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Evaluation of COVID-19 based on SEIR model

This article intends to establish a reasonable infectious disease model

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Abstract

for COVID-19, and establish reasonable predictive indicators through this model to express the virus infection status of the city over a period of time. Finally, predict the development status of the virus in 2021 and provide corresponding suggestions for government use. Firstly, this article studies a variety of mature infectious disease mod- els, and selects and improves the SEIR model that is closest to COVID-19. This article produced an understanding model of the COVID-19 in- fection mechanism. Secondly, the second question requires selecting reasonable indica- tors to evaluate the virus infection in the city. This paper selects the predictive index k, which itself is only related to the virus propagation time, and presents a change subject to the derivative of the logisic func- tion. This paper sets the parameters a, b and c as the parameters of k, and calculates the formula of the citya¿r´s predictive index k based on the specific infection development of the city. With the help of the formula of predictive index k, the citya¿r´s infected persons can be passed over a period of time. The number extrapolates the number of exposed persons to evaluate the level of virus infection in the city. According to the formula of predictive index k, the third question is directly calculated in Excel. The first nine months are the real data, the next three months are the test data, and the next year is the forecast data, and the k value of Guangdong Province is obtained. Image, and then get the forecast data for the second year according to the k value, and get the data image of Hubei Province in the same way. Finally, based on the model, this article gives suggestions for epidem- ic prevention in Guangdong Province.

Keywords

COVID-19, SEIR model, Gradient descent.

1. Introduction

1.1. Problem Background

The clinical characteristics of the pneumonia caused by the COVID-19 outbreak in 2019 showed that the virus-infected person had fever symptoms and impaired respi- ratory status, and the existence of super spreaders was not ruled out, and the presence of asymptomatic infections contributed to the epidemic Prevention and control have brought huge challenges. For the prevention and control of the epidemic, some schol- ars analyzed the impact of disinfection, personnel movement, and temperature on the spread of the virus. Accurately predicting the trend of the epidemic will play an im- portant role in the guidance of epidemic prevention and control.

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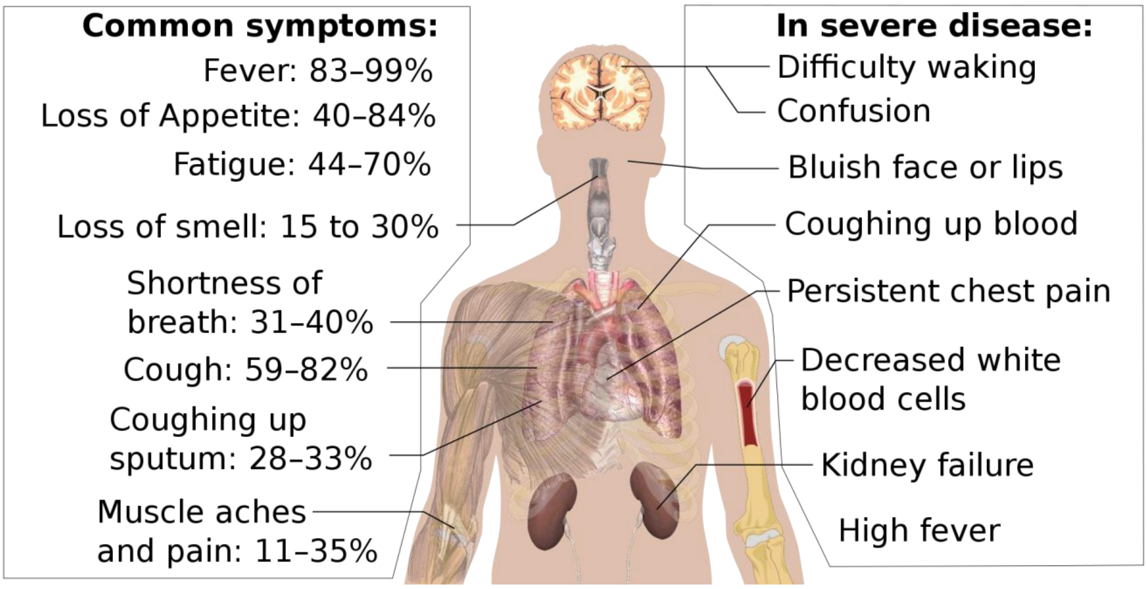

Figure 1: Symptoms of Coronavirus Disease 2019

1.2. Restatement of the Problem

Build a mathematical model to describe the situation of COVID-19.

