Study on the Dynamics of Virus Propagation in Combination with Big Data and Kinetic Models

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Abstract. With the continuous development of science and technology, in the context of current big data, the research on the law of traditional virus propagation dynamics had been developed to the bottleneck. The traditional law of virus propagation dynamics was less sensitive and the mathematical model was not easy to operate. Therefore, it was proposed to study the dynamics of viral propagation based on the combination of big data and kinetic models. The model was established by using differential equations and so on, and the accurate prediction law of virus propagation dynamics was completed by experimental tracking control. A graph of the number of patients over time was obtained by bringing the problem into the model, and the changes in the model results were derived from this graph. In this way, corresponding countermeasures was drawn based on the changes in the results. Finally, through simulation experiments, it was proved that the combination of big data and kinetic model of viral propagation kinetics scientifically and accurately studied the laws of viral propagation dynamics. The established mathematical model was easy to operate and had a good guiding significance for practice.

Keywords: Viral transmission · Big data · Kinetic model · Differential equation

1 Introduction

The research on the law of virus propagation dynamics has been developed to the bottleneck. The traditional law of virus propagation dynamics is less sensitive, and the mathematical model is not easy to operate. Therefore, we need to expand the field of view to see the virus propagation dynamics. With the continuous development of science and technology, in the context of current big data, a study is proposed to combine the big data and dynamics models to study the dynamics of virus propagation. The model is established by using differential equations and so on, and the accurate prediction law of virus propagation dynamics is completed by experimental tracking control. By establishing a differential equation model, the process of virus spread and propagation is described. Finally, the dynamics of virus propagation is studied through analysis. We bring the required questions into the model to get a graph of the number of patients over time, and based on this graph, we get the changes in the model results. In this way, according to the change of the result, the corresponding countermeasures

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can be obtained [1]. Finally, through the sensitivity analysis of the incubation period and the healing period of the infectious disease, it is found that the proposed virus propagation dynamics law combined with big data and kinetic model can scientifically and accurately study the law of virus propagation dynamics, and the established mathematical model is easy and has a good guiding significance for practical operation.

2 Theoretical Analysis of Big Data and Dynamics Models

Considering the total number of people in the region, we turn the problem into how to find the correct relational expression to express the total number of patients per day [2], to find out the normal number of people per unit time, the incubation period per unit time, the change of the number of people, the change of the number of patients diagnosed per unit time, the number of people who withdrew within the unit time, and the number of suspected patients per unit time, and the big data to establish the differential equation model and dynamics models were obtained.

①Treat all routes of transmission of the virus as contact with the pathogen;② The total number N of the areas examined during the spread of the disease is considered constant, that is, the number of people flowing into the area is equal to the number of people flowing out, and the time is measured in days;③ The virus in which the virus is in an incubation period is not contagious [3];④ the probability of a second infection of the healer is 0, they withdraw from the infection system, so they are classified as "exitors";⑤ Regardless of the birth rate and natural mortality rate during this period, the number of deaths caused by the virus is also classified as "exit";⑥ The isolated population completely severes contact with the outside world and is no longer contagious [4].

Changes in the normal number of people per unit time:

$$\frac{dS_1}{dt} = -\alpha_1 I(t)(1-\varpi)S_1 - \alpha_2\left[A(t)(1-\varpi) + A(t)\varpi\frac{1}{d_3}\right]S_1 \tag{1}$$

According to the above algorithm, the number of patients in the incubation period per unit time can be obtained:

$$\frac{dE}{dt} = -\alpha_1 I(t)(1-\varpi)\left[S_1 + A(t)(1-\varpi) + A(t)\varpi\frac{1}{d_3}\right] - \frac{2}{d_1+d_2}E \tag{2}$$

