Effectiveness of Community Contact Reduction

Abstract

The social contact network topology structure has a major impact on dynamic epidemic spread patterns and the efficacy of non-pharmaceutical interventions. People are commonly organized in small communities in accordance with the behavioral or functional units of individuals, meaning that most social contact networks tend to display property of the community structure. This paper explores the effect of the community structure-property of social contact networks on the epidemic spread and the effectiveness of interventions through empirical research and Monte-Carlo simulation on a large H1N1 outbreak on a Chinese university campus. To simulate this outbreak, a stochastic model is built on social contact networks between students, revealing that epidemic outbreaks commonly occur in local communities.

Introduction

Contagion is spread among the population mainly through close contact such as talking and physical touch for many types of communicable diseases. Since the intensity and frequency of close contact are primarily determined by individual social relationships, the study of patient social networks has a clear advantage in understanding the reasons for the epidemic outbreak and trend. In recent years, an increasing number of efforts have been made to create a variety of theoretical models that combine classical compartmental models with complex social network methods, such as the susceptible-infectious-recovery (SIR) model. These combined models take the idea from compartmental models that, according to their states, individuals are divided into different compartments and their states are transformed with time[1]. These techniques, on the other hand, overcome the limitation that assumes that populations in standard compartmental models are homogeneously mixed. Recent advances in the study of social networks provide useful tools to simulate and analyze the epidemic dynamics among the real population in which contacts between people are not simply randomly selected but have many complex characteristics[2-4].

The structure of the community is one of the significant properties that many real social contact networks possess. The structure of the Society, also known as hierarchical organization or modularity, refers to the fact that it is possible to break a network into sub-groups. Nodes are densely linked within these sub-groups, while the relation between subgroups is much more sparse[5]. Near and frequent population interactions in these social groups have been found to make these local areas the most at-risk settings for outbreaks of infectious diseases, especially respiratory infectious

diseases such as H1N1[6, 7]. How to protect people from being infected in such communities has been a public health priority to many countries. The group structure of social communication networks, on the other hand, defines the efficacy of non-pharmaceutical intervention approaches to slow the spread of infection in local populations. Non-pharmaceutical interventions have the added benefit of reducing the concern that viral drug resistance may be induced by pharmaceutical interventions. As such, many have, since the very beginning of the 2009 H1N1 pandemic, Countries, including China, have adopted control strategies, such as quarantining foreign travelers, closing schools, etc. These control strategies benefit greatly from reducing many of the population's social contacts in communities and thus preventing an epidemic outbreak. This technique, i.e. the quarantine of near contacts of infected individuals, has been shown to be effective against SARS infectious diseases. Obviously, when we take the tactics, it will cost more, stringent sooner or more. For us to choose when and how to conduct intervention methods, a quantitative assessment of the efficacy of various control measures is necessary. Because most interactions are within local social groups, the effects of community structures on the efficacy of control strategies must be examined.

A case analysis of a big 2009 influenza pandemic is conducted in this article. (H1N1) outbreak to describe H1N1 virus transmission patterns on a school campus that has community structure land. We are building a hierarchical social network among students in one apartment building where a severe H1N1 outbreak occurred, based on social contact information from a detailed epidemiological investigation of the outbreak. To simulate the spreading process of the epidemic in the network, finding community outbreaks within small social groups, a compartmental based stochastic model is proposed. In addition, the effect of three non-pharmaceutical interventions based on quarantine (including dormitory building quarantine only, plus prohibition of inter-room visits, and plus the transfer of all persons at risk to a treatment center) on the transmission is contrasted in order to identify the most successful control measures with appropriate control measures.

Data and Methodology

Data

A major H1N1 outbreak occurred on the campus of a Chinese university near Beijing from August 28 through September 17, 2009. In this outbreak, a total of 206 students are infected and about half (105) of them live in a six-story apartment complex. In this article, we concentrate primarily on the spread of the H1N1 virus in this one house, as it was the key hotspot for infection and a hub for student interactions during the outbreak. Students living in this building were divided into 14 classes and belonged to the same academic department. Adjacent rooms were allocated to the students of the same class and each room usually housed six students. Therefore, from a single dormitory room to a classroom to the entire building, students in this dormitory are organized hierarchically. We perform social contact between learners to further understand the social contacts between students.

Preliminary epidemiological examination to gather their near contacts prior to the onset of the disease in these reported cases. Thirty respondents recalled their close contact history in this investigation, involving 45 virus carriers in all. In Table 1, we list the interaction between these respondents and their infected contacts. 9 respondents were contaminated mostly by outsiders until the building was isolated. After the building was isolated, 21 respondents were mostly contaminated in other rooms by roommates and, to a lesser degree, by classmates. In addition, all infected patients are examined for their time delay from infected to hospitalized, finding that on average it took around 1.5 days.

