



The epidemic spreading on the multi-relationships network

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ABSTRACT

Different from traditional multi-community, the paper proposes a new multi-relationship network which is constructed to assess the effect of interlaced complex interpersonal relationships on the epidemic spreading process. Besides, an innovative MR-SIS epidemic model is proposed and analyzed in this paper. Empirically, we simulate MR-SIS spreading process on a multi-relationship network. The experiment results show that immunizing the nodes in overlapping sub-networks inhibits the epidemic spreading. Moreover, when considering the multi-relationship network structure and the above conclusion, this paper proposes a novel immunization to overcome the limitations of traditional immunization strategy, which has been proven a satisfying desirable performance on controlling disease transmission.

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1. Introduction

The past decade, the multi-community network [1–5], information cascades of complex networks [6], evolutionary games on multilayer networks [7] and the interdependent network have been attracting a lot of interest from researchers. Extensive research also has show that the community structure plays a pivotal role in epidemic spreading process [8–14]. In real-world networks, a social relationship community maybe has one or more individuals which connect to other community. Traditionally, this networks are defined as the multi-community networks, or overlay networks, [10,15–17] as shown in Fig. 1a, which simply describes the common example, the scientific collaboration network in which collaboration between individuals in different field [18]. Despite a large number of striking research up to now has been published, most studies in the field of multi-community have only focused on a single type relationship, meanwhile, in these studies, the multi-community network usually are defined as “interdependent network” [19–21], “network of networks” or “layered networks” [15,18]. However, due to the complex interpersonal relationship in the real world, each individual can’t be simply divided into a community by one or two relationships. On the other hand, the overlapping of different communities also increases the overall complexity of the network, such as friend network, classmate network and relative network. In addition, the complex interdependence of communities also is a important factor influencing the network, for example, the connection between different the city inner traffic networks not only depends on highway networks but also railway networks and airline networks. Essentially, individuals have very complicated social relationships, and individuals play different roles in different communities. As shown in Fig. 1b, each red node belongs to more than one community that is different from these red nodes linking two community on traditional overlapping network. In fact, everyone is the red node in the Fig. 1b, he has Notice the multiplicity and complexity of relationship, each individual has a variety of identities to face with different persons from different communities, hence he maybe a friend, a classmate, a workmate or a family. Because of the various

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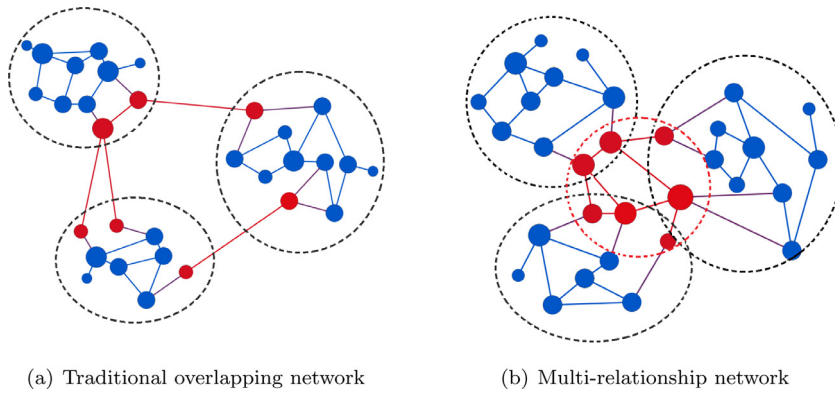


Fig. 1. The comparison figure of two types overlapping networks.

identities, every one is living in various relationship networks such as circle of friends, classmate net and family group. It is now well established that each relationship community has different effect for social intercourse, however, the influence of multi-relationship network on epidemic spreading process has remained unclear. Therefore, the objectives of this research are to investigate the specific influence of multi-relationship network on an infectious disease transmission process.

Inspired by traditional multi-community networks, this paper proposes a new network construction algorithm in which an individual has two kinds of identities between different overlapping sub-networks (such as the friend circle and family group in this paper). Hence, the multi-relationship network is constructed in this paper as follow:

1. Build n sub-networks in same size N_b . Each sub-network may be a WS small-world network or a BA scale-free network. This n independent sub-networks are defined as “basic sub-networks”, denoted by G_b , which are similar to the communities constructed by blue nodes in Fig. 1b.
2. From each basic sub-network, some nodes are randomly chosen out to form a new “overlapping sub-network” G_o with N_o , under the principle of scale-free (or small-world). Actually, every basic sub-network also is a overlapping one(which is described as the community of red nodes in Fig. 1b).
3. During the time Δt , in the same type of sub-network, the contact probability between two individuals is the same, but is different between different types of sub-networks.

From the above algorithm, this network

$$G = \sum_{i=1}^n G_{i_b} + \sum_{j=1}^m G_{j_o}, \quad (1)$$

is constructed by n basic networks and m overlapping networks in this network. Each individual perhaps belong to s overlapping networks in a basic network. Thus, let the probability of a individual in an overlapping networks be defined as $p = \frac{N_o}{nN_b}$, the probability of i individual in s overlapping networks be defined as $P_i(s) = \binom{m}{s} p^s (1-p)^{m-s}$. Let the contact probability be u_s in basic networks and be v_s in overlapping networks. Furthermore, let subscripts b and o respectively represent the different types of sub-networks: basic sub-networks and overlapping sub-networks.

Considering the above network structure, this paper proposes a novel SIS epidemic model which named as MR-SIS(Multi-relationship Susceptible-Infected-Susceptible) epidemic model, in which the effective spreading rate is calculated by different formulae(in basic networks $\lambda_1 = \frac{\beta u_s}{\gamma}$, but in overlapping networks $\lambda_2 = \frac{\beta v_s}{\gamma}$). Hence in the MR-SIS model, neighbors of each infected individual belong to different types of sub-networks, and they are infected by their neighbors with different rates λ (if the relationship between them is described as a link in basic network $\lambda = \lambda_1$, otherwise $\lambda = \lambda_2$).

This paper is organized as follows. In the next section, this MR-SIS epidemic model is detaillly introduced and discussed. Section 3 contains seven types topological structure degree distributions of multi-relationships networks, the simulation experiment of epidemic spreading on multi-relationships network and a new immunization strategy based on these nodes on overlapping sub-networks. Finally, this paper in Section 3 give the conclusions.

2. MR-SIS epidemic model

In classical SIS epidemic model, each individual has two states: *Susceptible* and *Infected* [22–24]. Let the number of susceptible (healthy state) individuals be denoted as $S(t)$, infected individuals $I(t)$ at time $t \geq 0$, initially with $S(0) = S_0$, $I(0) = I_0$ [25]. Suppose the probability β of a susceptible individual be infected by its infected neighbours. Meanwhile an infected individual also may recover to become a susceptible individual again with a probability γ [26,27]. The probabilities β and γ are inherent attributes of infectious disease, so they are two invariant constants for a kind epidemic. Then, define the virus

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