SEIR infectious disease model with temporary duration of immunity

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Abstract: *Based on the classical model of SEIR infection, this paper studies the model of SEIR infection with temporary duration of immunity by increasing the infectivity of the incubation period and the duration of immunity after infection. Based on differential equations, python language is used for modeling, and the modeling results are analyzed and compared with real data. The model can preliminarily predict the development trend of influenza in a period of time conforming to the above basic characteristics.*

Keywords*: SEIR model mathematical modeling; infectious disease model temporary duration; Python.*

1. Introduction

Infectious disease is to point to by the special microorganism pathogen invasion human body causes, have infectivity, namely the pathogen can infect a kind of disease to others through all sorts of ways. Infectious diseases have epidemiological characteristics, i.e. epidemic, local and seasonal. The source of infection carries pathogens and infects susceptible populations through certain transmission routes. Infection is a process of interaction between a pathogen and the body. The pathogen invades the organism, breaks through the defense function, grows, reproduces, causes the pathophysiological change. The pathogen of some diseases will turn the susceptible person into a latent infected person after contacting them, that is, carrying the pathogen but showing no symptoms of the disease, also known as the incubation period. After an infected person recovers from an infectious disease, the human body will have insensitivity to the pathogen of the same infectious disease, which is called immunity. The immunity state after the disease of different infectious diseases is different, some infectious diseases can be lifelong immunity after getting sick once, and some may still be re-infected after being cured.

Today's multiple infectious diseases, such as influenza, hepatitis B, tuberculosis, avian influenza and the novel Coronavirus pandemic, have all had a significant negative impact on human health, daily life and social and economic development. It is very important to establish the model of disease transmission, evaluate the characteristics of transmission of infectious diseases, predict the trend of transmission and evaluate the effectiveness of prevention and control measures. At present, infectious disease models mainly include SI, SIR, SIS, SEIR and other classical mathematical models, but these models are basic models with wide applicability and poor specificity, and cannot achieve very effective evaluation and prediction for some diseases with significant characteristics. On the basis of the characteristics of some diseases have to infection again, namely those infected after recovery is obtained with certain immune period of temporary immunity, this paper hopes to improve the classic SEIR epidemic model in order to realize to the alienation of the infectious diseases of mathematical modeling, to better forecast such diseases, and make more suitable for disease control and prevention measures.

2. Concept Explanation

In the classical SEIR model[1], it is assumed that the total population of a given region is a natural birth rate. A constant value of the death rate or other factors of population migration N. The total population is divided into the following four categories:

1) Susceptible to (S) : Refers to a healthy person who lacks immunity and is Susceptible to being Susceptible to infection after being sent from an infected person.

2) Exposed (E) : a person who has been Exposed to an infected person and is infected, but does not

show symptoms or have the ability to infect others.

3) Infected (I) refers to a person who is Infected and has the ability to infect others.

4) Recovered (R) : refers to the person who will be immune after the Recovered.

According to the above definition N=S+E+I+R.

It is assumed that the susceptible person becomes latent after effective contact with the infected person, the latent person becomes infected after average incubation period, the infected person can be cured and become the recovered person, and the recovered person is immunized and no longer becomes the susceptible person. To describe the conversion relationship among the four groups of people, the following coefficients (all greater than 0) are introduced:

1) Probability of infection β : refers to the probability of a susceptible person turning into a latent person after contact with an infected person, that is, the probability of being infected.

2) Interpersonal contact frequency R: refers to the number of susceptible persons contacted by an infected person.

3) Latent incidence probability α : refers to the probability of latent transforming into an infected person.

4) recovery rate γ : refers to the probability that the infected person will be immunized and become a recovery person after being cured.

Thus, the transformation diagram of various groups in the classic SEIR model can be obtained:

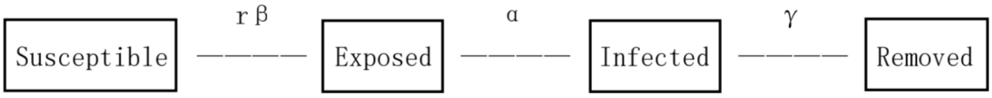


Figure 1: SEIR Model

According to the transformation diagram of SEIR model above, the following differential equation can be used to express the change rates of four groups of people over time:

