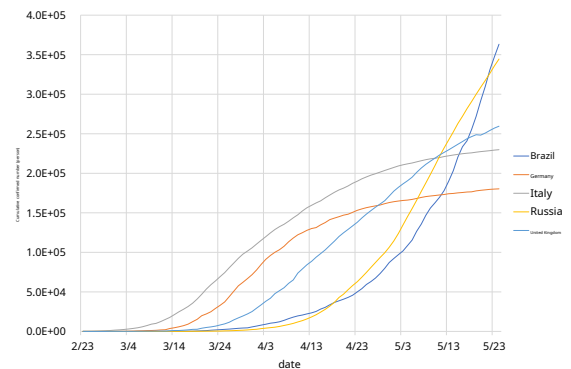


Figure 5: Cumulative number of confirmed cases in five countries

Generally speaking, the epidemic curve will follow the trend of rising first-reaching the peak-and finally falling. From the picture 5 It can be seen that among the five countries, Brazil and Russia are rising at a relatively obvious rate, and Brazil's growth rate is significantly higher than that of Russia. The rising trend of the other three countries still exists, but it is gradually flattening, and the epidemic situation in these five countries They have not reached their inflection point and peak position. Judging from the current situation, the prevention and control measures of the epidemic cannot be relaxed, and countries must persist in implementing the management policies related to the epidemic and implement various epidemic prevention measures.

The further establishment of relevant indicators for epidemic data will help to further understand the development of the epidemic in various countries. Cut off 5 month twenty four Day, U.S. cumulative

table 1: Epidemic data related indicators

	Cumulative confirmed number	mortality rate	Cure rate	Percentage
Brazil	438812	5.0%	23.6%	0.0022
Germany	182452	2.3%	42.9%	0.0022
Italy	231732	10.4%	23.5%	0.0038
Russia	379051	0.8%	10.4%	0.0026
United Kingdom	269127	11.1%	1.3%	0.0040
United States	1768461	4.5%	7.9%	0.0054

The number of confirmed cases has exceeded 176 Million. In terms of the cumulative number of confirmed cases, the United States not only ranks first among these six countries, it is also the country with the largest number of confirmed cases in the world. Judging from the mortality rate, Russia's mortality rate is the lowest, not enough 1%, The UK mortality rate is as high as 11.1%, Is the country with the most serious deaths among the six countries. At the same time, the cure rate in the UK is also the lowest among the six countries. This result is due to the lack of its medical system. The inadequacy of medical treatment makes the UK's ability to treat patients relatively low. Patients can only be admitted to the hospital when their symptoms are more severe and critical. It is not difficult to understand that the mortality rate and cure rate are very low for patients with severe conditions. Up. The cure rate in Germany is the highest, which has a lot to do with the improvement of the German industrial system. The independent production of anti-epidemic equipment such as masks and protective clothing ventilators can meet the needs of the German people to the greatest extent. Moreover, after the outbreak of the epidemic in Germany, strict prevention and control and adequate isolation were achieved. In addition to Germany, the cure rates in Brazil and Italy are also at a relatively high level (twenty three% about). The proportion in the above table refers to the proportion of the country's cumulative number of confirmed cases in the country's total population. It can be seen that the United States has the largest proportion of confirmed cases, followed by the United Kingdom.

5 Empirical analysis

5.1 data

This article starts with 2020 year 1 month twenty two Day to 2020 year 5 month twenty four Daily COVID-19 Epidemic data is used as a sample data set. COVID-19 Epidemic data From the Center for Systems Science and Engineering at Johns Hopkins University (CSSE) which provided COVID-19 Global database. The relevant national population data comes from United Nations Statistics Division.

5.2 SEIR Simulation evaluation of the model

When the model predicts the epidemic situation, this article uses the mortality rate, cure rate, the country's total population, and the current diagnoses, mortality, and The calculation formula of the cure rate is as follows:

$$\text{Mortality} = \frac{1}{n} \sum_{i=1}^n \frac{\text{Daily cumulative deaths}}{\text{Daily cumulative number of diagnoses}} \quad (11)$$

$$\text{Cure rate} = \frac{1}{n} \sum_{i=1}^n \frac{\text{Daily cumulative number of people cured}}{\text{Daily cumulative number of diagnoses}} \quad (12)$$

among them n is the number of days in the study interval.