To contain this epidemic, the school administration took several measures to control it. Emerging measures, including 1) isolating the apartment building from inter-building transmissions on 31 August; 2) banning students in the apartment building from contacting other students staying in separate dormitory rooms on 3 September; 3) quarantining all possible similar connexions when an infected student is sent to the hospital during the whole outbreak.

Table 1. The relationship between the respondents and their contacts to H1N1 virus carriers

	Respondents	contacts	Roommates	Classmates	Different classes	Different buildings
Whole period*	30	45	16	11	2	16
Before isolate	9	13	0	0	0	13
building After isolate building	21	32	16	11	2	3

Method

As shown in Table 1, social interactions between students in the apartment building indicate a property of a group structure, as a student is most likely to be infected by his or her roommates and is moderately likely to be infected in various rooms by his or her classmates and is less likely to be infected by students in different classes. We create a complex network in order to model social contacts between students in the building by representing students as nodes and social relationships between them as ties. Because of the group structure of social interactions between students in the apartment, we assign different probabilities for each student to contact his roommate, neighbors in the same classes, and others in the same house, respectively. Based on the epidemiological investigation, the probabilities are preset: we presume that the communication histories of the 30 respondents in Table 1 will represent other students' behaviors. Since people living in the same room should be in close contact with each other on a regular basis, we get the average number of contractors who are roommates, classmates but live in other rooms, whereas others living in the same building are p1= 5, p2= 3.5 and p3= 0.5, respectively. It displays the network model as Fig. 1.

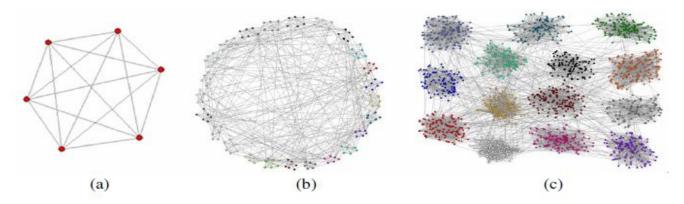


Fig. 1. (a) The social contacts network in one room. All students living in one room are fully connected. (b) The social contacts network in one class. Many edges exist in each room, and fewer edges between rooms. (c) The social contacts network in the building. The students are divided into different classes; many edges exist in each class, and fewer edges between classes.

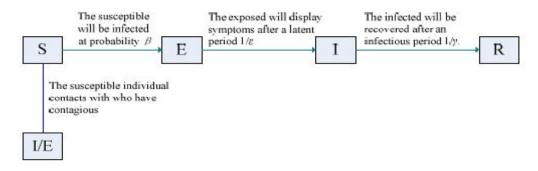


Fig. 2. The state change process of epidemic spreading in SEIR model

To simulate the disease spreading process on the network, a stochastic SEIR model was applied. People are divided into four groups in the SEIR model: Prone, Exposed (Incubation), Contaminated, and Recovered[27]. The epidemic spreading process of state change in the SEIR model is shown in Fig. 2. According to some observational studies of H1N1 transmission [28, 29] and the infectious duration as 1 / γ = 1.5 days, we set the latent period 1 / ϵ = 2 days based on our epidemiological investigation. The spreading rate β was set at 0.18, which means that between the daily counts of new infections in the actual epidemic and the simulation results, the coefficient of determination, a measure of how well the real data can be explained by the model, is maximum. We divide the outbreak into three periods according to the control strategies taken by the school administrator during the outbreak: 1) From August 28 to August 31, the apartment building was not isolated, and students in the building could be infected with infectors outside the building with a probability of λ = 0.004; (2) Infection can only be transmitted inside the apartment building from 1 September to 3 September; (3) After 3 September, communications between two students in separate rooms are cut

off with a likelihood of being contagious = 1, meaning that infection can not spread between rooms. The university administration investigated the infected people during the outbreak in order to identify their near connexions for quarantine. In practice, however, it is difficult to successfully classify all contacts since gathering contact histories of infected students is very time-consuming. As a proxy, a patient's roommates should be regarded as automatic near contacts and assumed to be quarantined as candidates. In our simulation, we presume that all roommates of an infected patient will be quarantined when the infected patient is hospitalized, and according to the investigation taken by the administration, the likelihood of finding and quarantining a neighbor exposed to an infected patient is = 0.8. In Table 2, related parameters are listed.

