An Advanced Infectious Disease Spreading Model—SEICD and Its Simulation

Ming Xi Zhao

Hebei Provincial North China Electric Power University 071003 Baoding, China

zhaomingxi2009@163.com

Abstract. Focus on describing the transmission of infectious disease, this paper mainly develop a new model--SEICD. The model is based on the classic infectious disease model called SEIR. In of the characteristics of most infectious disease, we make a series of improvements in depth. By the improved model, we adapt graph theory to describe the complex relationships of the real society,simulate the population changing of different states in the model, and analyze the influence the relative infectiousness k in the situation of infectious diseases spread. Considered all above, a best critical relative infectiousness kc to distinguish whether the regions under epidemic stress can be under control can be got.

1 Introduction

The improvements from SEIR model to SEICD model made in the following paper are briefly summarized below.

Firstly, during the incubation period of most infectious disease, the individuals can't infect others, the same as the feature of exposed (E) state. So we redefine the exposed (E) state as the incubation period. Then divide the exposed (E)into two parts: one part are definitely diagnosed and can becured without converting into the infected (I), while the other part without definite diagnosis will finally change into the infected (I).

Secondly, we divide the resistant (R) into two new groups named as the cured (C) and the dead (D). Because the infected (I) may be cured or dead gradually. During the I-to-C conversion and I-to-D conversion, the infectiousness is changing. So we use two vectors to respectively express the different degrees of infection in these two conversions. The elements of the vectors refer to how the infectiousness changes over time.

2 Advanced Infectious Disease Spreading Model--SEICD

2.1 Introduction of the classic SEIR model

In the original SEIR model[1],each individual is considered in one of these four discrete states: susceptible, exposed, infected and resistant. The transform between them is ruled like this: Initially susceptible individuals can become exposed. The exposed ones are defined as the people with "potential" virus and they can't infect others. However, they have the possibility to become infected and spread the virtue to other people. At the end of the model, the infected people finally turn resistant, which include the non-infections and no longer susceptible to the disease. In brief, we give a transformation figure as follows:
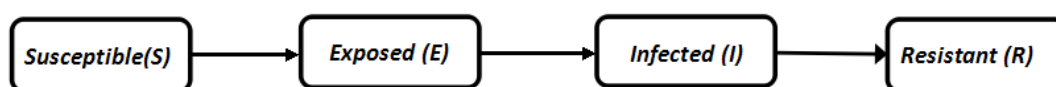

Figure 1 Transformation of the original SEIR model

As is shown in the graph: Susceptible ones have a rate to become exposed. After a few time, exposed individuals could manifested the features of disease and change to the infected group. Then, because of the treatment or death, the infected patients finally turn to resistant ones

2.2 Improvements of SEIR model

Considering the specifics of infectious disease, we make improvements in the following ways:

First, during the incubation period of most epidemics, the individuals can't infect others, the same as the feature of exposed (E) state. So we redefine the exposed (E) state as the incubation period. Then divide the exposed (E)into two parts: one part are definitely diagnosed and can be cured without converting into the infected (I), while the other part without definite diagnosis will finally change into the infected (I).

Second, we think that the resistant groups can be confused to the model. So we divide this part into cured (C) part and dead (D) part by the ratio of n and 1-n. That is to say, of people in group I, the possibility to be cured is n.

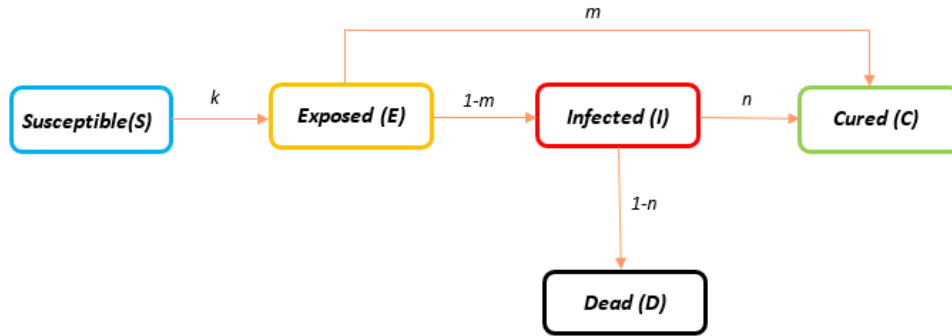The conversions are shown in the figure:

Figure 2 Relation schema of the epidemic spreading model

Figure 2 shows the relation of the four states and the conversion possibility between them. A susceptible person has a chance of k to touch the patients and become exposed. When exposed, he may be found and diagnosed by a possibility of m. According to the assumption, a person can be cured once he is diagnosed. So m can also represent the curing rate. However, if he is not diagnosed during the incubation period, he will turn infected and have a chance of 1-n to be dead.

