Research on Combating Epidemics based on Differential Equations and Cellular Automata

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Abstract. The new crown pneumonia epidemic has swept the world, panic, anxious, and uneasy emotions flowed into the psychology of everyone. This epidemic not only puts many countries in economic crisis, but may also put some small countries in danger of disappearing forever, and even make it impossible for large-scale people to return home. Therefore, the World Health Organization (WHO) and countries around the world need to join hands and work together to further explore ways to effectively control the epidemic. Analyze the relevant data of the four modes of disease (susceptible persons, latent persons, asymptomatic persons, and recovered persons), establish a differential equation model, and combine the results of question 1 to get the trend of the number of asymptomatic infections (present The trend of first rising and then falling) and specific data (it peaked at about 2733 people on the 42nd day after the outbreak; it dropped to 10 people about 70 days after the outbreak; it decreased to 0 at about 80 days). Then we simulated the distribution of asymptomatic infections based on the data reported by the Beijing Municipal Health Commission and combined with the cellular automaton model: the clustering state appeared in the first 10 days, and it gradually dispersed over time, and the distribution became more distributed after about 50 days. Evenly. Finally, it summarizes the applicable fields of this model in life and effective and accurate suggestions for epidemic prevention and risk reduction.

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1. Introduction

This In March 2020, the World Health Organization official [1] announced that the rapid outbreak of the new coronavirus (COVID-19) worldwide is a pandemic. The World Health Organization stated that the pandemic is "the global spread of new diseases." There is no strict qualitative and quantitative standard to measure the pandemic level. However, due to the insufficient economic strength and medical resources of each country, and different prevention and control policies, the WTO is very concerned...
about how to provide very effective quantifiable indicators for the epidemic situation. The approximate
distribution of the epidemic situation is shown in Figure 1:

![Figure 1 Approximate distribution of world epidemics](image)

Asymptomatic infection refers to those who have no relevant clinical symptoms, but the nucleic acid test of specimens such as respiratory tract is positive. Asymptomatic infections can also become the source of infection, and have a certain risk of transmission, but the length of the infection and the intensity of the infection are still unconfirmed, so many people are worried about whether asymptomatic infections will become a new source of infection. However, since it is difficult for the world to effectively identify asymptomatic infections, how to quickly and accurately identify and judge asymptomatic infections at the lowest cost and how strong their infectious ability has become the WTO and Issues of great concern to countries all over the world.

2. Problem analysis

Through the analysis of the specific circumstances of the epidemic, we believe that the identification of epidemics and pandemics is affected by factors such as the total population of the country, the number of confirmed infections, the number of deaths, and the duration of the epidemic. Then we obtained relevant data on the epidemic on the website of the Ministry of Health of the People's Republic of China [1], and used principal component analysis [2] to obtain the most important factors affecting the identification and the corresponding related function expressions. Finally, the corresponding data of the known epidemic (avian influenza) and pandemic (H1N1 influenza) are substituted into the conditions for identification.

As asymptomatic infections are contagious and difficult to be detected, we established an SEIR model for those diagnosed with asymptomatic infections, and analyzed the four states of the disease to obtain follow-up of asymptomatic infections. Change trend graph over time. At the same time, for the location of the asymptomatic infected persons, a cellular automata model was established to simulate the changes in the distribution status of asymptomatic infected persons, and the changes in the condition of the asymptomatic infections were analyzed, so as to provide accurate directions for proposing response plans.
3. Model establishment and solution

3.1. Principal component analysis method to define epidemic and pandemic

Principal component analysis [3] is to derive a few principal components from the original variables, so that they retain as much information of the original variables as possible, and they are not related to each other. We use the variance of $F_1$ (the first variable) to express, that is, the larger $\text{Var}(F_1)$, the more information contained in $F_1$, so $F_1$ is called the first principal component. If the first principal component is not enough to represent the information of the original $P$ indicators, then consider the selection. In order to effectively reflect the original information, the existing information of $F_1$ does not need to appear in, that is, $\text{Cor}(F_1, F_2) = 0$, then $F_2$ is called the second principal component. In this way, $P$ principal components can be constructed.

We have checked the relevant data of several typical epidemics on the website of the Ministry of Health of the People’s Republic of China, and used SPSS software to obtain the influence weight of each factor, as shown in Figure 2.

![Crushed stone diagram](image)

**Figure 2** Crushed stone diagram

It can be seen from the graph that the number of confirmed infected population and the number of deaths accounted for 98% of the weight of the defined epidemics and pandemics. Therefore, the two variables of the number of infected populations and the number of deaths are used to quantitatively judge epidemics and pandemics.

By dividing the data in the component matrix by the square root of the characteristic root corresponding to the principal component, the coefficient corresponding to each index in the two principal components can be obtained, namely

$$F = 0.371F_1 + 0.522F_2$$
Substituting the known epidemic (avian influenza) and pandemic (H1N1 influenza) data into formula (1) can be obtained. When $F \geq 10788$, the disease can be considered an epidemic; when $F \geq 57898$, it can be considered a pandemic.