Because there is still a lack of reliable COVID-19 For the data at the beginning of the outbreak, the start date of the model is set to the first occurrence of each country. 100 The date since the confirmed case, which indicates that the model start dates for the six observed countries are different. based on SEIR Model, this article predicts the development trend of the epidemic situation in six countries. The growth trajectory and prediction results of the cumulative number of confirmed cases in six countries are shown in the figure 6 And table 2 Shown.

table 2: Epidemic peak forecasts in six countries

	Brazil	Germany	Italy	Russia	United Kingdom	United States
Peak day	81	169	85	51	49	55
Peak value (*10 ₄)	2261.3	104.3	499.5	6290	2,965.8	13643

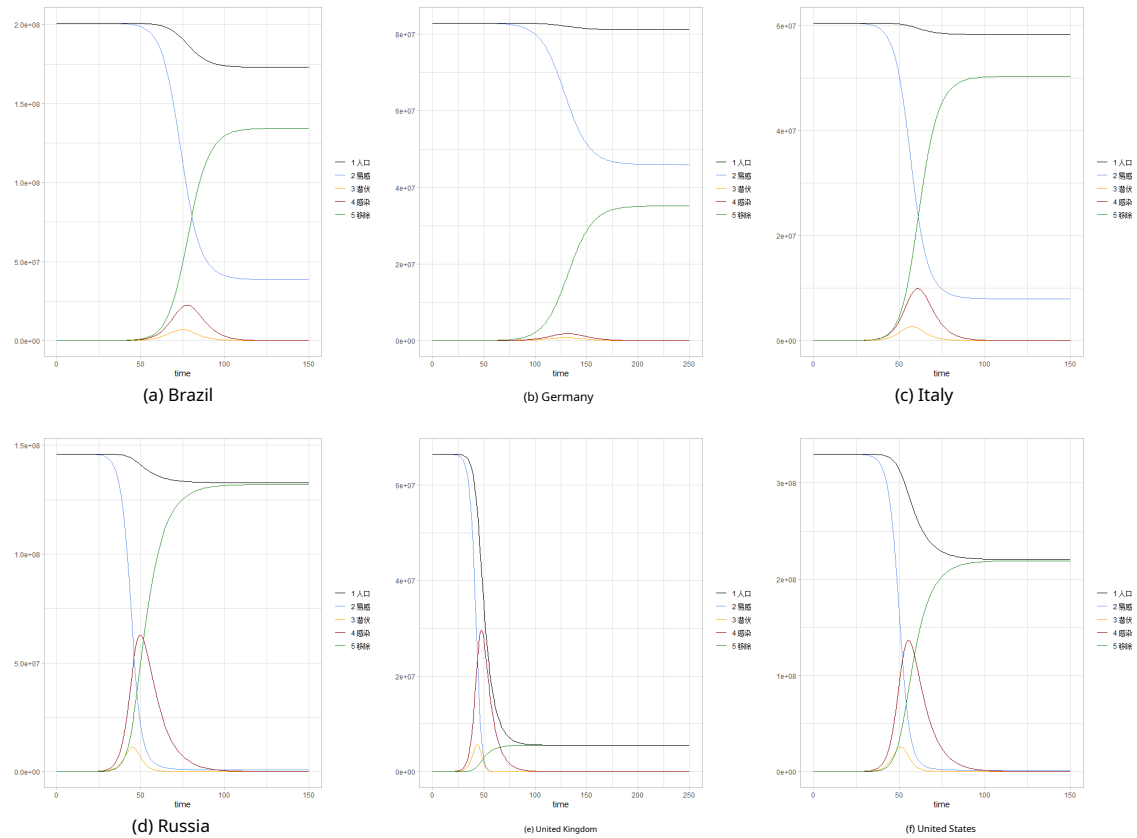


Figure 6: SEIRModel simulation

It can be seen that after the outbreak, the number of susceptible people in the UK will drop significantly, that is, the increase in the number of people in the incubation period is relatively large, and the number of infected people will reach a peak when the number of infected and susceptible people cross. The model predicts that the peak is reached after 49 days, that is, the cumulative number of confirmed diagnoses on the month and day reaches the peak, and the predicted peak is 2,965.8 ten thousand people. Compared with France, the number of susceptible people in Germany has decreased less, and there is no overlap between the number of infected and susceptible people. The model predicts that Germany's cumulative number of confirmed diagnoses reached a peak every day, and the time span was long. On the whole, the spread of the epidemic in Germany is relatively stable, and the number of people predicted to peak is also the least among the six countries. The number of people predicted to peak is 104.3 ten thousand people. Unlike other countries, the British SEIR curve, the number of susceptible people and the total population of the country fell sharply during the forecast period and eventually stopped at a low level, indicating that the spread of the epidemic in the UK is extremely rapid and the consequences of the spread (refer to its mortality and cure rate) are particularly serious. As of now, the cumulative increase in the number of confirmed diagnoses in the UK is still on the rise. If the UK government does not take more stringent measures, the predicted results of the model are likely to become a reality. The model predicts that the peak date in the UK will be very short, and it is set after the initial date. 49 days, and predict that the final cumulative number of confirmed diagnoses