According to the model, introduce an indicator to assess the level of COVID-19 in the city.

Based on the introduced indicators, predict the COVID-19 levels in multiple cities in 2021.

Provide a one-page report to the local government to describe the current situ- ation of COVID-19 in the city and provide suggestions on how to organize city events to slow the spread of COVID-19.

2. General Assumptions and Term explanation

2.1. Assumptions

To simplify the problem, we make the following basic assumptions.

The number of people infected with the virus per unit time is proportional to the current infected people.

The number of people infected with the virus per unit time is proportional to the current latent population.

Asymptomatic patients are included in the latent.

Patients in the incubation period per unit time are transformed into infected per- sons in a fixed proportion.

The infected person is converted into a removal state (cured or dead) in a fixed proportion within a unit time.

After a normal person is infected, it enters a period of incubation period. People in the incubation period will not show symptoms and can infect healthy people and are contagious.

When a patient is admitted to the hospital, it means that the patient is treated in isolation and is considered unable to contact others, so it will not infect healthy people.

Investigate the impact of population dynamics such as births, deaths, and mi- gration on the total population during the period of disease transmission in the region. That is: the total

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population remains unchanged.

2.2. Term explanation

The population within the epidemic area of infectious diseases is divided into the following categories:

Category S(Susceptible), refers to people who have not gotten the disease, but lack immunity, and are susceptible to infection after contact with infected people;

Category E(Exposed), refers to people who have been in contact with an infected person, have been infected with the virus but are in the incubation period, and have not shown signs of infection;

Category I(Infectious), refers to a person who has contracted an infectious disease and can spread to S class members and turn them into E class members;

Category R(Recovered), refers to a person who is isolated or has immunity due to illness.

3. Model Preparation

3.1. Notations

The primary notations used in this paper are listed in Table 1.

Table 1: Notations

Symbol	Definition
k	predicted index
t	virus spread time
S	number of susceptible people
E	predicted index
I	virus spread time
R	number of susceptible people
N	predicted index
β	proportion of susceptible people converted to exposed and infected
γ_1	proportion of exposed persons converted to infected persons
γ_2	proportion of infected persons converted into cured persons

3.2. Model Overview

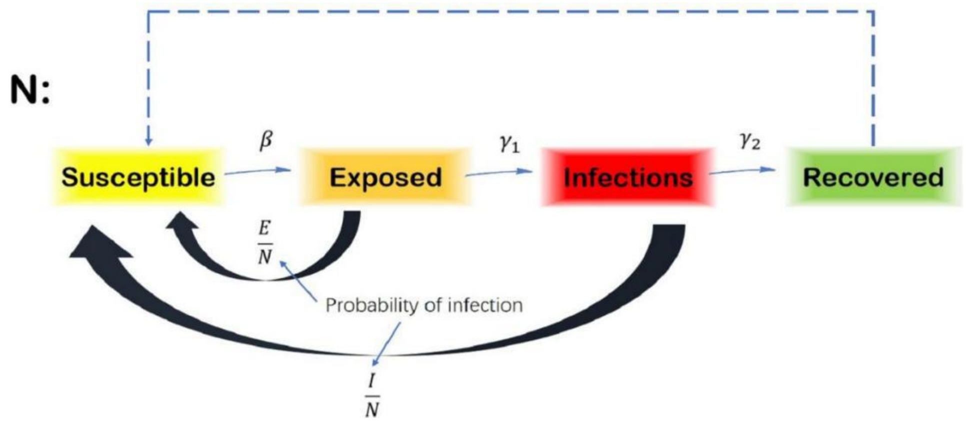

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Figure 2: Model Overview

4. Model Establishment

Different types of infectious diseases have their own characteristics. To be familiar with the transmission characteristics of a certain infectious disease requires in-depth

medical physiology research. Therefore, this article only builds a model according to the general mode of virus transmission. There are many well-known and mature in- fectious disease models, among which models established by differential equations are more suitable for practical applications. According to the transmission characteristics of COVID-19, this article selects suitable models from I model, SI model, SIR model, SIRS model, SEIR model, etc. And makes appropriate optimizations to establish the mathematical model of this article.

The I model is the simplest model, which starts from the number of infected peo- ple and effective contact rate. But the I model does not distinguish between infected people (patients) and uninfected people (healthy people). Therefore, as time increas- es, the number of patients will increase indefinitely, which does not meet the eighth assumption.

