Analysis and Research on the Progress of Epidemiological Dynamics based on SEIRS Predictive Model

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Abstract: In this paper, based on the nonlinear mathematical model SEIRS model, we describe the random transition between susceptibility, latent, morbidity and cure of the dynamic behavior of people under the action of infectious diseases. We select the infection rate, the number of contacts, the cure rate, mortality, immune cycle and other factors to solve the problem of the change of the number of patients in the system when the average number of people exposed to the initial latent person is different. By using dynamic simulation, it is concluded that the average number of contacts increases and the number of patients increases in the same cycle.

1. Introduction

Infectious diseases are diseases that can spread widely among people, people and animals, animals and animals. In the long years of human existence, the loss caused by plague to mankind is far more than the sum of wars. Cholera, smallpox, Spanish flu, SARS and COVID-19 have dealt a heavy blow to human production and life. The Centers for Disease Control and Prevention in China can be divided into A, B and C infectious diseases according to the mode of transmission and the ability of transmission. Every 10-30 years, a disease pandemic occurs in the human population. In today's living environment, shopping malls, supermarkets and schools may become areas where infectious diseases are rampant, so it is very important to establish a closed and systematic infectious disease transmission model to guide prevention [1].

This paper studies the following infectious disease scenario: in a closed system, the total number of people in the system is fixed. If there is a latent person in the system who spreads the disease, after a period of time, it will eventually lead to the infection of the disease in the whole system. The incubation period of disease refers to the period in which the human body is contagious but does not have symptoms of infection after being infected with the disease. The incubation period of measles is about 10-11 days, that of brucellosis is about 7-14 days, and that of cholera is about 1-3 days. The research content of this paper is that when the initial latent person is the staff, the number of infections

in the whole closed system after a period of time.

2. Problem analysis

The scenario studied in this paper is that when the initial latent person is a staff, there are more people exposed to the latent person per unit time in the closed system, and the system has a higher contact rate. Through the different contact rate to quantify the impact of different identities of the initial lurker. The state transition diagram of the power system studied in this paper is shown in figure 1[2].

3. Prediction model based on SEIRS

3.1 Data preprocessing

Table 1: Data preprocessing result

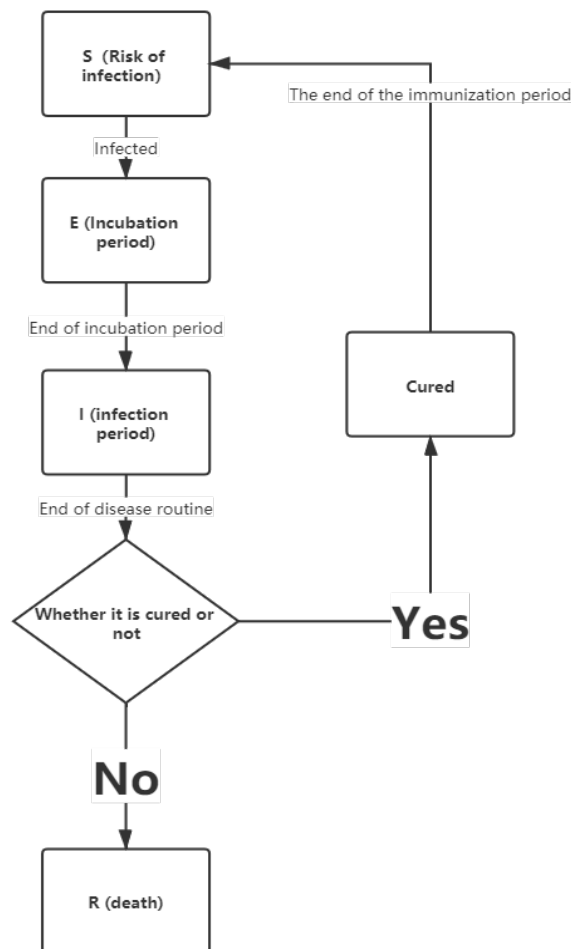|	Morbidity	Number of contacts	Cure rate	Antibody acquisition probability	Immune period	Course of disease	Incubation period
Staff	0.1	50	0.975	0.6	10-30	12-20	7-14
Non-staff	0.1	10	0.975	0.6	10-30	12-20	7-14

