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Dynamical behaviors of epidemics on scale-free networks with community structure

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Abstract

In this paper, we investigate in detail the epidemic spreading process in scale-free networks with community structure. In such a network, nodes tend to form sparsely linked local communities, each having dense internal connections. Different spreading rates in SIR model are adopted to describe the epidemic behavior of nodes in inner and inter communities, which makes the model more practical. In addition, in our model, we assume that if a node is infected in one community, its neighbors will move to other communities with probability p, which can decrease the epidemic size of the whole network without changing network structure. It is found in the simulation that the network without community structure is more robust than the ones with community structure.

Keywords: Epidemics; Scale-free networks; Community structure; Dynamical behavior

1. Introduction

Networks with a community structure, or modular networks, are relevant to many social and biological phenomena [1–7]. Community structure means that many nature or social networks can be divided into some groups such that the connections within each group are dense, while connections between groups are sparse. Such is indeed the case in many social networks, where individuals in a society tend to form groups according to their social characteristics. Within a group, each member is directly connected to most other members, but connections among different groups are relatively rare. In some degree, structure determines the characteristics and function of networks. Therefore, the finding of community structure provides a powerful tool for understanding the growth mechanisms and the functioning of complex networks.

For a given structure of complex network, issues of how the infection propagates and whether there exist effective control strategies to prevent or suppress the spread of the infection have been widely studied [8–16]. The simplest model for describing this issue is the two-state (SIS) model [8], in which the individuals can only

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exist in two discrete states: susceptible or infected. A key quantity in studying epidemic spreading in the SIS model is the critical point of epidemic outbreak. The epidemic can spread and persist only when the infection rate is greater than the critical point. The SIS model has been studied in both small world [9] and scale-free [8] networks, and the results show that in the case of scale-free networks, the infection can spread to the entire network even if the probability of the transmission is infinitely small. This result is in sharp contrast to the well-known threshold phenomenon in epidemiology. The result has been extended by Lloyd and May [10] to the SIR model, a three-state model where a node in the network can be in one of the three states: susceptible (S), infected (I), and refractory (R), an infected node can become refractory and is no longer susceptible to the infection. For a comprehensive review on the epidemic in complex networks, see Refs. [11,12].

The disease spreading on networks with community structures has been studied by many researchers [7,13,14]. Liu and co-workers have analyzed the spread of infectious disease on complex networks with household structure and found that the disease can spread on the scale-free network even when local recovery rate is greater than inner infection rate in every household [13,14]. This implies that no disease is spreading in every single household, but for the whole network, the disease is spreading. Huang et al. [7] have investigated the dynamics of information propagation on modular networks by using a three-state epidemic model with a unit spreading rate (i.e., the probability for a susceptible individual to be "infected" with the information is one). They have found that the information lifetime on the network can be maximized by the number of modules. Recently, Zhang et al. [15] have studied the SIS model in the community network and found that compared to the random network, the community network has a smaller threshold of epidemic outbreak and a strong prevalence to keep the outbreak endemic.

For a community structure network, infection rate in inner and inter communities are different. In reality, if a vertex is infected, its neighbors in the same community, may move to another community in order to avoid being infected. However, there is few works on this case. In this paper, we intend to fill this gap by investigating SIR model on scale-free networks with community structure by studying the role that removal has played on neighbors of infected node among communities. In the model, spread rates differ between inner-communities and inter-communities. Meanwhile, the neighbors of infected nodes in a community will move to other community with probability p. The results show that the aforementioned model can reduce the infection degree without changing the network structure.

2. Generate SF networks with community structure

Selection of this particular structure (scale-free networks with community structure) is based on the reason that scale-free network is heterogeneous. And a larger number of the previous works have pointed out that most real networks display the scale-free characteristics, which include Internet, WWW networks and power grids. BA [16] model can be used to explain the general growing mechanism, such as growth and preferential attachment which is general characteristic for all scale-free networks. Additionally, a property that seems to be common to many networks is community structure [11], especially for the social networks. Therefore, this particular structure is chosen in the paper. Scale-free networks can be generated with various methods. The first such model is given by Albert and Barabási (BA), which they identify the following as necessary for a network to have the scale-free property:

(1) *Growth*—the network grows over time.
(2) *Preferential attachment* (*PA*)—nodes with a high degree are more likely to create edges to new nodes than ones with a low degree.

Inspired by these two mechanisms mentioned above and the previous work by Yan et al. [17], we propose the generation model in our previous work [18]. It goes as follows. Start with c communities denoted $U_1, U_2, \ldots, U_c$ and each community is suppose to have a small number (m_0) of initial nodes. At every time step, we add into each community a new node with m ($<m_0$) edges that link the new node to n ($n<m$) different nodes within this community and $m-n$ different nodes within other $c-1$ communities already present in the system according to the PA rule $\Pi(k_i) = k_i / \sum k_j$, which means the probability Π that the new node will be connected to node i depends on the degree k_i of vertex i. In our study, we find the equilibrium status of systems