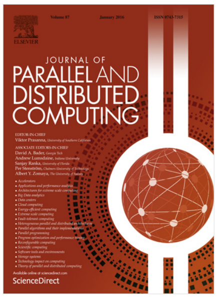

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Modeling and analysis of epidemic spreading on community networks with heterogeneity

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Abstract

A large number of real world networks exhibit community structure, and different communities may often possess heterogeneity. In this paper, considering the heterogeneity among communities, we construct a new community network model in which the communities show significant differences in average degree. Based on this heterogeneous community network, we propose a novel mathematical epidemic model for each community and study the epidemic dynamics in this network model. We find that the location of the initial infection node only affects the spreading velocity and barely influences the epidemic prevalence. And the epidemic threshold of entire network decreases with the increase of heterogeneity among communities. Moreover, the epidemic prevalence increases with the increase of heterogeneity around the epidemic threshold, while the converse situation holds when the infection rate is much greater than the epidemic threshold.

Keywords: community structure, heterogeneity, epidemic dynamics, mean-field theory

1. Introduction

With the development of network science, many common characteristics of real networks have been revealed, where one of the important characteristics is that a wide range of biological and social systems contains community structure [1–7]. Different individuals may form a community because of the same attributes, such as interest, age, profession and so on. As the large-scale outbreaks of epidemic diseases has occurred many times in different regions and different races in history, it can be said that the history of human history is a history of the struggle against different epidemic diseases. And with the progress of science and technology, the convenient transportation has also promoted the spread of the epidemic diseases to a great extent, for example, the severe acute respiratory syndrome (SARS) in 2003, the H1N1 influenza A virus in 2009, the H7N9 avian influenza virus in 2013, the Ebola virus in 2014 and the Middle East respiratory syndrome coronavirus (MERS-CoV) in 2015. The problem of epidemic spreading has gained great attention over the years and people want to predict the epidemic spread trend and take effective public health measures with limited vaccine supply. As the topology properties of networks have a profound impact on the dynamics of epidemic spreading, it is necessary to consider the effect of community structure on epidemic spreading. So far, a lot of results on epidemic dynamics in community networks have been obtained [8–12].

To simulate the real network, many different kinds of community network models were constructed based on classical networks, and some individual behavior characteristics in real networks (such as random walk, long-range jump and awareness) were also taken into account. Liu and Hu studied the SIS (susceptible-infected-susceptible) dynamics on a random community network model with probability $p(q)$ of intra- (inter-) community links. They found that the existence of community makes the degree distribution get broader, and the epidemic threshold decreases with the increase of community strength (p/q) [13]. Huang and Li studied the SI dynamics on scale-free network with community structure, they found that the community structure makes the growth of the infection slow and the epidemic prevalence reduce [14]. Salathé and Jones investigated the epidemic spread in empirical and artificial networks with community structure, and got the similar conclusion: the community structure has inhibiting effect on epidemic spreading, and the peak value of epidemic prevalence decreases with the increase of community strength. Moreover, they found that immunizing bridge nodes is more effective than simply immunizing highly connected nodes in networks with strong community structure [15]. To understand the influences of community structure and clustering coefficient on SIR (susceptible-infected-removed) dynamical processes, Wu and Liu presented a network model with adjustable clustering coefficient and adjustable community strength, and found that for a fixed community strength, the efficiency of epidemic spreading will decrease with increase of the clustering coefficient [16]. Chu et al. investigated the epidemic spreading on weighted scale-free networks with community structure, and found that compared to the internal weighting exponent, the external weighting exponent has higher impact on slowing the epidemic spreading [17]. On this basis, Min et al. further studied the spread of disease on weighted scale-free community network with two mixing styles [18] : a dense-weak style and a sparse-strong style. In [19], the authors studied the epidemic dynamics on a network with overlapping community structure and found that the epidemic prevalence increases with the increase of overlapping region. Some scholars constructed a random network composed of a sparse community

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