will exceed 2900 ten thousand people, this prediction result should get the government's attention. From the U.S. SEIR it can be seen from the model diagram that the peak number of infected people in the United States is at an extremely high level. After the model has stabilized, the country's total population is very close to the number of migrants. Citizens will be infected with the new coronavirus, and the number of susceptible people is extremely low. The model sets the peak date after the initial date. 55 days, and predict that the final cumulative number of confirmed diagnoses will exceed 130,000,000, which is the highest number of predicted cumulative confirmed cases among the six countries. Due to the relatively low cure rate in Russia, the 25—35 day, the number of people in the latent state and the infected state began to accelerate, and in the first 41—51 days the sky reached a peak and then began to decline. The model predicts that the peak number of infections in Russia will be at 500 more than 10,000, which is relatively high. Moreover, after the end of the epidemic, the total number of confirmed cases in Russia accounted for a relatively high proportion of the total number of people in the country. Italian SEIR According to the simulation results of the model, it can be seen that in the early stage of the epidemic, the number of people in both the latent state and the infected state is on an upward trend. 30 day-40 Around the sky began to accelerate growth, in the first 75 day-85 The sky reached a peak, then began to decline until it disappeared. After the epidemic ended, the cumulative number of confirmed diagnoses reached 499 ten thousand people. Brazil and Italy SEIR The results are similar, but the difference is that the model sets the peak date in Brazil after the start date 70—81 Day, a little earlier than the peak in Italy, but the cumulative number of confirmed diagnoses at the peak is much larger than that in Italy. The model predicts that the peak will reach 2261.3 ten thousand people, the result of the expansion of the epidemic is also quite serious.

5.3 LSTM Simulation evaluation of the model

for LSTM For each cell state in the time series, the unit starts from 4 Obtain the case count in consecutive dates, and output the subsequent 5 Forecasts for dates. Of this article LSTM The model is using *KerasTrained*. Apply the following five optimization algorithms: *Adam*, *SGD*, *AdaDelta*, *Adagrad* with *RMSProp*. And combine the following four loss functions: *MSE*, *MAE*, *Huber* as well as *Log Cosh*. Compared the above 20 Species group Combined performance in minimizing losses.

