Computer Methods in Medicine and Health Care G. Casalino and A. Nayyar (Eds.) © 2022 The authors and IOS Press. This article is published online with Open Access by IOS Press and distributed under the terms of the Creative Commons Attribution Non-Commercial License 4.0 (CC BY-NC 4.0). doi:10.3233/ATDE220545

Simulation of Infectious Disease Propagation Based on SEIS and Complex Network Models

Tingting YAN¹, Hui WANG, Qixia QU, Haomin ZHAO and Haitao LV School of Science, Shenyang Jianzhu University, Shenyang 110168, China

Abstract. In this article, we apply the stability theory of differential equations, based on the improved infectious disease transmission model SEIS, to describe the change in the number of infections when the lurker is a non-staff. In the process of the spread of infectious diseases, we establish the relationship between various groups, and establish the equation data solving algorithm. On this basis, a complex network model is established to describe the influence of the movement of various groups of people in the system on the number of infections when the lurker is a staff member. At the same time, the cellular automata simulation in accordance with the complex network models is carried out through the collected data. Finally, using the probabilistic model of the spread of infectious diseases, the impact of the protective effect on the spread of infectious diseases is analyzed when staff in public places take appropriate protective measures. Through the establishment of the probabilistic model and the curve fitted by the python program, we conclude that at the beginning of the spread of infectious diseases, the fastest and best protective measures can not only slow down the speed of the spread of infectious diseases, but also effectively reduce the infection in the later stages of transmission the proportion of the people.

Keywords. SEIS Model, complex network model, cellular automata simulation, probabilistic model

1. Introduction

This is an actual problem of the spread of infectious diseases in a particular closed system. In 2020, the sudden outbreak of COVID-19 caused the virus to spread again, and words such as the spread of infectious diseases became a hot topic [1, 2]. Daily data updates also make people realize that quantitative research on the spread of infectious diseases from visual charts can effectively help predict and control the spread of infectious diseases [3-6]. We establish an infectious disease transmission SEIS model, a complex network model, and a probability model that can be transmitted multiple times in a closed space to study the changes in the number of infections caused by different initial lurkers [7-10]. Through the model, we analyze the impact of protective measures on the spread of infectious diseases.

¹ Corresponding Author, Tingting YAN, School of Science, Shenyang Jianzhu University, Shenyang, Liaoning, China; Email: yantt@sjzu.edu.cn. This paper was funded by the National Natural Science Foundation of China, grant number 11604224, and Liaoning Provincial Department of Education, grant number LJKZ0596.

First, we build the SEIS model to study the change in the number of infections over time. The range of activities of other people and staff in public places is different, and the density of people is also different. The traditional SIS model cannot reflect the effect of this difference, so we improve the SEIR model and obtain the advanced SEIS model. Using the SEIS model, the problem of the number of infections when the lurkers are nonworkers was studied. Secondly, we establish a complex network model and use cellular automata to simulate the simulation results of the number of infected people over time. In the end, we assume that workers take certain precautions. Therefore, on the basis of the first two models, a probability model of virus transmission is established, and the protection effect numerical value is substituted into the model simulation analysis to consider the impact of protection measures.

2. SEIS Model

During the spread of infectious diseases, the total number of people in the closed system N remains unchanged, that is, birth rate and death rate are not considered. The population is divided into three categories: Susceptible, Lurker, and Infected, marked as S, L, I, respectively.

$$N = S + L + I$$

Taking into account the above assumptions, we first use differential equations to express the changes in the numbers of the three groups of people over time. First of all, for the susceptible people: the number of susceptible people(S) over time(t) = the number of people recovered(yI) - the number of infected people in the susceptible population $[rb(I + L) * \frac{S}{N}]$.

$$\frac{dS}{dt} = -rb(I+L) * \frac{S}{N} + yI \tag{1}$$

Secondly, for the lurker crowd: the change in the number $\left(\frac{dL}{dt}\right)$ of the lurker crowd(L) over time(t) = the infected population in the incubation period among the susceptible population $[rb(I + L) * \frac{s}{N}]$ - the number of people transformed from the lurker crowd to the infected(*aL*), where *a* is the probability of a lurker being transformed into an infected person. So the differential equation is obtained:

$$\frac{dL}{dt} = rb(I+L) * \frac{s}{N} - aL$$
(2)

Finally, for the infected population: the amount of $\text{change}(\frac{dI}{dt})$ in the number of infected people(*I*) over time(*t*) = the number of people transformed from latent people into infected people(*aL*) - the number of recovered people (yI):

$$\frac{dI}{dt} = aL - yI \tag{3}$$

Based on the above three formulas, we perform simulations. The above formulas constitute a Markov chain, that is, the changes in the number of people in Sn+1, Ln+1, and In+1 tomorrow are only related to the number of infected people today. Then we can express the number of people in the three groups of people on the N_{th} day as the following three formulas:

$$Sn+I = Sn-r * B * (In+Ln\frac{S_n}{N}) * + y*In$$
(4)

$$Ln + I = Ln + r^*B^*In\frac{s_n}{N} - a^*Ln \tag{5}$$

$$In+1 = In + a*Ln - y*In \tag{6}$$

Then we use python program to perform simulation tests, substitute numerical calculations, and get the effect diagram, as shown in Figure 1.