Changes in the number of patients diagnosed per unit time:

$$\frac{dI}{dt} = \frac{2}{d_1+d_2}E\frac{1}{d_3}I \tag{3}$$

Changes in the number of people who quit during the unit time:

$$\frac{dR}{dt} = \frac{1}{d_3}I \tag{4}$$

Changes in the number of suspected patients per unit time:

$$\frac{dA}{dt} = -\alpha_2\left[A(t)(1-\varpi) + A(t)\varpi\frac{1}{d_3}\right]S_1 - \alpha_1 I(t)(1-\varpi)\left[A(t)(1-\varpi) + A(t)\varpi\frac{1}{d_3}\right] \quad (5)$$

Where I_0, S_{10}, R_0, A_0, E_0 are initial values. The average incubation period of the infectious virus is $\frac{d_1+d_2}{2}$, that is, the patient in the incubation period per unit time is converted to the infected person by the proportional constant $\frac{2}{d_1+d_2} > 0$; The average course of death or recovery of the confirmed patient is d_3, that is, the recovery rate of the infected person per unit time is $\frac{2}{d_3} > 0$; The average course of treatment of suspected patients is d_3, that is, the recovery rate of suspected patients per unit time is $\frac{1}{d_3} > 0$; The contact rate parameter of each susceptible person and patient per unit time is $r > 0$.

The contact rate parameter $\alpha_2 > 0$ of the susceptible person and the suspected patient; Considering that the suspected patient's infection is converted into a latent patient, but the latent patient does not turn into a suspected patient; p is the strength of the isolation measure; $A(t)p\frac{1}{d_3}$ is a recovered suspected patient who has been quarantined; initial value setting: (These data are an estimate based on the total population and medical knowledge). $I_0 = 1$, $s_{10} = 1.1$ ten million, without considering the floating population;

R0 = 0; E0 = 0; A0 = 100; parameters setting: $\frac{2}{d_1+d_2} > \frac{1}{5}$, The average incubation period for infectious diseases is 5; $\frac{1}{d_3} = \frac{1}{20}$, The average course of death or recovery for a confirmed patient is 20.

$\frac{1}{d_3} = \frac{1}{20}$, Set the average course of suspected patients to 20; $\alpha_2 = 1.0 \times 10^{-11}$, The contact rate parameters of suspected patients and susceptible persons are also assumed to be fixed. Establish the calculus equation as follows:

$$\begin{cases} \frac{dS_1}{dt} = -\alpha_1 I(t)(1-\varpi)S_1 - \alpha_2\left[A(t)(1-\varpi) + A(t)\varpi\frac{1}{d_3}\right]S_1 \\ \frac{dE}{dt} = -\alpha_1 I(t)(1-\varpi)\left[S_1 + A(t)(1-\varpi) + A(t)\varpi\frac{1}{d_3}\right] - \frac{2}{d_1+d_2}E \\ \frac{dI}{dt} = \frac{2}{d_1+d_2}E\frac{1}{d_3}I \\ \frac{dR}{dt} = \frac{1}{d_3}I \\ \frac{dA}{dt} = -\alpha_2\left[A(t)(1-\varpi) + A(t)\varpi\frac{1}{d_3}\right]S_1 - \alpha_1 I(t)(1-\varpi)\left[A(t)(1-\varpi) + A(t)\varpi\frac{1}{d_3}\right] \end{cases} \quad (6)$$

$I_0 = 1$, $s_0 = 1.1$ ten million, without considering the floating population, $R_0 = 0$, $E_0 = 0, A_0 = 100$.

3 Virus Propagation Model

Since the spread of the virus is influenced by social, economic, cultural, customary habits and other factors [5], the most direct factors affecting the development trend of the epidemic are: the number of infected persons, the form of transmission, and the ability of the virus itself to spread, isolation strength, admission time, etc. When we build a model, we can't and don't have to consider all the factors. We can only grasp the key factors and make reasonable assumptions and modeling. Assume that the incubation period of an infective virus that is not completely known is d1–d2 days, and the healing time of the patient is d3 days. The virus can spread and spread through direct contact, oral droplets [6], and the number of people per day in this population is r. In order to control the spread and spread of the virus, the population is divided into four categories: normal population, patient population, cured human and death population, represented by H(t), X(t)R(t) and D(t), respectively. The controllable parameter is the isolation measure strength P (percentage of patients isolated during the incubation period). Therefore, the law of virus transmission can be divided into two stages: "pre-control" and "post-control".

