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An application of small-world network on predicting the behavior of infectious disease on campus

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A B S T R A C T

Networks haven been widely used to understand the spread of infectious disease. This study examines the properties of small-world networks in modeling infectious disease on campus. Two different small-world models are developed and the behaviors of infectious disease in the models are observed through numerical simulations. The results show that the behavior pattern of infectious disease in a small-world network is different from those in a regular network or a random network. The spread of the infectious disease increases as the proportion of long-distance connections p increasing, which indicates that reducing the contact among people is an effective measure to control the spread of infectious disease. The probability of node position exchange in a network (p_2) had no significant effect on the spreading speed, which suggests that reducing human mobility in closed environments does not help control infectious disease. However, the spreading speed is proportional to the number of shared nodes (s), which means reducing connections between different groups and dividing students into separate sections will help to control infectious disease. In the end, the simulating speed of the small-world network is tested and the quadratic relationship between simulation time and the number of nodes may limit the application of the SW network in areas with large populations.

1. Introductions

Dynamic modeling can effectively simulate virus transmission and has become a popular technique in infectious disease research (Hu, Yuan, Huang, & Huang, 2019). The compartment model proposed by Kermack and Mckendrick in 1927 pioneered the study of infectious disease modeling (Kermack and McKendrick, 1927, 1991a, 1991b). The SIR (Susceptible-Infected-Removed) is the most classic infectious disease model, which mainly divides individuals into three categories: susceptible, infected and removed. Later, infectious disease models are improved based on the SIR model, mainly SIS (Susceptible-Infected-Susceptible), SEIR (Susceptible-Exposed-Infected-Removed), SEIRS (Susceptible-Exposed- Infected-Removed-Susceptible) and SEIRS (Susceptible-Exposed-Infected-Removed- Susceptible) models (Tang et al., 2020).

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However, the process of virus transmission in the real world closely related to the number of infected individuals, the size of the transmission rate, and the way of contact between individuals. Research has shown that the crowd in the real society is not homogeneous, and the linkage relationship between people is not uniformly mixed, but shows some characteristics of complex networks, such as small-world characteristics, scale-free characteristics, and so on (Yan, 2023).

At the end of the 20th century, three articles on networks stimulated the interest of researchers in various fields to explore complex networks: the small-world (SW) network model in 1998, which is in between regular and completely random networks (Watts & Strogatz, 1998), the BA scale-free network model in 1999 (Barabasi & Albert, 1999), and navigable network model in 2000 (Kleinberg, 2000). Ten years later, Barabasi summarized the development of scale-free networks and future prospects (Barabasi, 2009). Recently, Broido et al. found fewer than 36 in about 1000 networks (4%) exhibit the strongest level of evidence for scale-free structure (Broido & Clauset, 2019), while a handful of technological and biological networks appear strongly scale free. For example, the evidence shows that the degree distribution of the network of sexually transmitted diseases conforms to the power exponential form (Schneeberger et al., 2004). In other words, diseases transmitted through the sexual route are more consistent with the structure of scale-free networks. Xie and Yao have studied the transmission of HIV in man who have sex with man (MSM) populations in different network structures and found that under the same degree distribution, the speed of disease transmission in scale-free networks is higher than that in small world networks. Therefore, if the MSM network structure tends towards scale-free networks, HIV will spread faster in such networks (Xie & Wei, 2013).

Traditional models of infectious disease transmission dynamics assume that all individuals in a society are homogeneous and do not take into account differences between individuals, and therefore cannot model the real situation well. Typical networks abstract real individuals as nodes, and the contact relationships between individuals as connecting edges between nodes, which can more closely model the linking relationships of social populations. Mean-field analysis is used to investigate dynamics on complex networks (Gleeson, Melnik, Ward, Porter, & Mucha, 2012). Combining complex network theory with propagation dynamics can better study the propagation mechanism of infectious disease in the real society, as well as accurately simulate and evaluate the effectiveness of the preventive and control measures taken (Li, Zhong, Ji, & Yang, 2021; Shen, Li, & Yao, 2016). In a small-world (SW) network, most nodes are not directly connected to each other, but most nodes can reach other nodes through a small number of steps. It has both a small shortest path length feature and a high clustering coefficient. As such, it is an intermediate version of two simpler types of networks, which are random network with a small shortest path length feature and a low clustering coefficient, and regular network with a high clustering coefficient and no short paths between "distant" nodes. The SW network was first proposed by Watts and Strogatz for modeling the properties of networks in many different areas, such as biology, sociology, computing, and earth sciences, with an emphasis on the behavior of infectious disease in SW networks. The SW effect has been found to have a significant impact on epidemics in single networks. There have been many cases of modeling infectious diseases using a SW network. Wu et al. investigated epidemic model with the diversity of the durations of infection and recovery of the individuals on small-world networks (Tang & Wu, 2019). Saramäki and Kaski proposed that the dynamic SW network model performs well in analyzing the spread of random infectious diseases, such as various types of influenza (Saramäki & Kaski, 2005).