We have analyzed the effect of three different control measures on H1N1 spread using our network-based model. In order to quantitatively analyze the influence of timeliness and severity of control measures on control results, we change the date of implementation of these measures in the simulation, on the one hand, and the parameters λ , η , θ , on the other hand. The effects of control measures are calculated as the number of students contaminated and isolated by the interventions is decreased.

Table 2. The parameters used in the social contacts network and SEIR model

Parameter value p ₁ 5		Interpretation			
		Average number of one's contactors who are roommates			
p_2	3.5	Average number of one's contactors who are classmates but are living in other rooms			
p_3	0.5	Average number of one's contactors who are students belong to other classes			
β	0.18	Spreading rate			
1/7	1.5	Average infectious period			
1/ε	2	Average latent period			
λ	0.004	The probability that a student is infected by outsiders in the first period			
η	1	The probability that edges between rooms are removed in the third period			
θ	0.8	The probability that close contactors living in other rooms can be found during the outbrea			

Result

Social Contact Network and Stochastic Simulation

The number of newly infected people in the building every day is illustrated in Fig. 3. The virus was primarily brought into the building from the outside during the first phase and spread to more and more students. In the second period, the transmission peaked and then rapidly reduced. If we take into account the 2-day latent H1N1 virus duration, we infer that after the administration isolated the building, the number of students exposed to infection decreased rapidly. In addition, after interaction between rooms was banned, the infection rate remained at an exceptionally low level.

Using a social contact network with a group structure, we simulated the H1N1 virus spreading process. Table 2 lists the associated parameters. As shown in Fig. 1, via roommate relationships, the students first form small groups, then form larger clusters by connecting rooms belonging to the same classes, and finally form the entire communication network for the building. It turns out that the simulation results, averaging over 100 experimental runs, match the overall outbreak trend very well, as shown in Fig. 3. The determination coefficient between the number of infected students in the actual outbreak and simulation results on each day is 0.79. Fig. Fig. 4 illustrates the relationship based on a typical single simulation run between infection transmission and social networks. It demonstrates that there is seldom inter-class transmission. There are regular internal transmissions in rooms within each class and the inter-room transmissions contribute to the spread of infection through the class.

Furthermore, we remember that the H1N1 outbreak's transmission mode is associated with the social communication network group structure. The infection has spread rapidly among densely linked groups of individuals. Fig. Fig. 5(a) suggests the distribution in dormitory rooms of contaminated numbers. In total, there were 68 dormitory rooms in which students were contaminated. Of these rooms, 44(64.7 percent) had only one infected case, while the other 24(35.3 percent) had more than two infected cases, despite the fact that the roommates of the infected students were promptly quarantined. The findings suggest that rooms are relatively independent units where the infection spreads rapidly.

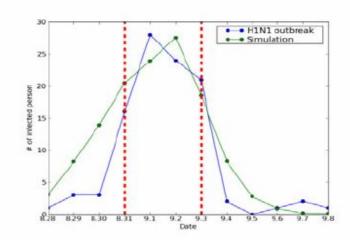


Fig. 3. The spreading process of the infection. Each point on the blue and green lines represents the number of the newly infected in the building each day of the situation of real outbreak and simulation, respectively. The outbreak is divided into three periods by the red dashed line.

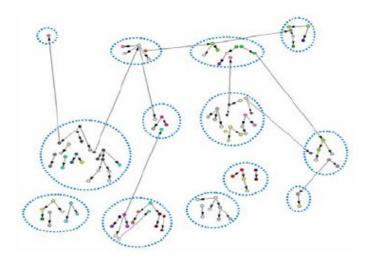


Fig. 4. The spreading process on the social contact network based on a typical single simulation run. Each point represents a student, and each edge represents a spreading path of the infection. The students are divided into various classes, denoted as circles. The students living in one room are marked with the same color.

The infection situation varied significantly across classes during the outbreak: the average number of infected in each class is 7.5 while the standard deviation is 9.0. Notice that the number of students is very uniform across schools, with an average of 136.7 and a standard deviation of 18.2. As shown in Fig. 5(b), fewer than 10% of infected students were in 12 classes and two classes witnessed major outbreaks of 15 (10 percent to 20 percent) cases and 32 cases (30 percent -40 percent). This disparity means that an outbreak with minimal inter-class intervention could occur in individual classes.

In general, in small communities such as rooms and classes, the simulation produced a transmission of H1N1 very similar to what was observed in the actual outbreak. We calculated the correlation coefficient of Pearson between the number of dormitory rooms (classes) that had different numbers of infections in actual outbreaks and simulation results. A value of 0.99 was obtained (0.95 for the class, both with p<0.005).