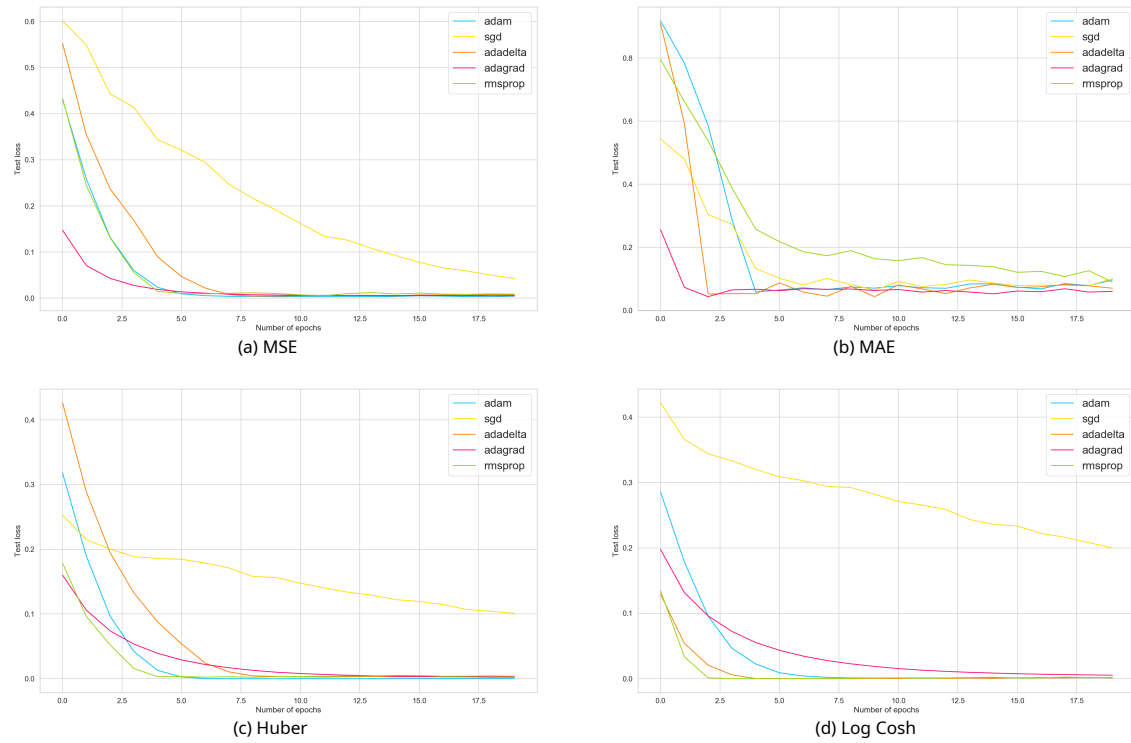


Figure 7: Performance comparison between different loss functions and optimizers

As shown in Figure 7, SGD is the worst-performing optimizer, the reason may be SGD is unable to adapt to the learning rate, no momentum is set, and training is unstable, causing it to always bounce around the local minimum. MAE is the worst loss function, each optimizer does not converge to close to zero. In spite of AdaDelta, AdaGrad with RMSProp, the performance is good in some specific situations, but this article chooses in the following empirical Adam Optimizer and MSE. The loss function is combined because its convergence speed performance is more consistent. And, by comparing the number of models in different training rounds (epoch) and the prediction step size (lookback), the final selection of training rounds is 70. The prediction step size is 4. This may be because the model running too little or too much will lead to under-training or over-training, making the data under-fitting or over-fitting. Will be the last 7 Day's data set is used as the test set, and the rest are used as the test set to train on the data of each country, LSTM. The training simulation results are shown in the figure 8.

5.4 SEIR versus LSTM Model prediction

will 2020 year 1 month 22 to 2020 year 5 month 18. The daily epidemic data is used as the training set and used separately SEIR Model and LSTM Model prediction 5 month 19 Day to 5 month 24. Japan, Brazil, Germany, Italy, Russia, the United Kingdom and the United States COVID-19. Accumulate the number of confirmed cases and compare their RMSE loss. As table 3, As shown, LSTM Model RMSE is much smaller than SEIR Model.

table 3: Forecasts for six countries RMSE Loss comparison

	Brazil	Germany	Italy	Russia	United Kingdom	United States
SEIR	15498478	4315	3905940	19031588	1082278	10278735
LSTM	12,229.01	1,905.93	2031.12	6,644.43	5,508.75	19200.5