Learning environments such as schools are characterized by frequent social gatherings and extensive interpersonal interactions, making them ideal breeding grounds for viruses (Liao et al., 2022). In this research, we use the SW network to predict the infectious disease behavior in universities. Multiple types of links exist between one student and another, which can be broadly categorized into two types: 'cliques', such as roommate relationships; and long-distance connections, such as those between students who sit close to each other in an elective course. The first type of link leads to a high degree of clustering of the nodes involved, while the second type of link may form short paths between distant nodes. These characteristics match well with the properties of the SW network, which has both small clusters and long-distance connections. Therefore, it is very feasible to use the SW network to model the connections between students at universities.

2. Methods

Based on the SI (Susceptible-Infected) model, two models are developed for the campus behavior using MATLAB software. The first model (Fig. 1) is a single SW network used to investigate the overall spreading trend of infectious disease. The second model (Fig. 2) consists of two SW networks with multiple shared nodes (labeled with diamonds in the figure) for studying the transmission of an infectious disease between two groups of people with connections. Each node in the network represents a susceptible (a student or a faculty member), and each connection represents a possible transmission route. Networks are constructed according to the method proposed by Watts and Strogatz (Watts & Strogatz, 1998): starting from a ring grid with n vertices and k edges per vertex, we randomly reconnected each edge with probability p. This construction allows us to 'tune' the graph between regularity ($p = 0$) and disorder ($p = 1$), thus exploring the intermediate region of $0 < p < 1$.

In this model, the locations of shared nodes in the two networks are chosen randomly. This is because people are unlikely to have exactly the same pattern of relationship with others in different surroundings. However, in a university, people with the same hobbies or life patterns may be familiar with each other and hence have a greater chance of being 'closer' in the network, which may be concerned in future research.

The process of modeling the spread of an infectious disease is as follows.
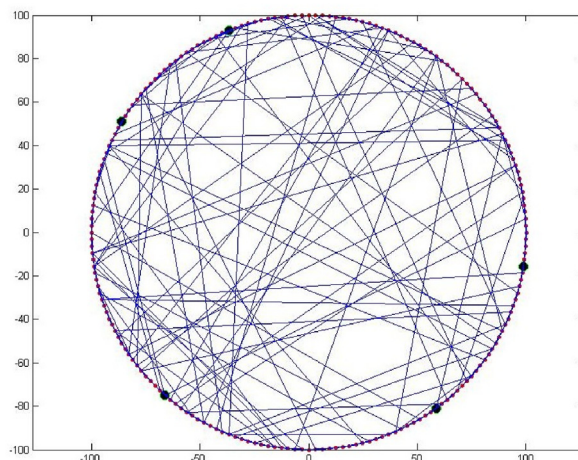
Fig. 1. Single SW network: Susceptible individuals are shown as small red dots and the initially infected individuals as large black dots. Blue lines represent connections between nodes. The circular layout does not reflect the spatial arrangement of the nodes. The total number of nodes in this figure is 200 and the average number of connections per node is 8.