2.3 The modification of the formula

It is shown that there are five groups of states in our EVD spreading model: S, E, I, C and D. Considering E-to-I conversion, I-to-C conversion and I-to-D conversion, the infectiousness is changing. So we define three vectors α_i, β_{ai} and β_{bi} to describe how the infectiousness changes over time:

$$\alpha_i = [\alpha_1, \alpha_2, \alpha_3, \ldots, \alpha_k]$$
$$\beta_{ai} = [\beta_{a1}, \beta_{a2}, \beta_{a3}, \ldots, \beta_{aw}]$$
$$\beta_{bi} = [\beta_{b1}, \beta_{b2}, \beta_{b3}, \ldots, \beta_{bs}]$$

where i refers to the number of states according to the exposed process and the infected process. α_i means the rate of the infection from exposed groups to other groups. According to the assumption we have made before, α_i is equal to 0. β_{ai} represents the cured(C) individuals from infected groups have changing rates to infect others, whereas β_{bi} refers to the dead(D) individuals from infected groups have changing rates to infect others.

Then we give several rules to discuss epidemic spread course:

Rule 1: One belonging to the exposed group has a rate of m to become cured (C)without being infected, i.e.

$$R_{1-e,t} = m * E_{sum,t} \quad (1)$$

$R_{1-e,t}$ means the increase between time slots of cured groups from exposed individuals. $E_{sum,t}$ means during the t time slot, the size of the exposed groups.

Rule 2: The change of the dead part are only decided by the infected groups, i.e.

$$R_{2,t} = (1 - n) * I_{sum,t} \quad (2)$$

$R_{2,t}$ refers to increase between time slots of dead groups. $I_{sum,t}$ refers to the size of exposed groups in the time slot.

Rule 3: When exposed people convert into infected groups, they infect others in two ways, β_{ai} and β_{bi}, i.e.

$$I_{a,t} = n * E_{a,t} \quad (3)$$
$$I_{b,t} = (1-n) * E_{a,t} \quad (4)$$

$I_{a,t}$ represents one part of the infected groups who will change their rate of the infection by β_{ai} while $I_{b,t}$ by β_{bi}.

Rule 4: Susceptible individuals i get infected by the connected infected groups with certain rate, and the rate can be calculated in this way:

$$P_s(i) = k \sum_j \omega_{ij}[n\beta_a(j) + (1-n)\beta_b(j)] \quad (5)$$

where $P_s(i)$ refers to the probability of susceptible groups changing into exposed groups. ω_{ij} represents the possibility of i contacting with j.

Rule 5: The relative infectious parameter k has a relatively simple interpretation when k approaches to zero[2], the probability that an infected one j infects others is equal to:

$$1 - \prod_{n=1}(1 - k\beta\omega_{ij}) \approx \sum_{n=1} k\beta(n)\omega_{ij} \quad (6)$$

In this way, the process of calculation can be greatly simplified.

3 Simulation of Infectious Disease Spreading Model

3.1 Descriptions of relationships between individuals by graph theory

To describe the relationships between the groups in our model, we apply the graph theory. In brief, we use nodes and edges to describe the relationships between individuals. In this way, we can make our model more reliable. Here we will take weighted small world graph [2] into account. This graph is, as is shown to us, based on the small-world graph which can be used to describe the small town's relationship that one has close connections with his neighbors, and only a few people need just one or two other nodes to connect with.

