



Identification of highly susceptible individuals in complex networks



Shaoting Tang, Xian Teng, Sen Pei*, Shu Yan, Zhiming Zheng

LMIB and School of Mathematics and Systems Science, Beihang University, Beijing, China

HIGHLIGHTS

- We investigate the susceptibility of individuals in SIR and rumor spreading models.
- We explore the impact of community structure on spreading processes.
- We compare the performance of degree, betweenness centrality, PageRank and k-shell in locating highly susceptible individuals.
- We find that k-shell is superior in identifying high risk population for SIR model, but degree performs better for rumor spreading model.
- Our finding highlights the significance of both topological features and spreading mechanisms in identifying highly susceptible population.

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ABSTRACT

Identifying highly susceptible individuals in spreading processes is of great significance in controlling outbreaks. In this paper, we explore the susceptibility of people in susceptible-infectious-recovered (SIR) and rumor spreading dynamics. We first study the impact of community structure on people's susceptibility. Although the community structure can reduce the number of infected people for same infection rate, it will not significantly affect nodes' susceptibility. We find the susceptibility of individuals is sensitive to the choice of spreading dynamics. For SIR spreading, since the susceptibility is highly correlated to nodes' influence, the topological indicator *k*-shell can better identify highly susceptible individuals, outperforming degree, betweenness centrality and PageRank. In contrast, in rumor spreading model, where nodes' susceptibility and influence have no clear correlation, degree performs the best among considered topological measures. Our finding highlights the significance of both topological features and spreading mechanisms in identifying highly susceptible population.

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1. Introduction

Developing efficient methods to prevent epidemic outbreaks or accelerate information dissemination is the ultimate goal of research on spreading dynamics across various domains [1–15]. For diseases and information that spread through social networks, the structure of underlying contact network can greatly affect the spreading processes [13–15]. Previous studies have inspected the role of topology in epidemic threshold and critical behavior. For example, in uncorrelated networks, the epidemic threshold is $\lambda = \langle k \rangle / (\langle k^2 \rangle - \langle k \rangle)$, where $\langle k \rangle$ and $\langle k^2 \rangle$ are the first and second moments of the degree distribution [14]. Later on, in view of the wide occurrence of intrinsic heterogeneous complex networks in real world,

* Corresponding author.

E-mail addresses: tangshaoting@buaa.edu.cn (S. Tang), peisen@buaa.edu.cn (S. Pei), zzheng@pku.edu.cn (Z. Zheng).

Table 1

Statistics of social networks. We display the node number N , link number L , and average degree $\langle k \rangle$ for Facebook and Enron social networks. The critical infection rate of SIR model β_c is calculated by $\langle k \rangle / (\langle k^2 \rangle - \langle k \rangle)$. β_S and β_R are adopted infection rates in SIR and rumor spreading simulations respectively.

Network	Topological statistics			β_c	β_S	β_R
	N	L	$\langle k \rangle$			
Facebook	4,039	88,234	43.7	0.0095	0.03	0.3
Enron	36,692	367,662	20.0	0.0072	0.02	0.3

researchers started to investigate the effect of microstructure on spreading dynamics in more detailed perspectives: the community structure appearing in social networks [16], k -shell decomposition of networks for identification of influential spreaders [3], link salience skeleton correlated with the frequency of a link's appearance in infection hierarchies [17], as well as weak ties which is significant for information dissemination [18].

Due to the existence of complex microstructure, individuals with different topological features should play distinct roles during the spreading processes. Previous studies mainly focus on the spreading ability of individuals. Many topological measures are employed to identify influential spreaders in networks, such as degree [4,13], betweenness [19], k -shell index [3,20], PageRank [21,22], etc. In fact, individuals situated in different positions of the contact network will also vary in susceptibility to epidemics. Identifying the highly susceptible individuals in contact networks is of great significance in controlling epidemic outbreaks. Therefore, it is indispensable to explore the factors that affect people's susceptibility.

In this paper, we study the susceptibility of individuals in SIR and rumor spreading dynamics through extensive simulations in real-world social networks. First, we explore the impact of community structure on people's susceptibility. Even though the community structure can diminish the infected population and slow down the spreading processes, it is not the pivotal factor affecting nodes' susceptibility. Although the location of epidemic source has an impact on the precise infected probability of each single person, there exist a group of nodes that can always get infected with relatively high probabilities no matter where the spreading originates. We are particularly interested in these populations and consider them as highly susceptible individuals. To quantitatively depict the property of these people, we define the susceptibility of each individual as the average probability to be infected by a randomly chosen spreading source. Then we further explore the topological properties of the highly susceptibility individuals. By examining their topological traits including degree, k -shell, betweenness centrality and PageRank, we find the susceptibility of individuals is sensitive to the choice of spreading dynamics. For SIR spreading, the susceptibility is highly correlated to nodes' influence. Therefore, nodes located in the core region of networks are more likely to be infected. However, in rumor spreading model, degree can better identify highly susceptible individuals. Our results indicate that it is necessary to acquire the information of spreading mechanism to better locate highly susceptible population in practice.

2. Impact of community structure on spreading processes

Most of social networks in reality have notable community structure. We first explore the impact of community structure on individuals' probabilities to be infected in spreading processes. We examine the epidemic flows in two social networks with community structure: (1) the friendship network between users of the social network Facebook (Facebook) [23], (2) the Enron email communication network (Enron), in which nodes are email addresses and edges represent email communications [24]. These social networks have been used in previous studies. Topological statistics of networks are shown in Table 1. In our following study, we treat all these networks as undirected.

The community structure is extracted by a fast heuristic method based on modularity optimization [25]. The layout of community structure for Facebook social network is shown with different colors in Fig. 1(a). To simulate spreading processes among populations, we first apply susceptible-infectious-recovered (SIR) [26,27] model on the above social networks. In SIR model, the population can be classified into three possible states: susceptible (S), infected (I), or recovered (R). Starting from a single epidemic source node, at each time step, the infected individuals (I) would infect their susceptible neighbors (S) with probability β_S and then become recovered (R) and gain permanent immunity with probability λ . Such process continues until there are no infected individuals in the system. In our simulations, without loss of generality, we set $\lambda = 1$. Previous studies have adopted this model to describe diffusion of contagious diseases. For information dissemination, recent works have shown that, although some information spreading processes are greatly affected by human-related factors [28–32], a few information memes showing viral behavior can also spread like infectious diseases [33]. Hence the SIR model is applicable not only to epidemics but also to those information memes which are not seriously affected by human-related factors.

In simulations, the selection of infection rate β_S could significantly affect the spreading outcomes. Below the critical value $\beta_c = \langle k \rangle / (\langle k^2 \rangle - \langle k \rangle)$, the proportion of infected individuals will vanish in the limit of a very large population. For β_S much larger than β_c , the epidemic will infect almost all the people in the network. In our study, we use relatively small values of β_S to guarantee medium scale infection coverage. Otherwise most of the nodes will be infected with high probabilities, making their susceptibility indistinguishable. In Table 1, we report the critical infection rate β_c and adopted value β_S in our simulations. The infection rate β_S is slightly above its corresponding critical value β_c to generate moderate coverage.

For Facebook network, we select three nodes in different communities as spreading sources and apply 10^5 realizations of SIR model. The infected probability of each individual is approximated by the frequency of getting infected in these

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