The SI model is improved on the basis of the I model, distinguishing the infected and uninfected. However, the SI model does not take into account that patients can be cured. As a result, healthy people in the population can only become patients, and patients cannot become healthy people. This does not meet the fifth assumption.The common SI model is shown below:

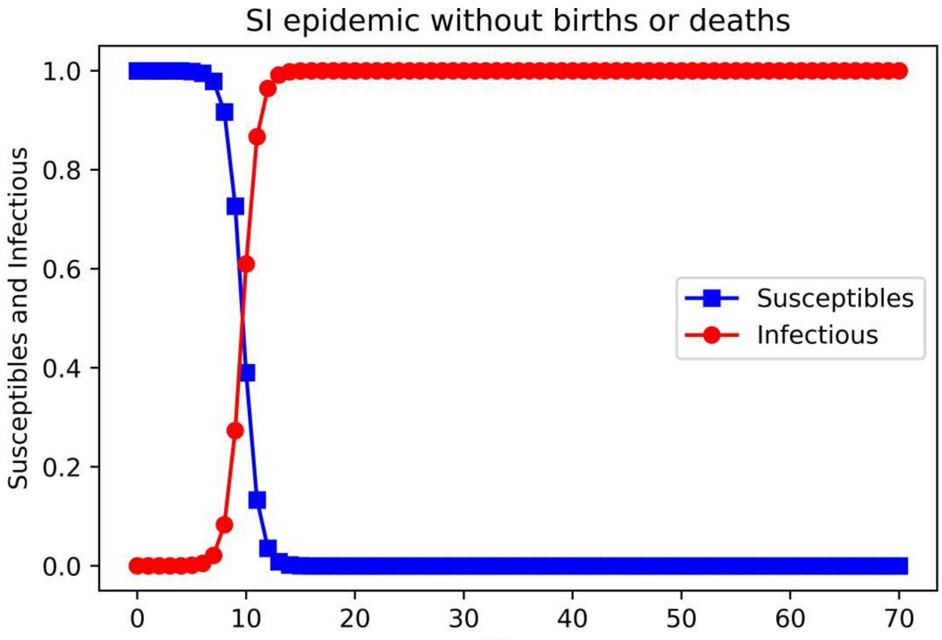

Figure 3: SI model

The SIR model is improved on the basis of the SI model, taking into account the situation that the patient has a strong immunity after healing, that is, the number of removers (including the dead and the cured) is increased. However, it did not consider the exposers that appeared during the infection process, which did not meet the sixth assumption.

The SIRS model is improved on the basis of the SIR model. If the infectious disease studied is non-lethal, but the immunity obtained after recovery cannot be maintained for life, the recovered person may become susceptible again.

The SEIR model is improved on the basis of the SIR model, adding exposers.

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Taking into account the assumptions listed in this article, the SEIR model is chosen as the basis for this modeling. The common SEIR model is shown below