(1) $dS/dt=-r\beta SI/N$

(2) $dE/dt= r\beta SI/N-\alpha E$

(3) $dI/dt=\alpha E-\gamma I$

(4) $dR/dt=\gamma I$

3. Modeling Process

3.1. Classical SEIR model

Reference for journals and research papers on SEIR diseases such as prediction model of research, when modeling the spread of the disease more ability, the latent time and cure time needed for the specific description of the critical nature of into parameter, and according to its mathematical properties and easy for calculation purpose put forward modeling the assumptions listed differential equations to represent the transmission process of disease. In the analysis and modeling of existing differential equations, previous scholars have adopted different methods. And this is usually not the focus of computer science papers. However, as a mathematical direction of the article, it is necessary to introduce the mathematical modeling methods for differential equations in detail. Based on the principle of data visualization, this paper presents the modeling results in the form of charts to visually represent the content and trend of data, which also requires the programming ability of researchers.

Python was chosen as the main tool for modeling and drawing. First, Python has a very powerful library that allows you to draw diagrams without using any external plug-ins. It is also very maneuverable and allows you to fine-tune modeling details in a concise way to ensure accuracy. Second, Python also has compatibility advantages that other computer languages do not. Because Python is an interpreted language, it is inherently highly integrated and visible. Basic mathematical modeling can be done by downloading a Python compilation environment on each computer. At the same time, it also has high readability, no tedious grammar requirements, and is friendly to beginners. Each Mac comes with a python2.7 compilation environment that runs on a terminal and has a very low barrier to entry.

This paper will first model the classical SEIR model, and then conduct personalized optimization on this basis. First, the corresponding differential equation is established according to the actual situation. Referring to the basic SEIR model, four differential equations before optimization can be obtained. In fact, the explanations of these equations have been explained in detail in the concept explanation section, which is covered here[2].

$$\begin{cases} N\frac{ds}{dt} = -N\lambda si \\ N\frac{de}{dt} = N\lambda si - N\delta e \\ N\frac{di}{dt} = N\delta e - N\mu i \\ N\frac{dr}{dt} = N\mu i \end{cases}$$

Figure 2: Differential equations of SEIR model

In order to better use the differential equation in mathematical modeling and image rendering, the classical SEIR model differential equation is transformed into form. The notation of the parameters has been changed, and both sides of each equation are multiplied by N, the total number of people, essentially the same as the classical SEIR differential equation. In particular, the number of daily contacts λ, the average number of effective contacts of susceptible persons per infected person per day; Daily incidence δ, the proportion of people who become sick in a day to the total number of people exposed; Daily cure rate μ, the ratio of the number of patients cured per day to the total number of patients, i.e. the average number of days cured is $1/\mu$.

Create the appropriate modeling environment in Python. Here we will introduce python's Scipy toolkit to solve differential equations. To be more specific, Scipy.integrate.odeint () is a specific method that Python can use to solve differential equations by numerical integration to solve ordinary differential equations. Specific use methods are as follows[3]:

The main function of odeint() :

* func: callable(y,t,...) , that is, in the derivative function f(y,t), the derivative of y at t is expressed as a function.

* y0: in array format, is the initial condition y0.

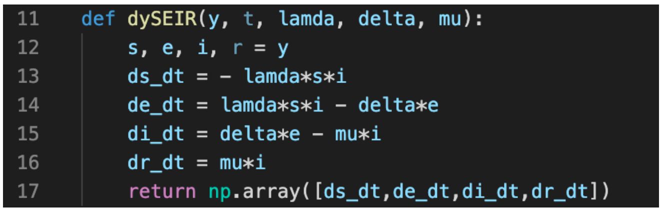
* t: also represented in array form, the sequence of time points corresponding to the function value is solved. The first element of the sequence is the initial time t0 corresponding to the initial condition y0. In addition, time series must be monotonically increasing or monotonically decreasing, allowing for repeated values.

* args: conduction parameter to derivative function. When the derivative function f(y,t, p1,p2...) Including variable parameters p1,p2... , args=(p1,p2...) Parameters P1,p2... Conduction to the derivative function func.

Return value of odeint() :

* y: in the form of array, in the shape of (Len (t),len(y)), that is, the y value of each moment in the time series is given.