(a)   (b)
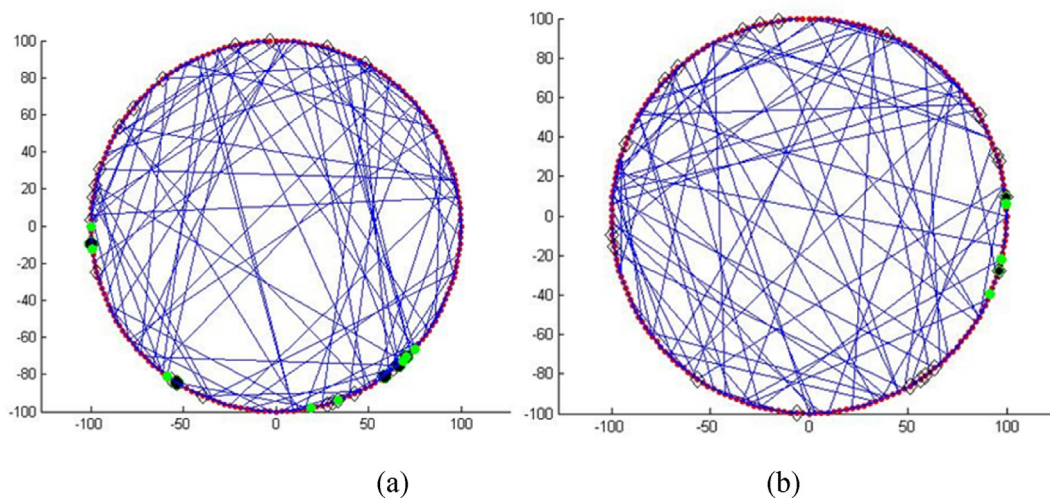
Fig. 2. SW networks with several shared nodes. The nodes labeled with diamonds represent the shared nodes.

1) Create an $N*N$ adjacency matrix of the graph to represent the connections between nodes. (This step is done during the creation of the SW network.)
2) Randomly designate $N*p_0$ nodes as the initial infected nodes for the first model and one of the two networks in the second model. Label them as 'infected'.
3a) Find all connections to the infected nodes in the network. Assume that each node contacts with all the nodes linked to it at each time step. Therefore, each connection node is infected with probability p_1. Find the newly infected node and mark it as 'infected'.
3b) Find all connections to the infected nodes in the network of the second model and conduct the process of 3a.
4a) Select $N*p_2$ (p_2 is the probability) nodes, then randomly swap their positions in the network and keep their attribute ('infected' or not) unchanged.
4b) Randomly specify the locations of shared nodes in both networks of model 2. For any infected shared nodes, mark the corresponding node in the other network as 'infected'.
5a) Repeat step 3.
5b) Repeat step 3 in the other network.
6) Count the number of infected nodes.

The parameters of the models are listed in Table 1.

Table 1
The parameters in the modeling process of the two models.

Parameter	Description
N	Total number of nodes in the network
k	Average connections per node
p	The proportion of long-distance connections
p_0	The initial proportion of infected nodes in the network
p_1	Probability of a susceptible getting infected with each connection to infected node in a time step
p_2	Probability of the exchange of nodes' positions in a time step
s	Shared nodes between the two networks in the second model
$T_{1/2}$	The average time T when half of the nodes are infected
r	The linear correlation coefficient

In a real campus with thousands of students, the connections between students may be much more complex than in the model. However, in order to speed up the calculations and to present the network in a clearer graph, we simplify the model to 200 nodes with an average of 8 connections per node.

3. Results

The first model focuses on the attributes of the model (i.e. the SW network) in the analysis of infectious disease spread. Therefore, four issues are studied: 1) the spread of an infectious disease in the model after a single time step; 2) the spread of an infectious disease after several time steps; 3) the relative relationship between the proportion of long-distance connections, p, and the spreading speed of an infectious disease; 4) the computing speed of the model as N grows; 5) the relationship between the proportion of node positions exchange in a time step. Fig. 3 shows the result of the first model, the newly infected individuals are shown as green dots.

Just like in real situations, infectious disease occurs primarily in people who are in close contact with an infected person, but sometimes it also occurs in seemingly unrelated people (note the green dot in the upper right of the figure).
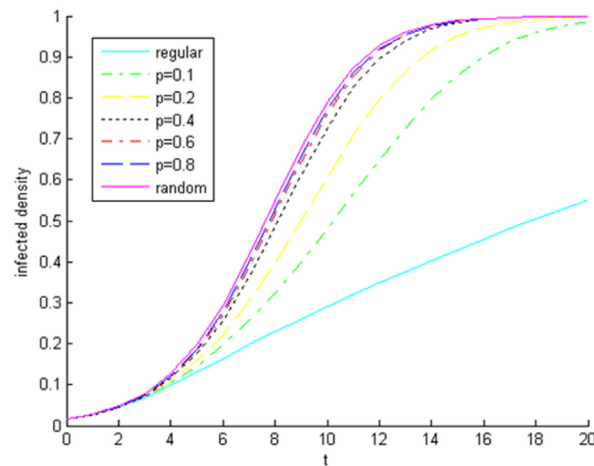
The spread of infectious disease over several time steps has been studied. In most cases, pathogens seem to "crawl" along the circular regions of the network over time, while "jumping" from one region to another with a small probability. This reveals the properties of SW networks.