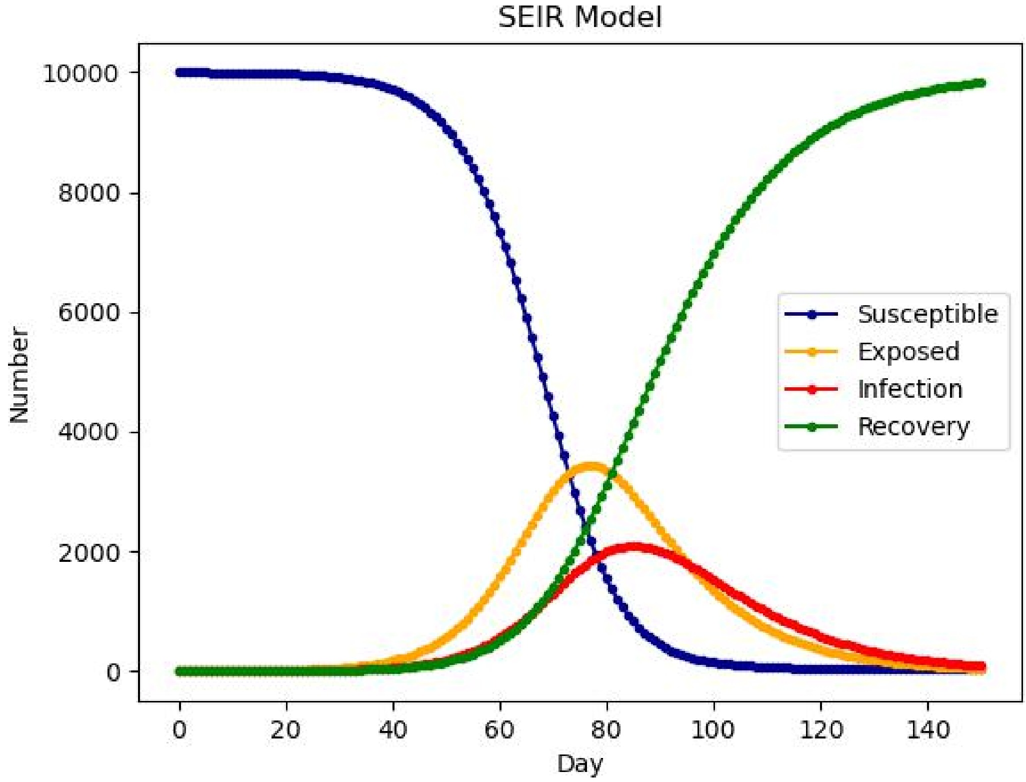

Figure 4: SEIR model

The universal SEIR model is as follows:[1]

$$\frac{dS}{dt} = -\beta SI$$

$$\frac{dE}{dt} = \beta SI - \gamma_1 E$$

$$\frac{dI}{dt} = \gamma_1 E - \gamma_2 I$$

$$\frac{dR}{dt} = \gamma_2 I$$

In response to the special situation of COVID-19, exposed persons can infect sus-ceptible persons. We make the following adjustments to the formula:

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$$\frac{dS}{dt} = -\frac{\beta S (I + E)}{N}$$

$$\frac{dE}{dt} = \frac{\beta S (I + E)}{N} - \gamma_1 E$$

$$\frac{dI}{dt} = \gamma_1 E - \gamma_2 I$$

$$\frac{dR}{dt} = \gamma_2 I$$

5. Assess the Level of COVID-19

Question two requires the introduction of an indicator to assess the current level of COVID-19 in cities. The level of COVID-19 in the city at this stage should not be the number of confirmed patients (I) that day, but the number of potential lurkers (E) in the population based on the change in the number of confirmed patients. Relevant de- partments quickly formulate plans based on the number of lurkers, in order to use the lowest cost and the fastest speed to curb the development momentum of the epidemic and maximize the protection of susceptible people(S).[2]

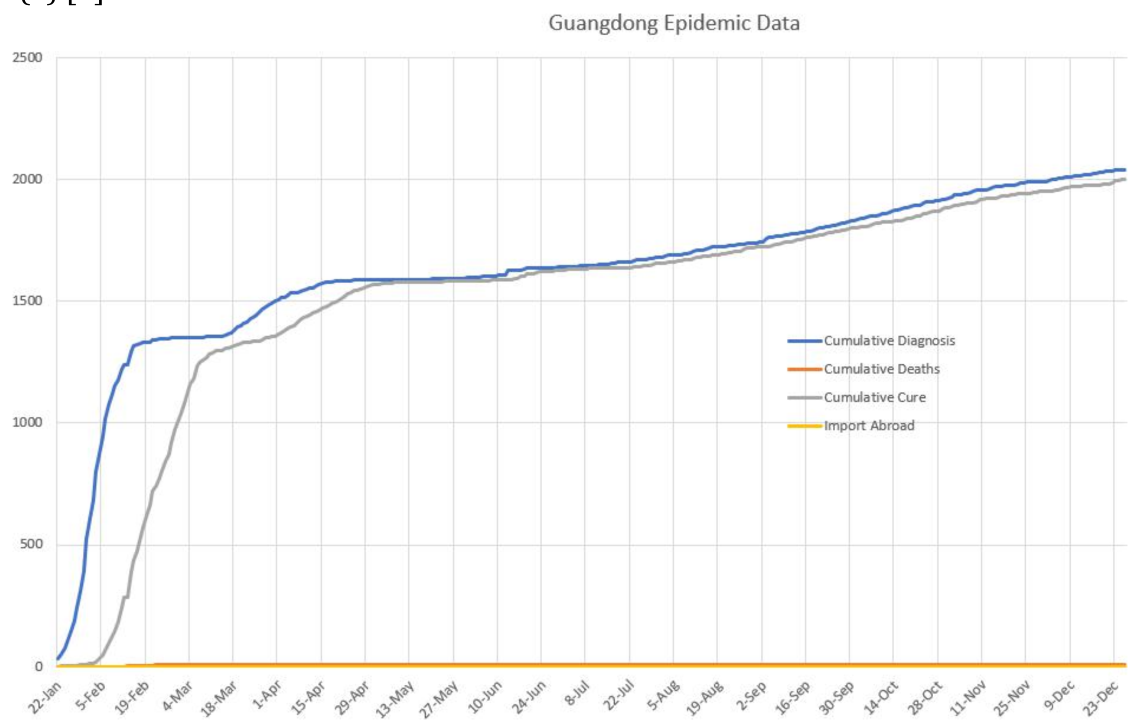

Figure 5: Guangdong Epidemic Data

Therefore, this paper introduces the prediction index k (t) as an indicator. k repre- sents the ratio of confirmed patients (I) to latent patients (E) at a certain time, and the relationship is as follows:

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$$k(t) = \frac{ce^{-a(t+b)}}{(1+e^{-a(t+b)})^2}$$

Among them, a, b, and c are model parameters.

Since the incubation period of COVID-19 is 7-14 days, the relationship can also be determined:

$$I(t) = \gamma_1 E^{\cdot} t - \bar{t}^{\Sigma}$$

Among them, *t* represents latency.

the loss function using the number of infected persons is:We assume that the growth of infectious diseases conforms to the logisic function, and the prediction index k(t) obeys the logisic derivative function. Use preset parameters to fit the k-t curve, and get the loss function of the number of infected people as:

$$Loss = \frac{\sum^{n}}{n}_{i=1} (I_{r,i} - I_{s,i})^2$$

Among them, $I_{r,i}$ and $I_{s,i}$ are the true number of infections and predicted number of infections on day *i*.

Through the epidemic data of Guangdong Province, we get the curve of the prediction

index k (t)

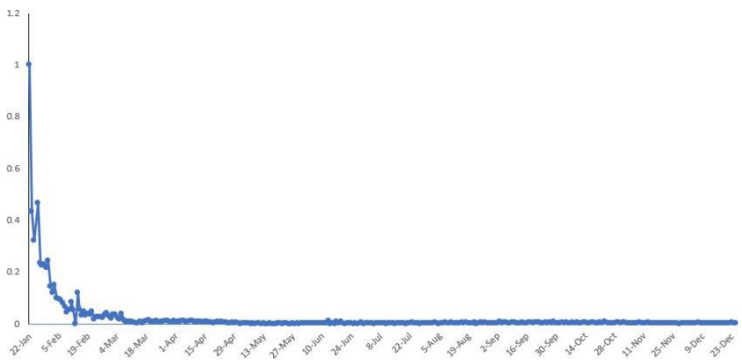

Figure 6: k (t)

Analysis of the epidemic situation in Guangdong Province based on the image: Before January 22, that is, at the beginning of the COVID-19 outbreak, the epidem- ic situation in Guangdong Province was urgent. From January 22 to early February, Guangdong initiated Level I response to major public health emergencies, and car- ried out necessary prevention and control isolation measures, such as restricting or stopping markets, rallies, theater performances and other crowd gathering activities, The population takes preventive work to prevent the virus from spreading excessive- ly between people, and the epidemic is basically under control. After February 10, the development of the epidemic was effectively controlled. After February 15th, the number of people cured in Guangdong Province increased rapidly, while the number of existing infections declined rapidly.

6. Forecast COVID-19 Levels

According to the formula,

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$$k(t) = \frac{ce^{-a(t+b)}}{(1+e^{-a(t+b)})^2}$$

The calculation is performed directly in Excel. The first nine months are the real data, and the last three months are the test data. The k value image of Guangdong province is obtained as follows:

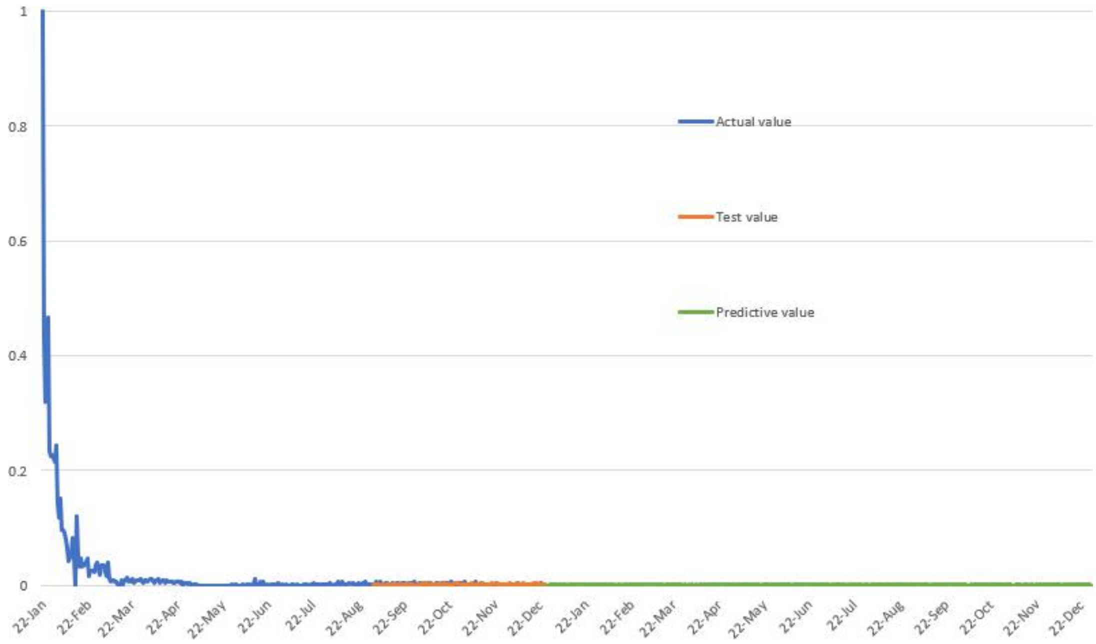

Figure 7: K Value Map of Guangdong Province

Using the previous curve, the development trend of the COVID-19 epidemic was predicted. The prediction recurrence formula is as follows:

$$S(n+1) = S(n) - \frac{\beta(n)S(n)I(n)}{N}$$
$$E(n+1) = E(n) + \frac{\beta(n)S(n)I(n)}{N} - \gamma_1 E(n)$$
$$I(n+1) = I(n) + \gamma_1 E(n) - \gamma_2 I(n)$$
$$R(n+1) = R(n) + \gamma_2 I(n)$$

According to the formula, directly perform calculations in Excel, and get the pre- diction image of Guangdong Province as follows:

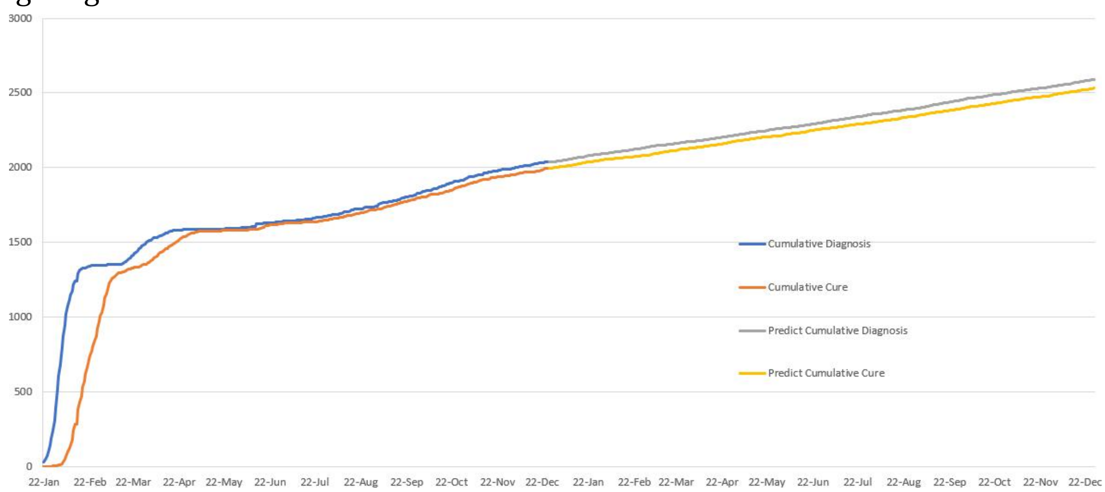

Figure 8: Guangdong Province Forecast Image

With reference to the current epidemic prevention status, the possibility of a new large-scale

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epidemic outbreak is unlikely. It is predicted that the epidemic will be ef- fectively controlled in 2021, but due to the influence of mutant viruses and other influ- ences, the possibility of local outbreaks is possible.

