Computer Simulation and Epidemic Preventive Countermeasures Using SEIR Model and Big Data Technology

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Abstract. Object: Evaluation of various new type of coronavirus pneumonia (COVID-19) normalization prevention measures and methods: Based on the actual data and transmission characteristics of the COVID-19 epidemic, this paper constructs an SEIR model for the transmission of new coronary pneumonia, which focuses on parameters such as asymptomatic infection. Result: Simulate the implementation of different types of public health preventive policies, and explore normalized preventive countermeasures.

1. Research Background
In early December 2019, a case of pneumonia of unknown cause appeared in Wuhan City, Hubei Province, and it spread widely in China and many countries around the world. It has become a public health emergency of international concern [1]. On January 7, 2020, the Chinese Center for Disease Control and Prevention (CDC) isolated a new type of coronavirus from a throat swab sample of a Wuhan patient [2]. On February 11, 2020, the Coronavirus Research Group of the International Committee on Taxonomy of Viruses named this coronavirus "SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2)", and the WHO announced that it would name the pneumonia caused by this virus infection as Coronavirus disease 2019 (coronavirus disease 2019, COVID-19) [3].

As a new infectious disease, COVID-19 has had a huge impact on global health and economy. Research on its etiology and epidemiological characteristics is of great significance to the control of the epidemic. The establishment and application of mathematical models can help people understand the internal mechanism of the process of disease transmission, and then provide a basis for decision-making for public health departments to take preventive measures.

2. Literature Review
Mathematical models of epidemic diseases uses a series of assumptions, preset parameters and variables, and constructs equations to quantitatively explain the characteristics of the spread of infectious diseases. It uses some data that existed at the beginning of the epidemic to estimate parameters and assist in the discovery of transmission mechanism of infectious diseases in the population. It can simulate the trend of the epidemic under certain assumptions [4].

At present, Mathematical models of epidemic diseases can be divided into two categories according to their mathematical expressions: deterministic models and network dynamics models. At present,
deterministic models represented by general growth models and chamber models still occupy an important academic position. However, with the development of artificial intelligence and computer technology, network dynamics models represented by cellular automata [5] and artificial neural networks have gradually been paid attention to and applied.

The basic assumption of the deterministic model is that the total population of the target area is a constant or an asymptotic constant, and the model expression is mainly based on differential equations. According to the modeling basis, the deterministic model can also be subdivided into phenomenological models and mechanical models.

The phenomenological model mainly relies on empirical observations and emphasizes the reproducibility of the empirical observations by model research objects; while the mechanistic models consider the dynamic mechanism of epidemic transmission, based on a series of differential equations to quantify the parameters that affect the process of disease transmission. Then explain the development process of the epidemiological state in the target population.

This new crown pneumonia epidemic has an incubation period and asymptomatic infections. Therefore, most researchers are based on classic deterministic models (such as SEIR model, SIR model, GGM model, etc.) [6] to carry out epidemic simulation and development prediction. Training-based artificial intelligence (AI) or machine learning methods also have certain auxiliary applications [7].

This paper uses the classic SEIR model in infectious disease research as the theoretical basis to construct a model of the spread and spread of the new coronavirus pneumonia epidemic, and construct the basic framework and theoretical system for the research on the spread and intervention mechanism of the new coronavirus epidemic. According to the research idea of "dissemination law-early warning mechanism-response ability", multi-source heterogeneous information such as the influencing factors of the new coronavirus pneumonia epidemic, the transmission mechanism, and the transmission characteristics are effectively integrated. This paper proposes the spread, spread and prevention strategies of new coronavirus pneumonia under different conditions.

3. Model construction

Data source
The data in this article comes from the official website of HUBEI HEALTH COMMITTEE (http://wjw.hubei.gov.cn/)

Model building
The SEIR model is currently the most representative mathematical model for research on the dynamics of infectious diseases in a fixed population [8]. The model takes into account the characteristics of the incubation period of infectious diseases. This paper considers the latent state E on the basis of the SIR model, and assumes that the latent person E and the infected person I have the same probability of infecting the susceptible population S. Construct a SEIR [7] model based on the above theories, $\gamma$ is the contact rate (the average number of contacts per person); $\beta$ is the probability of infection (after contact with patient I); $r$ is the probability of recovery; $\alpha$ is the probability of a latent person becoming a sick person; $\beta_2$ is the probability of infection (after contact with latent person E); $\gamma_2$ is the average number of people in contact with the lurker every day; $k$ is the patient's mortality [9];
Establish a differential equation.