The virus pre-control model is a virus model similar to that of natural propagation [7], and the post-control model is a differential equation model after interventional isolation intensity [8]. The transformation relationship of various types of people in the two models is shown in the following Fig. 1.

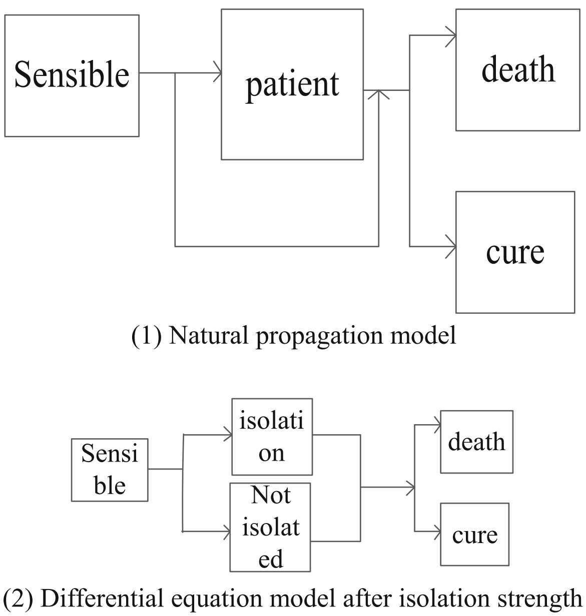

Fig. 1. Virus propagation model

Based on the above model, use the model you created for the following data: d1 = 1, d2 = 11, d3 = 30, r = 10; numerical simulation [9, 10], assuming the initial number of cases is 890, suspected patients are 2000 isolation measures intensity p = 60%. The patients were hospitalized 1.5 days later, and the simulated results of the suspected patients were isolated after 1.5 days and the simulation results of isolation measures p = 40%. The sensitivity of the above parameters to the calculation results was analyzed and used for subsequent improvement of the model [11, 12]. The model program is as follows.

```
ORG0000H
LJMPSTART
ORG0003H
LJMPPINT0
ORG001BH
LJMPPTI1
START:MOVTMOD,#10H
MOVSCON,#00H
MOVTH1,#03CH
MOVTL1,#0B0H
MOVDPTR,#TAB
SETBEA
SETBEX0
SETBIT0
DISP:MOVA,R4
MOVB,#10DIV  AB
MOVCA,@A+DPTR
MOVSBUF,A
LCALLDELAY
JIXU:
MOV   TH1,#03CH
```

4 Analysis of Results

Suppose that the time of the first patient in a certain area is T0, in the period of (T0, T), it is a period of near-free propagation, the isolation intensity is 0, and the number of infections per patient per day is a constant. Let us now consider the changes in several groups of people during the period from t to t + Δt. And by analyzing the state transformation relationship of various groups of people, the differential equation is established. When d1 = 1, d2 = 11, d3 = 30, r = 10, I0 = 890, A0 = 20, p = 60%,the patient was admitted to hospital two days later, and the suspected patient was quarantined two days later. This will give you a graph of the number of patients over time: (see below) (Fig. 2).