With Scipy, a powerful toolkit, Python programs have the ability to solve differential equations. The classical SEIR equations can now be expressed in Python (where the variable names correspond to the above equation) :



```
def dySEIR(y, t, lamda, delta, mu):
    s, e, i, r = y
    ds_dt = - lamda*s*i
    de_dt = lamda*s*i - delta*e
    di_dt = delta*e - mu*i
    dr_dt = mu*i
    return np.array([ds_dt,de_dt,di_dt,dr_dt])
```

Figure 3: Code implementation of SEIR model

The classical SEIR model is not directly output here. In the modeling process of the optimized SEIR model, the two models will be output together for easy comparison.

3.2. SEIR model with temporary duration of immunity

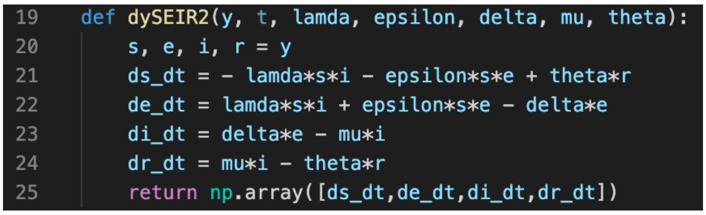
In essence, there are two essential differences between the optimized SEIR model with temporary immunity duration and the classical SEIR model: First, considering that many infectious diseases are contagious during the incubation period, the susceptible person (S class) is infected by effective contact with the infected person (I class), and the effective contact with the latent person (E class) may also be infected and turn into the latent person (E class). The second is to consider that many infectious diseases in the cured after the recovery (R) the duration of immunity is not permanent, that is to say, the recovery (R) after a certain period of time will become susceptible again (S).

To address the first difference, a new parameter (Epsilon) was introduced to represent the average number of susceptible persons each lurker has effective daily contact with. This parameter is mathematically similar in nature to λ. It simply changes the object from latent (class E) to susceptible (class S). Therefore, we only need to add $\varepsilon \cdot s \cdot e$ and subtract $\varepsilon \cdot s \cdot e$ when solving to ensure that the basic condition of SEIR model, the total population, remains the same. Similarly, to address the second essential difference, a second new parameter (Theta) was introduced to represent the immune failure rate of each convalescent (class R). That is to say, it can represent how many convalescent patients with immunity period (R type) lose immunity and become susceptible (S type) per unit time. Therefore, when listing the differential equations, we only need to add $\theta \cdot r$ and subtract $\theta \cdot r$ in the solution to meet the optimization requirements under the condition that the major premise population remains unchanged.

$$\begin{cases} \frac{\mathrm{ds}}{\mathrm{dt}} = -\lambda si - \varepsilon se + \theta r \\ \frac{\mathrm{de}}{\mathrm{dt}} = \lambda si + \varepsilon se - \delta e \\ \frac{\mathrm{d}i}{\mathrm{dt}} = \delta e - \mu i \\ \frac{\mathrm{dr}}{\mathrm{dt}} = \mu i - \theta r \end{cases}$$

Figure 4: Differential equations of improved SEIR model

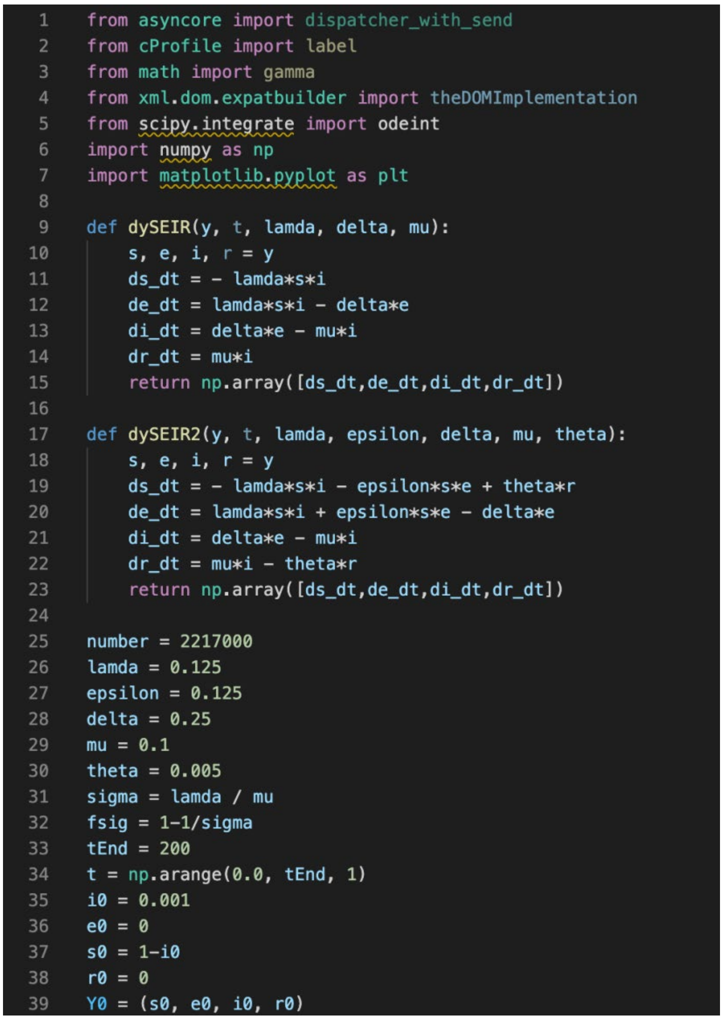
Thus, differential equations corresponding to SEIR infectious disease model with temporary immunity duration can be obtained, as shown in the figure above. The derivative function of the differential equation is expressed in the Python environment, and the following results are obtained:



```
def dySEIR2(y, t, lamda, epsilon, delta, mu, theta):
    s, e, i, r = y
    ds_dt = - lamda*s*i - epsilon*s*e + theta*r
    de_dt = lamda*s*i + epsilon*s*e - delta*e
    di_dt = delta*e - mu*i
    dr_dt = mu*i - theta*r
    return np.array([ds_dt,de_dt,di_dt,dr_dt])
```