In addition, to better simulate the relationship in the real world, the weighted small- world graph add several nodes can have connections with further nodes, while most nodes still only keep in touch with his neighbors.
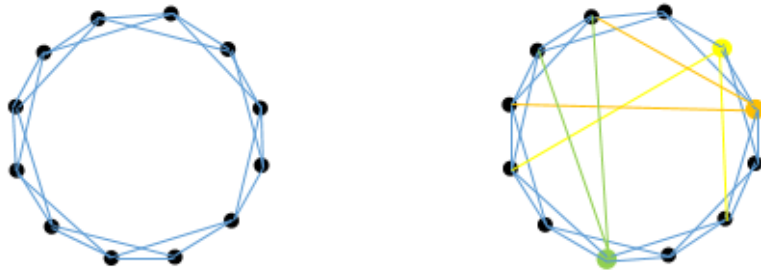

Figure 3 Small-world graph and weighed small-world graph

3.2 An example of Infectious Disease Spreading Model

By studying the features of epidemic disease, we give several reasonable parameters as follows:

- Graph size *N*: 1000
- Mean degree of the graph *d*: 6.0
- Infectiousness vectors:

$$\alpha_i = [0,0,0,0]$$
$$\beta_{ai} = [0.5, 0.25, 0.12, 0.05]$$
$$\beta_{bi} = [0.5, 0.6, 0.7, 0.8]$$

- Relative infectiousness *k*: 0.5

The size N is large enough to describe the population changing of the different states in the epidemic spreading model. Mean while, a larger size will enlarge the time of computing. Figure4 shows that the disease spreads in a relatively slow speed.
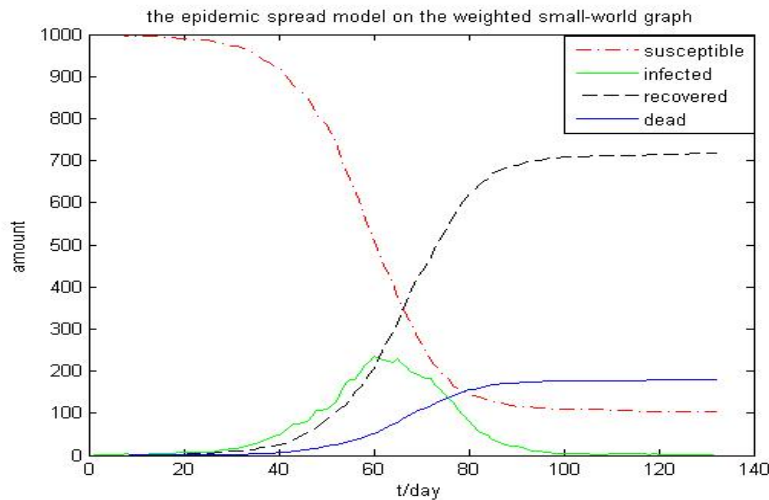
Figure 4Changes in number of people in state S, I, C, D on the weighted small-world graph

To study the different value of the relative infectiousness k how to influence the states of the model, we carry out another simulation about the relationships between k and the fraction of affected individuals. We get the k changed from 0 to 2, stepped by 0.01.We can get the conclusion that with the growth of k, all fractions based on four kinds of the graphs are increasing and get close to 1, which means if k is large enough, the spread of disease will get out of our control. On the contrary, if we keep the relative infectiousness under a certain value, the spread of the disease can be governed and finally eradicated. In this simulation, we can find the critical relative infectiousness kc is close to 0.6. That is to say, only if the relative infectiousness k is smaller than kc, can disease beer adicated completely.

4 Conclusion

This paper mainly develop a new infectious disease spreading model called SEICD, and give the formulas to conclude the population change of different types of individuals. For different kinds of infectious disease, we can assign different weights to the parameters. After simulation, we can get a best kc to control the infectious disease. In this way, infectious disease become no longer severe.

References

[1] Müller, M., & Zemp, J. (2009). Lecture with Computer Exercises: Modelling and Simulating Social Systems with MATLAB.
[2] Wang, Y., Chakrabarti, D., Wang, C., & Faloutsos, C. (2003, October). Epidemic spreading in real networks: An eigenvalue viewpoint. In *Reliable Distributed Systems, 2003. Proceedings. 22nd International Symposium on*(pp. 25-34). IEEE. Jaquet, V. & Pechal, M. (2009) Epidemic spreading in a social network.