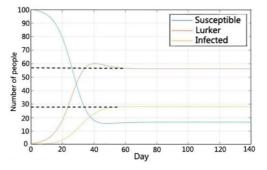


Figure 1. Changes in the number of three categories of people.

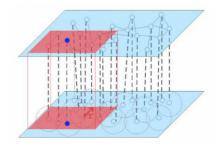


Figure 2. The complex network structure of virus transmission.

3. Complex Network Model

The complex network model takes into account the superposition of individual information and viral spread. In real life, people can move. Therefore, we adopt a dynamic network model to describe the network structure of virus spreading. The network layer individuals walk randomly, but the individuals can only have contact with other neighbors within a given radius r, that is, each individual can only have connections with other individuals within the same radius r at the current moment. The network structure of virus transmission is shown in Figure 2.

The individual movement is regarded as the movement of the node on the plane. The position of the node over time is set to $R_i(t)$ and the moving speed is set to $V_i(t) = (V_i(t)cos\theta_i(t), V_i(t)sin\theta_i(t)), i = 1, 2, \cdots$. In this model, it is further assumed that the modulus of the moving speed of individuals is constant and the modulus of all individuals is the same. That is, short-range jump is set to $V_i(t) = v$, $i = 1, 2, \cdots, N$. At the initial

moment, i.e. t = 1, N nodes are randomly distributed on the two-dimensional plane. At each time, the nodes follow the wandering (refresh $\theta_i(t)$). Each node updates its position and direction angle as follows:

$$\begin{cases} r_i(t + \Delta t) = r_i(t) + v_i(t)\Delta t \\ \theta_i(t + \Delta t) = \xi_i(t + \Delta t) \end{cases}$$
(7)

Among them, $\xi_i(t)$ is N independently distributed random variables, uniformly taken from $[-\pi, \pi]$. Assuming that in a closed system, the movement of individuals in public places must be long-distance jumps. Therefore, the probability of a person's longdistance jump is $P_{jump} = Q_1/Q_2$ and the probability of short-distance jump is $1 - P_{jump}$. The movement follows the above formula (7). Consequently, there is $V_i(t) =$ $(Vcos\theta_i(t), Vsin\theta_i(t))$. For a long-range jump, there is $V_i(t) =$ $(2Vcos\theta_i(t), 2Vsin\theta_i(t))$ with the probability of $P_{jump} = Q_1/Q_2$.

4. Cellular Automata Simulations

To collect data, we perform cellular automata simulations based on the complex network model, as shown in Figures 3 and 4.

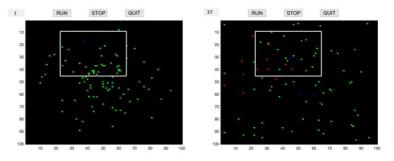


Figure 3. Cellular automata simulations at time = 1 (left) and at time = 31 (right).

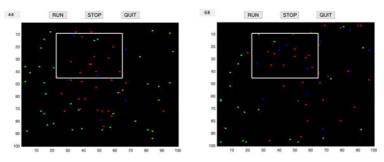


Figure 4. Cellular automata simulations at time = 44 (left) and at time = 68 (right).

Through simulation, the change of the number of various groups of people in the system with time when the initial lurker is a staff member is obtained, as shown in Figure 5:

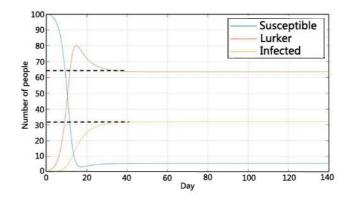


Figure 5. Changes in the number of three categories of people.

5. Comparative Analysis

By comparing the trend charts of the three categories of people when the initial lurker is a staff member and a non-staff member, we can clearly see that when the initial lurker is a staff member, in the early stage of infection, the susceptible people are in the incubation period. The early change rate of the population increases exponentially, and the number of susceptible populations also plummets. When non-staff are the initial lurkers, the change is gentler. This is because although the moving range of the staff itself is not as large as that of the non-staff, but because he is in a public place, the density of people and the degree of contact are higher than those of the non-staff. In addition, because of the closed space, we assume that the total number of people remains unchanged and there is no change in immunity. Therefore, in the two trend graphs, the changing numbers of the three types of people tend to be in a dynamic balance in the end.