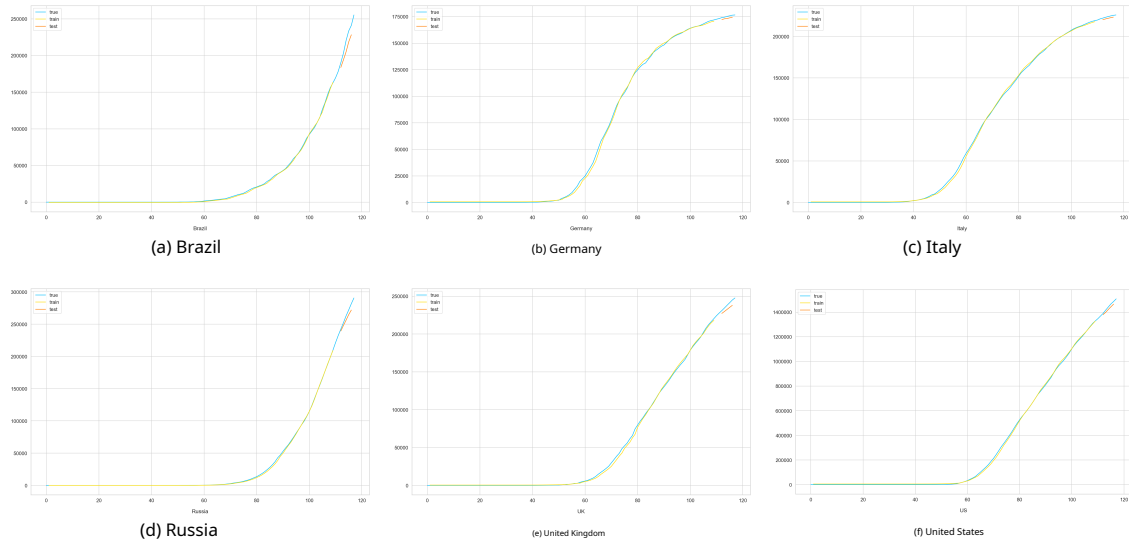


Figure 8: LSTMModel simulation

Use separately SEIRModel and LSTMModel for the future 55 days of the world COVID-19. The cumulative number of confirmed diagnoses is predicted because the data of all countries/regions are considered, so that the model extracts more information, which makes the model more accurate.

table 4: Forecast of the global number of confirmed cases

	05/25	05/26	05/27	05/28	05/29
SEIR	106816753	120811582	136419044	153760588	172947403
LSTM	4897492	4996472	5102424	5210817	5310362

6 discuss

From the perspective of mathematical models, SEIRThe model is used to estimate infectious diseases, and LSTMThe model is used in time series forecasting analysis. versus SEIR Compared with the model, LSTMThe model can better fit the existing data because it is trained on the existing data, but it cannot accurately judge and fuse infectious features. So think LSTMThe model is more suitable for short-term forecasting. on the other hand, SEIRThe model introduces more variables and factors by considering the interaction and association of multiple populations, which is more in line with the development of infectious diseases, but when different intervention measures are considered, the prediction results will be very different.

This article has some limitations. Mathematical models quickly merge multiple inputs to produce prediction results. However, this process involves assumptions about uncertain factors. For example, it is difficult to accurately determine the extent to which people comply with local government quarantine policies or measures, and public behaviors that may affect the actual contact rate and subsequent contact rates, such as hand washing, Wear a mask, social distance, etc. These models also lack sufficient data to estimate the isolation ratio of specific populations. In fact, the evolution of infectious diseases is quite complicated, and our research only considered the most classic SEIRModel, did not expand it, for LSTMThe model does not consider the influence of parameters such as the number of hidden layers and the number of iterations on the model. In addition, there are many unconsidered factors, such as the mode of transmission of the virus, demographic characteristics, and natural environment. For example, air pollution may accelerate the spread of the virus. The detection rate of the virus, the quantity and quality of medical resources (such as test kits and medical professionals who perform the tests) also vary among countries.

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