Fig. 4 shows how the proportion of long-distance connections, p, affects the spreading speed of an infectious disease. As predicted, as p increases from 0.05 to 0.40, the spreading speed rises significantly. However, as p continues to rice, the relative relationship between p and spreading speed decreases. The average time T when half of the nodes are infected $T_{1/2}$ is an important indicator for the model. Therefore, the relationship between $T_{1/2}$ and the proportion of long-distant connections p is listed in Table 2. All data in the table are averaged over 100 simulations.

Simulating speed is also among the important factors when deciding which model to choose in a practical situation. Simulating results show that the number of nodes N and the computing time of the model roughly fits a quadratic function, in which $t \sim N^2$ (Table 3). The data are averaged over 100 independent runs when N value is no more than 2000 and 10 runs when $N > 2000$.
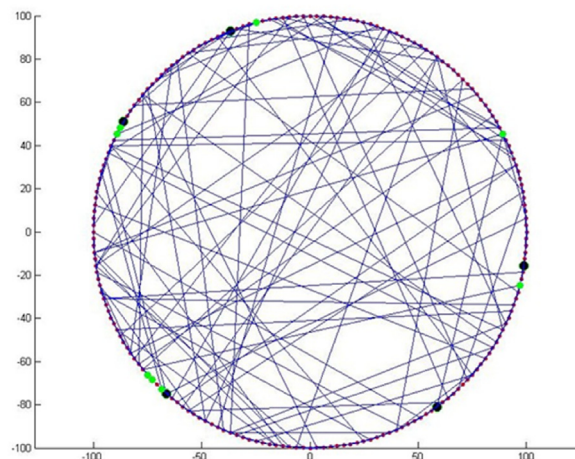
Fig. 3. Single SW network after a time step. $N = 200$, $k = 8$, $p = 0.1$, $p_0 = 0.025$, and $p_1 = 0.2$.

Fig. 4. The spread of an infectious disease over time. Lines are obtained with $N = 200$, $k = 8$, $p_0 = 0.015$ and $p_1 = 0.1$. $P = 0$ is used to simulate the spread in a regular network and $p = 191/199$ is used for a random network. All the data are averaged over 500 independent runs.

In the SW network, p_2 reflects the intensity of activities within the network. Simulating results show that in an independent network, p_2 had no significant effect on the spreading speed over two time steps, which suggests that reducing human mobility in closed environments does not help control infectious disease (Table 4). In the simulation, $N = 200$, $k = 8$, $p_0 = 0.025$, $p_1 = 0.1$, all data are averaged over 2 time steps.

The second model focuses on two questions in this study: 1) the relative relationship between the number of shared nodes (s) and the spreading speed of an infectious disease from one network to another; 2) the relative relationship between the proportion of long-distance connections (p) and the spreading speed of an infectious disease from one network to the other.

Fig. 5 shows how s affects the spreading speed of an infectious disease from one network to another. As predicted, the spreading speed rises significantly with s increasing from 5 to 80, and the correlation coefficient between s and the infective density shows a linear correlation. Table 5 lists the linear correlation coefficient (r) according to different value of p, data in the table are averaged over 10 independent individual simulations.

4. Conclusions and discussions

The simulation results show that the SW network has unique properties. As shown in Fig. 4 and Table 2, the spreading speed of infectious disease in the SW network is intermediate between the normal network and the random network, and a very small p value can have a great impact on the spreading speed of infectious disease. This is due to the nature of long-distance connections in the SW network. These connections link distant parts of the network together to form short paths for the spread of infectious disease. This property is also reflected in the simulation of infectious disease spread over several time steps.

This characteristic of the SW network illustrates the importance of isolation (medical quarantine) as an effective method of cutting off an infected person's long-distance connections with others. It reduces the p value of the network and thus slows down the transmission process considerably. Therefore, reducing the contact among customers is considered as the effective measures to control COVID-19 propagation in supermarkets (Xu & Chraibi, 2020). Social distancing is a recommended solution by the World Health Organization (WHO) to minimize the spread of COVID-19 in public places (Rezaei & Azarmi, 2020). It was found that infectious diseases can be substantially suppressed by increasing the quarantine rate (Nagatani & Tainaka, 2021).

