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Diffusion centrality in interconnected networks

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Abstract

The identification of influential or vulnerable nodes in a network is garnering considerable attention nowadays owing to the recent increase in the connectedness of society. Further, knowledge of the properties of interconnected networks is fundamental because of its viable application to the understanding of modular structures that often appear in real-world networks. In this paper, we focus on analysis of centrality, which is defined as the relative importance of a node in a network, and its effect on the probabilistic diffusion dynamics in interconnected networks. We propose a numerical framework in which the importance of the type of the centrality changes along with the diffusion regimes. It is well known that a critical point exists that, when crossed by the infection rate, results in epidemics [1, 2]. During the subcritical regime where the infection rate is below the critical point and no epidemics occur, the nodes with the highest number of infections (vulnerable nodes) can be indicated by the alpha centrality, which can be approximated by the degree centrality when the infection rate is almost zero, and the eigenvector centrality when the infection rate approaches the critical point. This theory is examined in numerous simulations using several types of interconnected network. The simulation results fit the estimation of our numerical framework in a small toy network during the subcritical regime. However, interconnection between some networks and the complexity of a network reduce the accuracy of our approximation of the numerical framework, as predicted by our numerical frameworks. Our simulation results also imply that during the critical regime when the infection rate is around the critical point, the type of centrality that can indicate the vulnerable nodes differ according to the topology of the network. In addition, during the supercritical regime, in which the infection rate is sufficiently large, the importance of centrality cannot be discriminated because the number of infections on each node becomes almost the same.

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1. Introduction

Centrality refers to a series of indices used to quantify the relative importance of a node in a network. Many types of centralities have been proposed so far in the fields of graph theory and network analysis [3]. Nowadays, research about the relationship between centrality and dynamics is garnering a lot of attention because a large number of Internet-based services are being developed and getting popular all over the world. Identification of the node with the greatest importance in a certain dynamic provides beneficial aspects, such as more effective marketing strategies in the massive Internet market and efficient vaccination strategy to prevent the spreading of computer viruses. Recently, Klemm et al. [4] proposed an analytical framework used to measure the role of an individual node in various types of network dynamics, such as probabilistic diffusion dynamics.

In this paper, we propose a theoretical framework to identify the influential and vulnerable nodes using the concepts of centrality and the Susceptible-Infected-Susceptible (SIS) model [2,5,6,7], one of the numerical models of the probabilistic diffusion dynamics. The probabilistic diffusion dynamics are often applied to fields dealing with epidemics and computer viruses spreading in networks [8, 9]. In the SIS model, the states of the nodes in a network are represented by a state vector in which each component corresponds to the condition of each node; the infected or susceptible state of a node is represented by one or zero, respectively. In the probabilistic diffusion process, each infected node can change the states of its susceptible neighbors at an infection rate β during each time step. In addition, the infected nodes enter the susceptible state at a recovery rate δ. Many previous studies [9-11] on the SIS model have focused on the threshold of infection spreading in networks. For example, Mieghem et al. [10] rigorously proved that the phase transition on a single network occurs in conditions where the effective infection rate β/δ is equal to the inverse of the maximum eigenvalue of the adjacency matrix $1/\lambda_1(\mathbf{A})$. When $1/\lambda_1(\mathbf{A}) < \beta/\delta$, infection spreads throughout the network and settles to a specific steady state. On the other hand, when $\beta/\delta < 1/\lambda_1(\mathbf{A})$, the number of infected nodes decreases and finally tends to zero.

In this paper, we propose a framework that indicates that a specific type of centrality can identify the vulnerable nodes in the SIS dynamics, and the type of the indicator varies as the regime of the infection changes. We also verify the framework using numerical simulations in several types of interconnected networks.

2. SIS model

The SIS model [2,5,6,7] is a well-known model that is used to express probabilistic diffusion dynamics across networks in a quantitative manner. In the SIS model, the nodes in a network are assigned two states, susceptible (S) and infected (I). A susceptible individual node is influenced by its surrounding neighbors and enters the infected state at infection rate β. The infected nodes enter the susceptible state again at recovery rate δ. A number of theories have been put forward to find the threshold of epidemics spreading in networks using the SIS model [9-11]. Recently, Mieghem et al. proposed a rigorous mathematical framework using the N-intertwined mean-field approximation [10] based on the continuous Markov chain theory. In their model, the tipping point τ_c of the effective infection rate β/δ can be obtained as

$$\tau_c = \frac{1}{\lambda_1(\mathbf{A})} \tag{1}$$

where $\lambda_1(\mathbf{A})$ represents the maximum eigenvalue of the adjacency matrix $\mathbf{A}$.

In the SIS model, the transition probability matrix $\mathbf{M}$ can be expressed as follows:

$$\mathbf{M} = (1-\delta)\mathbf{I} + \beta\mathbf{A} \tag{2}$$

Therefore, defining $\mathbf{p}(t)$ as a probability vector at time t, the probability vector at time t+1 can be calculated as

$$\mathbf{p}(t+1) = \mathbf{M}\mathbf{p}(t) \tag{3}$$

Using formula (3) and the initial probability vector $\mathbf{p}(0)$, the probability vector at time t can be described as follows:

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