Figure 5: Code implementation of improved SEIR model

Thus, the derivative function, the core of differential equation mathematical modeling, has been constructed. The parameters are then assigned and the graph is printed. The final code result is shown below:



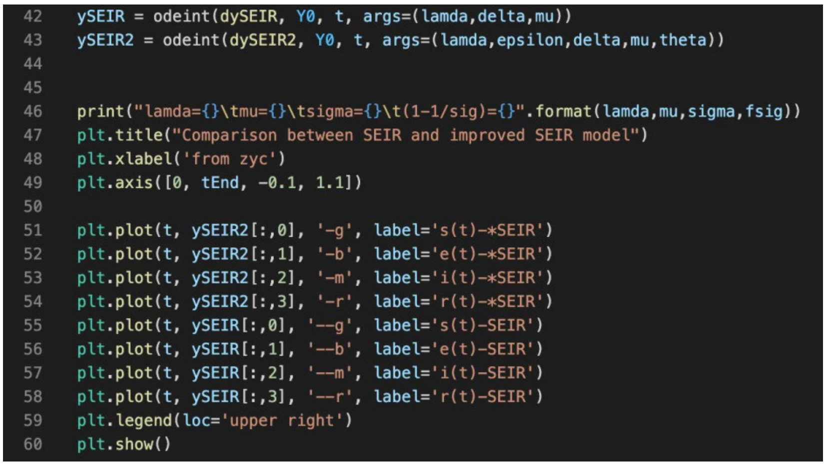
```python
from asyncore import dispatcher_with_send
from cProfile import label
from math import gamma
from xml.dom.expatbuilder import theDOMImplementation
from scipy.integrate import odeint
import numpy as np
import matplotlib.pyplot as plt

def dySEIR(y, t, lamda, delta, mu):
    s, e, i, r = y
    ds_dt = - lamda*s*i
    de_dt = lamda*s*i - delta*e
    di_dt = delta*e - mu*i
    dr_dt = mu*i
    return np.array([ds_dt,de_dt,di_dt,dr_dt])

def dySEIR2(y, t, lamda, epsilon, delta, mu, theta):
    s, e, i, r = y
    ds_dt = - lamda*s*i - epsilon*s*e + theta*r
    de_dt = lamda*s*i + epsilon*s*e - delta*e
    di_dt = delta*e - mu*i
    dr_dt = mu*i - theta*r
    return np.array([ds_dt,de_dt,di_dt,dr_dt])

number = 2217000
lamda = 0.125
epsilon = 0.125
delta = 0.25
mu = 0.1
theta = 0.005
sigma = lamda / mu
fsig = 1-1/sigma
tEnd = 200
t = np.arange(0.0, tEnd, 1)
i0 = 0.001
e0 = 0
s0 = 1-i0
r0 = 0
Y0 = (s0, e0, i0, r0)
```