Surprisingly, however, the decline rate slowed down as p continued to grow. When p reaches 0.60, no statistically significant difference between the $T_{1/2}$ value of the SW network and that of the random network. We noticed that the characteristic path length L goes down significantly when a regular network ($p = 0$) becomes a SW network with several long-distance connections added. As Watts and Strogatz pointed out, "for small p, each short cut has a highly nonlinear effect on L, contracting the distance not only between the pair of vertices it connects, but also between their direct neighbors, neighbors of neighbors and so on (Watts & Strogatz, 1998; Watts & Strogatz, 1998)." Thus, we suppose that the spreading is closely related to the characteristic path length of a network.

Then we studied the relationship between the mobility of nodes in a single network (p_2) and the spreading speed. Beyond our expectations, p_2 has no significant effect on the spreading speed in a single network over 2 time steps. This result reflects the fact that in an enclosed environment, reducing human mobility cannot help reduce the spreading speed in a single network significantly. For example, if some students are found infected in a classroom or dormitory building, methods such as quarantine should be taken firstly, as this reduces the p value. On the contrary, if the students are only allowed to live or study where they are, but long-distance connections are not forbidden, the spreading speed will remain high. The similar result was

Table 2
Relationship between $T_{1/2}$ and p.

p	regular	0.05	0.10	0.20	0.40	0.60	0.80	0.90	random
$T_{1/2}$	17.88	13.49	11.83	10.52	9.63	9.29	9.27	9.25	9.23

Table 3
The average elapsed time for a single simulating over 20 time steps.

N	100	200	500	1000	2000	5000	10,000
t/s	0.0241	0.0509	0.249	0.706	2.56	16.86	Out of memory

Table 4
The number of 'infected' nodes (N) over 2 time steps.

p_2	0	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1
N	16	17	17	16	16	16	16	16	16	16	17
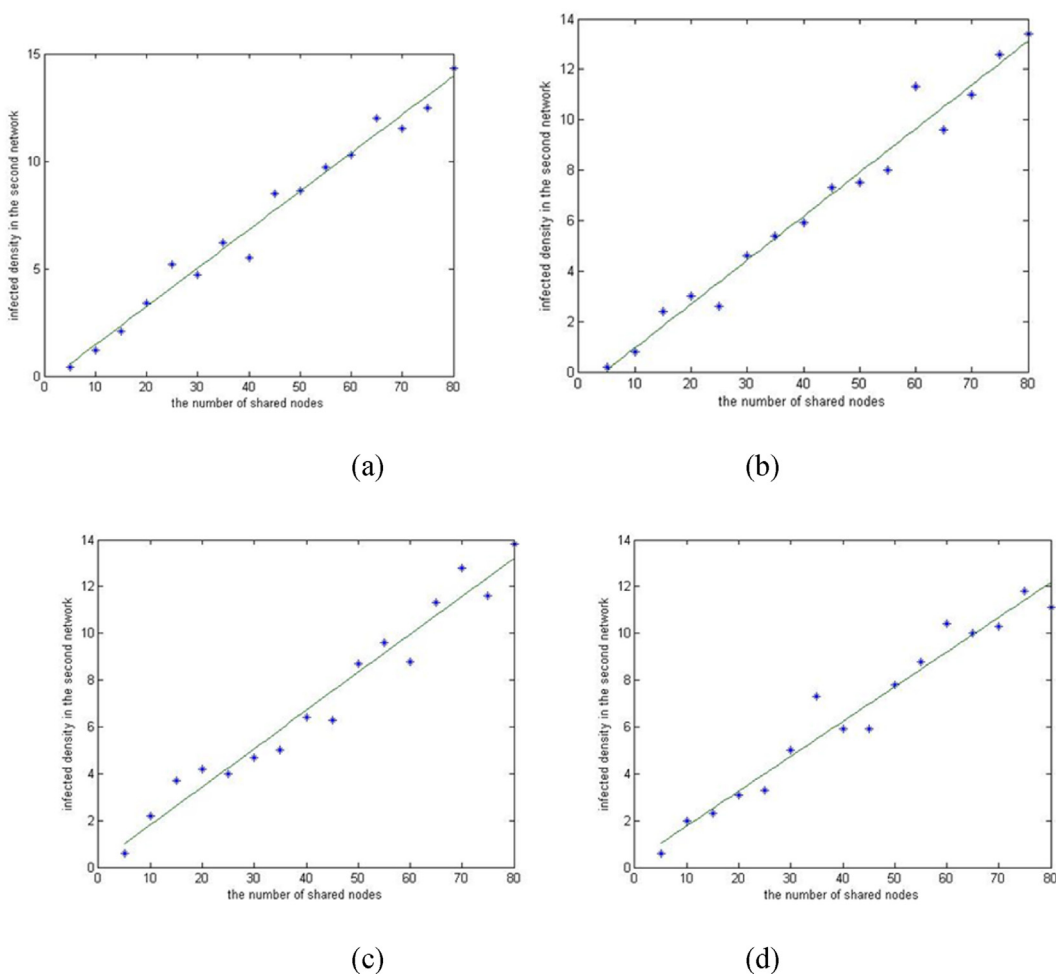
Fig. 5. The relative relationship between s and the infective density of the second network after a time step, $N = 200$, $k = 4$, $p_0 = 0.05$, $p_1 = 0.2$, $s = 5:5:80$. (a) $P = 1$, (b) $p = 0.5$, (c) $p = 0.1$, (d) $p = 0$.