6. Probability Model

Assuming that staff in public places have appropriate protective measures, the transmission rate of this infectious disease will be reduced. Therefore, a probabilistic model based on the simulation of the movement of people is established. Among them, the short-distance transmission rules of the virus are as follows:

(1) r_1 represents the effective transmission distance of the virus, and ρ_0 is the density of people infected with the virus within the range of r_1 ;

(2) the probability of people being infected with the virus is determined by equation (8);

$$R_{per}^{t+1} = R_{per}^t + \left(\beta \cdot f(\overline{\Delta t}) \cdot \left(1 - \frac{1}{m}S_{per}^t\right) \cdot \left(1 - S_{per}^t\right) \cdot \frac{1}{\rho_0}\right) \cdot P_{protect}$$
(8)

In the above formula (8),

 $(1)\frac{1}{\rho_0} \in [0,1]$ represents the probability that a susceptible person being infected with the virus within the effective transmission distance r1 at time t.

(2) $R_{per}^t \in [0,1]$ represents the probability of a person being infected with the virus at time t.

(3) $S_{per} \in [0,1]$ indicates the protective effect of the protective measures adopted by the staff, which will reduce the probability of infection S_{per} . Considering that the protective measures of other personnel are not as good as those of the staff, the protective effect of the protective measures adopted by other personnel is set as $\frac{1}{m}S_{per}$.

(4) β is the basic probability of spread of the virus in close contact.

(5) $P_{protect}$ represents the proportion of people taking protective measures in the system.

The effect of protection on the spread of infectious diseases is shown in Figure 6.

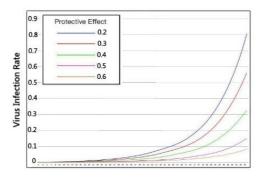


Figure 6. The effect of protection on the spread of infectious diseases.

7. Conclusion

In a closed system, the population is divided into three categories: Susceptible, Lurker, and Infected. Based on the improved SEIS model, the changes in the number of infected people over time when the lurkers are non-staff are simulated. In addition, through the establishment of a complex network model and the simulation of cellular automata, the changes in the number of infected people over time when the lurkers are staff are simulated. Finally, a probabilistic immune model is established to analyze the impact of protective effects on the spread of infectious diseases when workers in public places have appropriate protective measures. Through the establishment of the probabilistic model and the fitting of the curve diagram with the help of the python program. Through analysis, we conclude that in the early stage of infection, when the latent person is a staff member, the number of people in the incubation period increases rapidly, and the number of susceptible people drops sharply. When the lurkers are non-staff, the changes in the numbers of the three groups are relatively gentle. Moreover, at the beginning of the spread of infectious diseases, the fastest and best protective measures can not only slow down the speed of the spread of infectious diseases, but also effectively reduce the proportion of infected people in the later stages of transmission.

References

- [1] Rismanbaf A. Potential treatment for COVID-19: A narrative literature review. Arch Acad Emerg Med. 2020;8 (1):e29.
- [2] Chakraborty T, Ghosh I. Real-time forecasts and risk assessment of novel coronavirus (COVID-19) Cases: A data-driven analysis. Chaos Solitons & Fractals. 2020;135:109850.
- [3] Kaul G, Kapoor E, Dasgupta A, Chopra S, Management of multidrug-resistant tuberculosis in the 21st century. Drugs of Today. 2019;55(3):215-224.
- [4] Lim S, Tucker C S, Kumara S. An unsupervised machine learning model for discovering latent infectious diseases using social media data. Journal of Biomedical Informatics. 2017;66:82-94.
- [5] Funk S, Salathé M, Vincent A A, Jansen V A A. Modelling the influence of human behaviour on the spread of infectious diseases: A review. Journal of The Royal Society Interface. 2010;7:1247-1256.
- [6] Klovdahl A S. Social Networks and the spread of infectious diseases: The AIDS example. Social Science & Medicine. 1985;21:1203-1216.
- [7] Cao H, Zhou Y C, Song B J. Complex dynamics of discrete SEIS models with simple demography. Discrete Dynamics in Nature and Society. 2011;653937.
- [8] Hui J, Zhu D M. Dynamics of seis epidemic models with varying population size. International Journal of Bifurcation and Chaos. 2007;17:1513-1529.
- [9] Stefan G H, Joshua C, Richard J M. A complex network perspective on clinical science. Perspectives on Psychological Science. 2016;11:597-605.
- [10] Pelikan M, Goldberg D E, Lobo F G A. Survey of optimization by building and using probabilistic models. Computational Optimization and Applications. 2020;21:5-20.