Using the same method, we analyzed Hubei province and got:

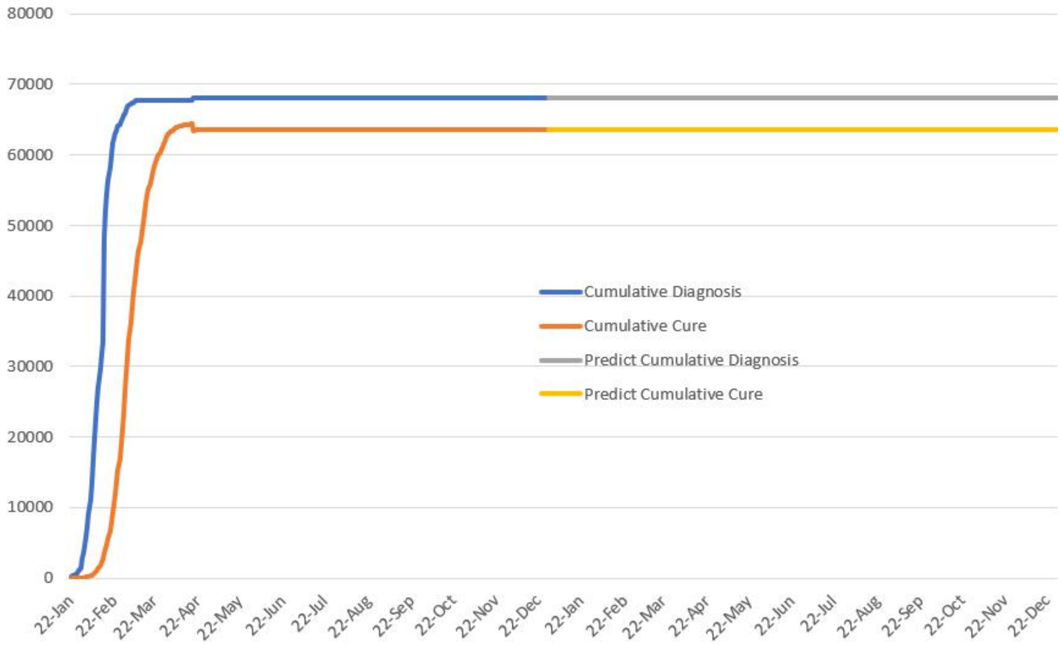

Figure 9: Hubei Province Forecast Image

Although Hubei Province was the outbreak point of the epidemic in China at first, due to the later epidemic prevention measures in place and no imported cases, accord- ing to the current state, it will be in a state of zero for a long time. If there is no special emergency, the epidemic has been controlled.

7. A Report to the Local Government

Dear government staff:

Our team has established an infectious disease model for the COVID-19 virus, and conducted a comparative analysis of the data in your city.

Based on the predictive index k set by the model and the development of urban in- fections in the past week, we predict the virus level that your city may develop in the next month. According to the model, the number of people who will be converted from exposed persons to confirmed infections in the city in the next month will account for approximately x% of the citya¸r´s population. If not controlled, these infected persons and the susceptible people converted by exposed persons will account for approxi- mately Y% of the citya¸r´s population. In view of the fact that the virus development situation in Guangdong province last year was similar to the current situation and the control situation is better, it is recommended that the government make adjustments according to its own medical resources and population. Suggested measures are as follows:

Strictly control personnel returning from abroad.

Strictly implement closed management of each community.

Strictly implement and promote basic epidemic prevention measures, such as wearing masks, washing hands frequently, etc.

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Expand existing closed isolation conditions to prepare for future outbreaks of new infections.

If you want a more detailed analysis, please share more detailed data with us. The data we need include the number of people diagnosed daily in the past week, the number of suspected observation subjects, the number of people in isolation, and the total population more detailed data.

We believe that under strict policy implementation, the city will soon emerge from the haze of COVID-19.

Yours sincerely,

A mathematical model team

8. Strengths and Weaknesses

8.1. Strengths

First one,the model construction method conforms to scientific principles.

Second one,the selected indicators are very concise and easy to understand.

8.2. Weaknesses

Only one,some assumptions are still different from the actual.

References

[1] Ning Qing, Bao Hong, Xu Cheng. A review of the research methods of the new crown virus epidemic prediction model[A]. China Computer Users Association Network Application Branch. China Computer Users Association Network Ap- plication Branch 2020 24th Annual Conference on New Network Technologies and Applications Proceedings [C]. China Computer Users Association Network Application Branch: Beijing Key Laboratory of Information Service Engineering, Beijing Union University, 2020:5.

[2] Li Weiwei,Du Rong,Chen Shudong,Sun Shuang.Analysis of transmission charac- teristics of new coronavirus pneumonia and forecast of epidemic development trend[J].Journal of Xiamen University (Natural Science Edition),2020,59(06):1025- 1033.