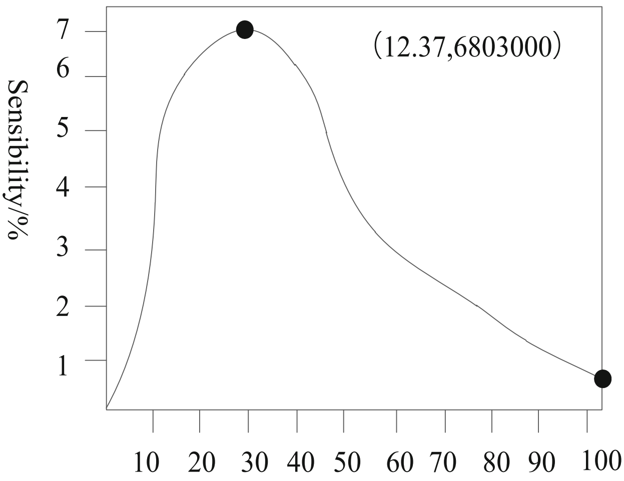

Fig. 2. Graph of the number of patients over time

From the figure we can see that the number of patients changes sharply with time. This shows that this is the development trend of the initial stage of virus transmission. Then you can see the highest point (Day 12.37) when the number of patients reached a maximum of 6803,000 people. By taking patient admission treatment and suspected patient isolation measures, we can clearly see from the figure that the number of patients is decreasing, and the number of patients has dropped to 540,800 after 100 days.

In order to further verify the sensitivity of the study of viral propagation kinetics, sensitivity simulation experiments were carried out on the dynamics of viral propagation. The simulation results are shown below (Fig. 3).

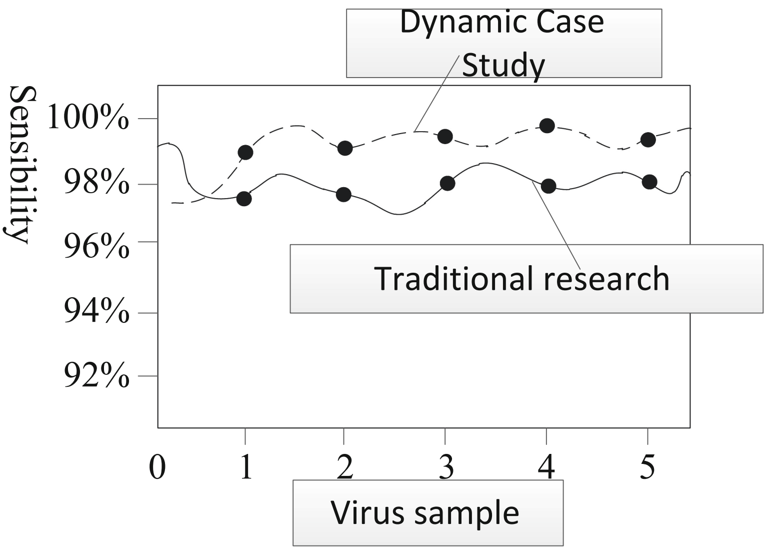

Fig. 3. Sensitivity simulation results

Through the above results, the following conclusions can be made, and the problems in the medical field can be transformed into the field of mathematics for analysis and discussion, and the development trend of infectious diseases and the prediction results for the future can be quantitatively obtained, which has strong theoretical and reliability. The parameters involved in the model have corresponding data sources. It can be easily calculated by combining certain data, and the relationship between the variables is clear, which is easy to solve the model. Since the mathematical model is based on continuous differential equations, an accurate analytical solution will not be obtained. We will fit the parameters under the premise of reasonable parameters. Considering the total number of people in the region, the population is divided into five categories: confirmed patients, suspected patients, healers, deaths and normal people, and these categories are divided into contagious and non-infectious. Countermeasures can be drawn based on the changes in the results. In addition, the sensitivity analysis of the incubation period and the healing period of the infectious disease was carried out. It was found that the change of the incubation period would have a greater impact on the results of the whole model, and the change of the healing period would only shorten the duration of the infectious disease, but has little effect on the cumulative number of patients.

5 Conclusions

With the continuous development of science and technology, in the context of current big data, the research on the law of traditional virus propagation dynamics has been developed to the bottleneck. The traditional law of virus propagation dynamics is less sensitive and the mathematical model is not easy to operate. Therefore, it is proposed to study the dynamics of viral propagation in combination with big data and kinetic models. Based on the traditional infectious disease model, using the differential equation method as the theoretical basis, combined with the different measures taken, the curve relationship between the number of patients and time is fitted, and the corresponding countermeasures should be taken. Sensitivity simulation experiments were carried out on the study of virus propagation kinetics. The results show that the study can scientifically and accurately study the laws of virus propagation dynamics. The established mathematical model is easy to operate and has a good guiding significance for practice.

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