3.2. Distribution and outcome prediction of asymptomatic infection

Let's consider the places where the epidemic is most severe now: the United States and Spain. From question one, we can see that the most important factor in the prevention and control of the epidemic is the number of confirmed cases and the number of deaths. According to some current studies, among the confirmed cases of new coronavirus pneumonia, the proportion of asymptomatic infections accounts for 10%-13%. Therefore, all close contacts of people who have been diagnosed with new coronavirus pneumonia and those who have died of new coronavirus pneumonia can be regarded as the key test objects, and they can be isolated and tested for the virus to obtain a more accurate proportion of asymptomatic infections. Then take places with high crowd density (such as airports, train stations, supermarkets, etc.) as the sampling objects, and randomly select people according to their proportions for testing. This is the most time-saving and can also screen out asymptomatic infections as quickly as possible to prevent the virus from spreading to more people.

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3.3. Analysis of EIR Model's Trend of Asymptomatic Infections

In the SEIR model with asymptomatic infections [4], we divide the population into 4 states, which are susceptible, infected, asymptomatic, and recovering (cured after infection).

A susceptible person becomes a latent person with a probability of $\beta$, a latent person becomes an asymptomatic person with a probability of $\sigma$, and an asymptomatic person recovers with a probability of $\gamma$.

Let $N$ be the total number of people, so

$$N = S + E + I + R$$

From this we can build a SEIR model

$$\frac{dS}{dt} = -r \beta IS / N$$
$$\frac{dE}{dt} = r \beta IS / N - \alpha E$$
$$\frac{dI}{dt} = \alpha E - \gamma I$$
$$\frac{dR}{dt} = \gamma I$$

$N = 1000, I = 1, r = 30, \beta = 0.1, \gamma = 0.5, \alpha = 0.2$ The four state changes are shown in Figure 4.

As can be seen from the figure, the number of asymptomatic infections and latent persons presents an upward trend and then a downward trend, susceptible persons present an obvious downward trend, and recovered persons present a prominent upward trend.

Since the new crown pneumonia virus is also contagious during the incubation period, we set the infection probability of the latent person to $\beta_2$, and the healthy person that the latent person contacts every day is $r_2$, and the improved SEIR model is
\[
\begin{align*}
\frac{dS}{dt} &= -r \beta IS / N - r_2 \beta_2 ES / N \\
\frac{dE}{dt} &= r \beta IS / N - \alpha E + r_2 \beta_2 ES / N \\
\frac{dI}{dt} &= \alpha E - \gamma I \\
\frac{dR}{dt} &= \gamma I
\end{align*}
\]

After analyzing the relevant data of this epidemic, we take \( r_2 = 30, \beta_2 = 0.1 \), and get the change trend shown in Figure 5:

It can be seen from the figure that the asymptomatic infection reached a peak about 42 days after the appearance, about 2733 people; about 70 days after the appearance, it dropped to 10 people; it disappeared in about 80 days.

3.4. Distribution simulation of asymptomatic infection by cellular automata model

One by one, define them on a grid, and the network at each point represents a cell and a state. We use the discretization of cellular automata, the synchronization of dynamic evolution, and the locality of interaction to move it, and rely on the state of itself and its neighbors to simulate the distribution of cells.

We imagine the movement of cellular automata as the trajectory of asymptomatic infections, and use the data provided by the Beijing Municipal Health Commission and an improved SEIR model to simulate the distribution of asymptomatic infections over time. The changes are shown in Figure 3, Figure 4, and Figure 5.
Comparing these three pictures, we can find that as time goes by, the distribution of asymptomatic infections has become more and more scattered, and the number is gradually decreasing, indicating that as the number of infections and deaths decreases, the epidemic will eventually be brought under control.

4. Model checking
When the epidemic breaks out, we can immediately take corresponding measures to control the development of the epidemic. When the epidemic broke out 10 days later, my country implemented a
strict "home order"[9]. Figure 9 shows the changes of asymptomatic infected persons after the implementation of the “home order”

It can be clearly seen from the figure that after the implementation of the “home order”, the high-incidence period of asymptomatic infections has obviously moved backward (from the original 20 days to 50 thousand), and the peak number of asymptomatic infections has dropped significantly. (From the original more than 4,500 to about 2,300), this has bought us more precious time to fight the new crown pneumonia epidemic, and greatly reduced the consumption of social public resources, so that useful resources can be used in the right place. Make a little contribution to mankind's early victory over disease.

5. Model evaluation and promotion
A large amount of data has been well classified, and the two most important factors that define epidemics and pandemics have been selected to make our model more convincing.

Comprehensive use of principal component analysis, differential equation model, cellular automata model, so our model is very valuable and practical.

Random simulation of the distribution of asymptomatic infections was made. Since it may not match the real data, the model was improved to ensure that the movement of asymptomatic infections is not random.

In the process of model solving, the previous model was continuously optimized, and the model was tested to make the model achieve better results.

There are some vacancies in the data, which we fill in by experience, so there are inaccuracies.

Since the world is a complex system, making some assumptions while simplifying the model may cause errors.

In addition to the factors considered in the article, the definition of epidemics and pandemics is also affected by other factors (such as economic issues between countries) that are not considered in this article.

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