Figure 1: State transition diagram

3.2 The establishment of the model

The differential equation of SEIRS can be expressed as [3] [4]:

$$\frac{ds}{dt} = -\frac{r\beta}{N} + \xi R$$

$$\frac{dE}{dt} = \frac{r\beta SI}{N} - \sigma E$$

$$\frac{dI}{dt} = \sigma E - \gamma I$$

$$\frac{dI}{dt} = \sigma E - \gamma I$$

$$\frac{dR}{dt} = \gamma I - \xi R$$

Through the iteration of Markov chain, the following equations are obtained:

$$S_n = S_{n-1} - \frac{r}{N}\frac{\beta S_{n-1}I_{n-1}}{N} + \xi R_{n-1}$$

$$E_n = E_{n-1} + \frac{r\beta S_{n-1}I_{n-1}}{N} - \sigma E_{n-1}$$

$$I_n = I_{n-1} + \sigma E_{n-1} - \gamma I_{n-1}$$

$$R_n = R_{n-1} + \gamma I_{n-1} - \xi R_{n-1}$$

3.3 The establishment of the model

Using AnyLogic software for simulation calculation and analysis, the following results are obtained. When the staff is initially infected, the results are as follows:
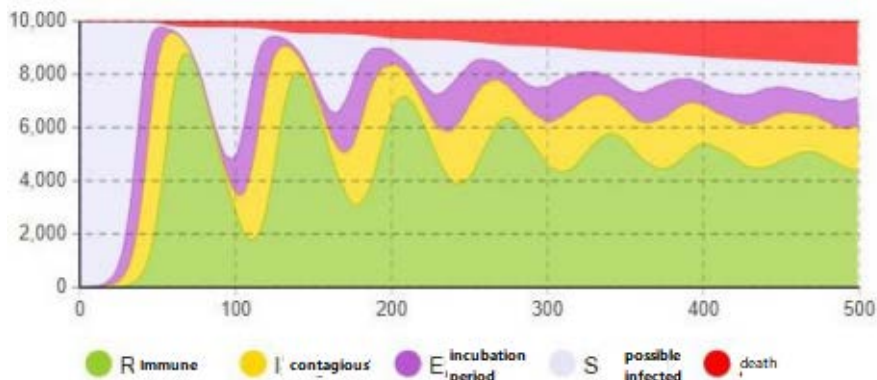

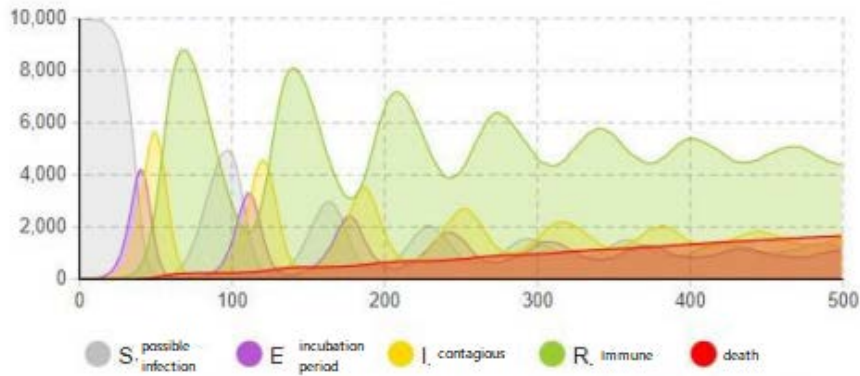*Figure 2: Changes of SEIRS when the staff were initially infected.-1*