Figure 6: Complete Python Code Part one



```python
ySEIR = odeint(dySEIR, Y0, t, args=(lamda,delta,mu))
ySEIR2 = odeint(dySEIR2, Y0, t, args=(lamda,epsilon,delta,mu,theta))


print("lamda={}\tmu={}\tsigma={}\t(1-1/sig)={}".format(lamda,mu,sigma,fsig))
plt.title("Comparison between SEIR and improved SEIR model")
plt.xlabel('from zyc')
plt.axis([0, tEnd, -0.1, 1.1])

plt.plot(t, ySEIR2[:,0], '-g', label='s(t)-*SEIR')
plt.plot(t, ySEIR2[:,1], '-b', label='e(t)-*SEIR')
plt.plot(t, ySEIR2[:,2], '-m', label='i(t)-*SEIR')
plt.plot(t, ySEIR2[:,3], '-r', label='r(t)-*SEIR')
plt.plot(t, ySEIR[:,0], '--g', label='s(t)-SEIR')
plt.plot(t, ySEIR[:,1], '--b', label='e(t)-SEIR')
plt.plot(t, ySEIR[:,2], '--m', label='i(t)-SEIR')
plt.plot(t, ySEIR[:,3], '--r', label='r(t)-SEIR')
plt.legend(loc='upper right')
plt.show()
```

Figure 7: Complete Python Code Part Two

4. Data Sources

Based on the establishment of the mathematical model above, the prediction of some infectious diseases can be realized. After consulting data and reading papers, it is found that influenza completely meets the basic requirements of SEIR model and two optimization conditions. In other words, if there is a high degree of coincidence between the prediction results of the above modeling and the actual statistical data in the prediction of the spread of influenza, the accuracy and correctness of the modeling in this paper can be proved to a certain extent. Therefore, the author collected some data of influenza transmission on the website for the model to use.

This paper selected the data related to influenza in Beijing from 2017 to 2018 as the research content. According to the document "China Center for Disease Control and Prevention [2019] 103" of the Chinese Center for Disease Control and Prevention, research based on surveillance of influenza-like cases and hospitalized SARS cases in Beijing suggests: In the 2017-2018 season, about 2.271 million people were infected with influenza in Beijing, with a total infection rate of 10.5%, symptomatic incidence of 6.9%, and incubation period of about 3-5 days. A study on hospitalized cases of influenza in Beijing from 2016 to 2018 showed that the case fatality rate of hospitalized patients with influenza was 0.5%, and the duration of immunization was about 6 to 8 months.

After processing the data collected here, the parameters available in the optimized SEIR model can be obtained. In fact, these actual parameters are already substituted in the final code above (lines 25-30)[4].

5. Modeling Results

After compiling and running the Python code shown above, we have the following chart as a result of modeling trends in the spread of influenza:

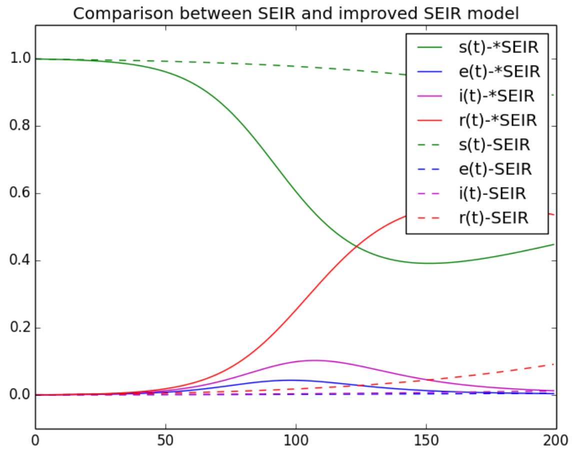


Figure 8: Prediction curves for infectious diseases

In the image, the solid line represents the optimized SEIR model with temporary immunity duration, while the dotted line represents the classical SEIR model. The legends and notes are shown in the figure: the green curve represents the susceptible (S), the blue curve represents the latent (E), the purple curve represents the sick (I) and the red curve represents the recovered (R). It should be noted that the ordinate of the image is not the specific number of people in each category, but the proportion represented respectively. This makes it easy to change the total number of people N.

According to the above figure, the difference of influenza trend prediction between the model before and after optimization is analyzed. There was a significant difference between susceptible, latent and recovered patients. First look at the susceptible person's curve. Before optimization, the susceptible curve must be monotonically decreasing. Because there is no supplemental source of susceptible people. An improved version of the model adds a source of replenishment for susceptible people, namely, those who have passed the time limit of immunity. The green dotted line shows a monotonically decreasing trend, while the green solid line shows a rebound after a sharp decrease, which is the result of taking the duration of immunity into account.