\[
\frac{dS}{dt} = -\beta \gamma S I N - \beta^2 \gamma^2 S I N \tag{1}
\]

\[
\frac{dE}{dt} = \beta \gamma S I N - \alpha E + \gamma^2 \beta^2 S E N \tag{2}
\]

\[
\frac{dI}{dt} = \alpha E - (k + r)I \tag{3}
\]

\[
\frac{dR}{dt} = rI \tag{4}
\]

\[
\frac{dD}{dt} = kI \tag{5}
\]

\[
N = S(t) + E(t) + I(t) + R(t) + D(t) \tag{6}
\]

The difference equation of the difference model under the time series obtained by solving the above differential equation:

**The susceptible person S:**

\[
S_{t+1} = S_t - \beta \gamma \frac{S_t I_t}{N} - \beta^2 \gamma^2 \frac{S_t I_t}{N} \tag{7}
\]

a) The Lurk E:

\[
E_{t+1} = E_t + \beta \gamma \frac{S_t I_t}{N} - \alpha E_t + \gamma^2 \beta^2 \frac{S_t I_t}{N} \tag{8}
\]

b) The Patient I:

\[
I_{t+1} = I_t + \alpha E_t - (k + r)I_t \tag{9}
\]

c) The Dead D:

\[
D_{t+1} = D_t + kI_t \tag{10}
\]

d) The Recovered R:
\[ R_{t+1} = R_t + rt \quad (11) \]

Let the total population \( N = 1400000000 \); Infected at the beginning \( I = 1 \); Susceptible \( S = N - I \); The rest are all 0; Number of contacts of infected persons \( \gamma = 4 \); probability of infection \( \beta = 0.6 \); probability of latent persons being transformed into infected persons \( \alpha = 0.125 \); number of contacts of latent persons \( \gamma_2 = 8 \); probability of latent persons infecting normal persons \( \beta_2 = 0.03 \); probability of recovery \( r = 0.143 \); Daily fatality rate \( k = 0.0254 \).

The Matlab program is established according to the above model, and the prediction results are as follows.

![Figure 2. Simulation without isolation measures.](image)

After taking isolation measures, re-estimate the parameters [10], change the probability of infection \( \beta = 0.3 \), and the number of contacts of latent persons \( \gamma_2 = 0.8 \), and the prediction results are as follows.

![Figure 3. Simulation of isolation measures.](image)
4. Research result

![Figure 4](image_url)

Figure 4. Trends of China's sick, cured, and dead over time.

Comparing the prediction graph obtained from the code with the actual data curve area, the curve fits the actual data curve, the shape is similar, and the degree of fit is better, indicating that the obtained prediction result is more in line with the actual situation.

Since the model has obtained more accurate predictions, individual parameters can be changed on the basis of the above models to realize the impact of prevention and control measures on the epidemic, and then predict the development of the epidemic after the measures are taken. By implementing the isolation measures, the prediction curve shown in Figure 4 was obtained, which shows that the isolation measures have brought great effects, and the number of infected and non-infected people has plummeted. It can be concluded that isolation measures can be taken to prevent asymptomatic infections from threats.

5. Discussion and suggestions

Mathematical models of epidemic diseases play an important role in theoretical research and scientific prevention and control guidance on the spread and development of infectious diseases. Future research on Mathematical models of epidemic diseases needs to meet the complexity of infectious disease transmission and prevention and control process requirements, need to strengthen the rapid recognition and prevention and control of infectious diseases, promote real-time sharing of epidemic information, explore the application of multi-model combination, make full use of computer science and intelligent frontier number growth and sub-linear growth 3 stages to make a model fit with the actual data of the epidemic, in revealing the new crown we have made useful exploration in revealing the mechanism of pneumonia epidemic transmission and development trend prediction [11].

In summary, the deterministic model often gives better results in accordance with the actual statistical results in the application, and is also widely used in the prediction of the development of the new crown pneumonia epidemic and plays a good role in data theoretical support and scientific prevention and control guidance; The network dynamics model is more suitable for the complex requirements of infectious disease transmission trend simulation in terms of research methods and applicable objects,
and also brings into play the results of technological development by learning from previous epidemic data or current limited data, and continues to provide theoretical support and data support for public health decision and policy makers.

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