obtained in random-walk simulations, which indicate that the infection hardly spreads if the movement of all people is limited to a certain group and the infection spreads everywhere if people freely move between different groups (Nakagiri, Sato, Sakisaka, & Tainaka, 2022).

Table 5

The linear correlation coefficient (r) between s and infective density.

p	random	0.5	0.1	regular
r	0.9903	0.9880	0.9806	0.9783

The property between different networks in the second model indicates that though the variation of p has little effect on the spreading speed between different networks, we should pay enough attention to the connection blocking between different networks. This is because the spreading speed between different networks is proportional to the number of shared nodes (s). More importantly, the real-world network is a small-world network, and the number of shared nodes and the spreading speed are highly decentralized. Therefore, the probability of an infectious disease outbreak is likely to exceed our prediction. Especially on university campus, students usually have many opportunities to participate in different activities and establish connections with different groups of people, which mean that the number of shared nodes will be very large, and thus campus epidemic should be taken seriously. The similar result can be obtained in other SW network, for example, The similar result can be obtained in other SW network, for example, Nagatani and Tainaka found that infectious diseases can be substantially suppressed by decreasing the migration rate (Nagatani & Tainaka, 2021), and It is found that the infection curve can be flattened more and more by prohibiting longer-distance travels successively (Nagatani, 2021). We show that the movement restrictions are effective control measures against epidemic spreading. Methods such as decreasing mobility of students and staff, eliminating group activities and dividing students into separate sections can keep the infectious disease under control. They can reduce the number of shared nodes in the networks, and thus slowing down the spreading process considerably. In the case of COVID 19, universities in China took these measures to prevent outbreaks on their campuses. Nonpharmaceutical interventions (NPIs), such as social distancing, reduce not only COVID-19 cases but also other circulating infections such as influenza and RSV (Huang et al., 2021). Preventing and controlling infectious disease brought about by network connections is a theme for future city construction (Wang, 2021).

There are limitations to the model in this paper. A real-world situation is far more complicated than the model. There are many factors such as weather, medical condition, public awareness and so on affect the network. However, the model does not include all the parameters that are relevant to the real-life situations. During the actual spread of an infectious disease, the conditions of a node or a group of nodes (e.g. sick or not) will affect the connections to it/them (Han, 2007; Pastor-Satorras & Vespignani, 2001). For example, a sick person may be quarantined for medical observation or may be cured, but the models in this research are proposed under the premise that the connections in the networks are static. Therefore, when modeling the real spread of infectious disease, we must consider how the reality will affect the connections in the network.

Another limitation is the quadratic relationship between the simulating time and the number of nodes. This will limit the application of the SW network in areas with large populations. For example, some universities have a population over 10,000. To solve this problem, we assume that a "small-world function" can be given to estimate the spreading behavior in the SW network.

In short, the behavior patterns of infectious diseases in SW networks are different from those in a regular network or a random network, and the connections between networks play an important role. Like other network models, it was found that the spread of infectious diseases increases with the increase of long-distance connection ratio, indicating that reducing human to human contact is an effective measure to control the spread of infectious diseases. The spreading speed between different networks is directly proportional to the number of shared nodes, which means that prohibiting long-distance travel is another effective measure to control infectious diseases. However, the probability of node position exchange ($p2$) inside a network has no significant impact on the spreading speed, indicating that reducing human mobility in a closed environment does not help control infectious diseases.

CRediT authorship contribution statement

Guojin Wang: Writing − review & editing, Writing − original draft, Validation, Data curation, Conceptualization. **Wei Yao:** Writing − review & editing, Software, Project administration, Methodology, Funding acquisition, Conceptualization.

Declaration of competing interest

The authors declare no conflict of interest.

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