The convalescent do the same. The recovery curve in the original model must be monotonically increasing. Because the convalescent can't change into anything else once they become convalescent. In the improved version, however, survivors who pass the immunity period become susceptible and enter the cycle again. Combined with the image, the red dotted line shows a monotonically increasing trend, while the green solid line shows a decrease after a significant increase, which is also the result of considering the duration of immunity.

Finally, there are the lurkers. In the optimized model, the lurk peak came more quickly, reaching around 90 days. Look at the classic SEIR model. The increase in lurkers was minimal. This is caused by the new source of lurkers. Contact between the susceptible and the lurker can also bring in new lurkers.

The image results predicted by the SEIR infectious disease model with the duration of immunization were then compared with the actual data statistical results in the figure below.

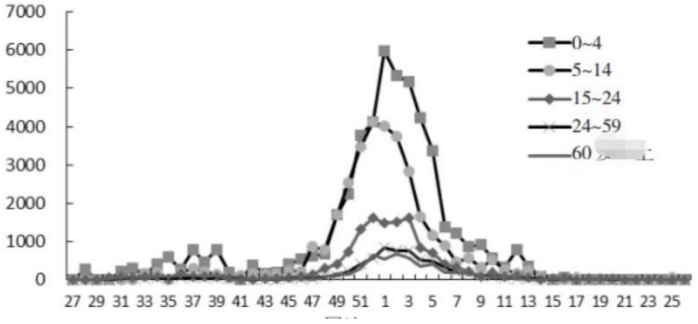


Figure 9: Weekly distribution of influenza incidence during the 2017-2018 in Beijing

It should be noted before the analysis that the prediction model in this paper is simulated from an initial situation of about 45 weeks to the end of 17 to 19 weeks.

As you can see, the ordinate of the actual data uses the actual number of people rather than the ratio. The peak of infection occurs around 100-110 days after the disease begins to spread. After conversion, the total number of patients is about (4000+2500+1000+500+500)*20=8500*20=170000, while the proportion is 170000/2000000, about 0.085. This is close to the vertical coordinate of the peak in the predicted image. The prediction model is also accurate in predicting the peak duration, which is also about 150 days. This shows that the SEIR model with temporary duration of immunity is more successful in predicting the trend of influenza transmission. It has the ability to predict the spread of infectious diseases that meet the requirements.

6. Discussion and outlook

The SEIR infectious disease model with temporary immunity period established in this paper has the ability to solve practical problems, but it is also inaccurate and inconsistent with the actual situation in some details. For example, the immune failure rate of the convalescent is fixed at a constant. In practice, the value of this parameter should increase gradually over time. Also not considered is the case fatality rate. This is also the common fault of SI, SIS and SEIR models of this type: the premise is that the total population is unchanged, that is to say, there is no birth or death in the process of disease transmission. However, this is an impossible condition for many infectious diseases.

In addition, there are some problems to be optimized in the process of mathematical modeling. For example, python, the modeling language chosen this time, is actually quite powerful, but only one of the toolkits was used for the fitting. Although it can meet the accuracy requirements, there is a big gap between it and the actual data. The author puts forward an idea here: if we can use neural network, let the machine learn according to the existing data so as to correct and optimize. The resulting parameters are bound to be more accurate and better choices[5].

Here, the author hopes that future researchers can take this paper as a reference to solve the remaining problems mentioned above and make the model more accurate in prediction, which may be put into practical application in the future.

7. The Conclusion

The purpose of this study is to establish that 1) many infectious diseases are infectious during the incubation period. In addition to effective contact with the infected person (class I), the susceptible person (class S) may be infected by effective contact with the latent person (class E) and become latent person (class E). 2) The duration of immunity for many infectious diseases recovered after cure (Class R) is not permanent, that is to say, the recovered (class R) is the optimized version of SEIR infectious disease prediction model, which has a certain probability of returning to susceptible (Class S). By using

Python language and its built-in Scipy toolkit, the author has successfully established a mathematical prediction model that meets the standard accuracy to predict influenza, a particular infectious disease. The end result is Python code and a chart predicting the 2017-2018 flu epidemic in Beijing. This work has contributed to the improvement of SEIR models and the prediction of the spread of infectious diseases with specific characteristics.

Reference

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