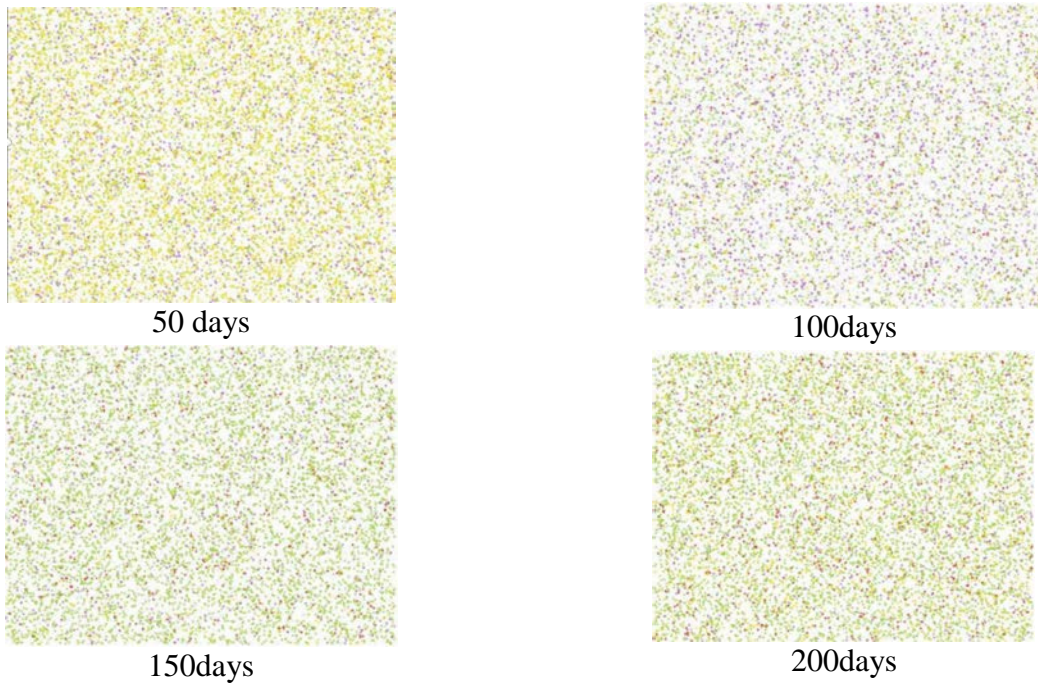*Figure 3: Changes of SEIRS when the staff were initially infected.-2*

50 days

100days

150days

200days

Figure 4: Infection in different days

4. Conclusion

At present, the global epidemic situation is still not optimistic, and epidemic disease is also a thorny problem that human beings are facing at present. Combined with the background of the epidemic situation, this paper uses matlab simulation and AnyLogic software to study the influence on the spread of infectious diseases in a closed system when the classification of transmission population is different and in the case of different levels of protection, which reflects the law of the spread of infectious diseases and provides ideas and schemes for researchers of related theories.

References

[1] Huang Guangqiu, Sun Siya, Lu Qiuqin. A function optimization method based on SEIRS epidemic model-- SEIRS algorithm [J]. Computer Research and Development, 2014 Jing 51 (12): 2671-2687.
[2] Wang Xia, Hong Fengling, Yan Weiping. Global stability of a class of SEIRS epidemic model [J]. The Progress of

Applied Mathematics, 2013 Jing 2 (02): 83-88.

DOI: 10. 12677/AAM. 2013. 22011.

[3] Yu Yumin, Song Suluo. Study on a kind of SEIRS epidemic model [J]. Journal of Zhengzhou University (Science Edition), 2011 Jing 43 (2): 4-9.

[4] Wang Ting, Wang Hui, Hu Zhixing. A kind of nonlinear SEI RS mathematical model of infectious disease transmission [J]. Journal of Henan University of Science and Technology (Natural Science Edition), 2017, 38 (2): 84-88, 94.