Appendices

Appendix .A Tools and software

Paper written and generated via LATEX, free distribution.

Graph generated and calculation using MATLAB R2019a and Python 3.8.

Appendix .B Real-time Data Crawling of the Epidemic

This Python program is used to crawl epidemic-related data, including the daily cu- mulative diagnosis, cumulative deaths, cumulative cures, and the number of imported patients overseas.

Program 1: data.py

```
import json
import requests
import xlwt
```

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```
import re import os

from collections import Counter

if __ame ______== "___main__":

if not os.path.exists('./Epidemic data across the country'): os.mkdir('./Epidemic data across the country')

province_name =
['Beijing','Shanghai','Jiangsu','Guangdong', 'Zhejiang','Shaanxi','Shanxi','Hebei','Henan',

'Hubei','Hunan','Anhui','Shandong ','Chongqing', 'Sichuan','Liaoning','Jilin','Heilongjiang','Tianjin', 'Fujian','Yunnan','Guizhou','Qinghai','Hainan','Tibet', 'Guangxi','Ningxia','Gansu','Xinjiang','Inner

Mongolia','Jiangxi']

for item in range(len(province_name)): province = province_name[item]

url = 'https://api.inews.qq.com/newsqa/v1' \ '/query/pubished/daily/list?province='

headers = {

'User-Agent': 'Mozilla/5.0 (Windows NT 10.0; Win64; x64) ' 'AppleWebKit/537.36 (KHTML, like Gecko) ' 'Chrome/84.0.4147.105 Safari/537.36'

}

data = {

'province': province

}

page_text = requests.post(url=url, data=data, headers=headers).json()

# fileName = province+'.json'

# fp = open(fileName,'w',encoding='utf-8')

# json.dump(page_text,fp=fp,ensure_ascii=False)

data = page_text['data']

# print(data) date_num = len(data)

book = xlwt.Workbook(encoding='utf-8')

sheet = book.add_sheet('Epidemic data', cell_overwrite_ok=True)

col_name = ['Province','Date','Cumulative diagnosis',        'Cumulative death','Cumulative cure','Overseas import']

for i in range(0, 6): sheet.write(0, i, col_name[i])

for i in range(date_num): sheet.write(i + 1, 0, province) y = data[i]['date'].split('.')[0]

m = data[i]['date'].split('.')[1]

        sheet.write(i    +  1,   1,   y+'æIJ´L'+m+'æ°Uˇe')

        sheet.write(i    +  1,   2,   data[i]['confirm'])

        sheet.write(i    +  1,   3,   data[i]['dead'])
```

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```
sheet.write(i + 1, 4, data[i]['heal'])
ex = 'Confirmed cases (.*?) cases | New (.*?) cases' match = re.findall(ex, data[i]['description'])
if len(match) == 0: sheet.write(i + 1, 5, 0)
else:
sheet.write(i + 1, 5, int(match[0]))
print('%s End of crawl'%province)
book.save('./Epidemic data across the country/'+ province + 'Epidemic data' + '.xls')
```

```
print('End of crawl ')
```

Appendix .C Draw Pictures

This python program is used to draw the image of the SEIR model.

Program 2: Draw Pictures.py import scipy.integrate as spi

```
import scipy.integrate as spi
import numpy as np
import matplotlib.pyplot as plt
N = 10000
beta = 0.6
gamma = 0.1
Te = 14
I_0 = 1
E_0 = 0
R_0 = 0
S_0 = N - I_0 - E_0 - R_0
T = 150
INI = (S_0,E_0,I_0,R_0)
def funcSEIR(inivalue,_):
Y = np.zeros(4)
X = inivalue
Y[0] = - (beta * X[0] * X[2]) / N
Y[1] = (beta * X[0] * X[2]) / N - X[1] / Te
Y[2] = X[1] / Te - gamma * X[2]
Y[3] = gamma * X[2]
return Y
T_range = np.arange(0,T + 1)
```

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```
RES = spi.odeint(funcSEIR,INI,T_range)
plt.plot(RES[:,0],color = 'darkblue',label = 'Susceptible',marker = '.')
plt.plot(RES[:,1],color = 'orange',label = 'Exposed',marker = '.')
plt.plot(RES[:,2],color = 'red',label = 'Infection',marker = '.')
plt.plot(RES[:,3],color = 'green',label = 'Recovery',marker = '.')
plt.title('SEIR Model')
plt.legend()
plt.xlabel('Day')
plt.ylabel('Number')
plt.show
```