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Threshold conditions for SIS epidemic models on edge-weighted networks

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HIGHLIGHTS

- A pairwise model of SIS epidemic models with a general transmission rate is formulated.
- We obtained the epidemic threshold by the linear stability analysis.
- We developed a method to judge the sign of the leading eigenvalue of a matrix.
- The difference between SIS and SIR models on weighted networks is shown.

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ABSTRACT

We consider the disease dynamics of a susceptible–infected–susceptible model in weighted random and regular networks. By using the pairwise approximation, we build an edge-based compartment model, from which the condition of epidemic outbreak is obtained. Our results suggest that there exists a remarkable difference between the linear and nonlinear transmission rate. For a linear transmission rate, the epidemic threshold is completely determined by the mean weight, which is different from the susceptible–infected–recovered model framework. While for a nonlinear transmission rate, the epidemic threshold is not only related to the mean weight, but also closely related to the heterogeneity of weight distribution.

1. Introduction

The susceptible–infected–susceptible (SIS) model and the susceptible– infected–recovered/removed (SIR) model are two widely considered models. The theory of complex network can provide an analytic framework for the role of nodes or edges in the epidemic spreading, and get novel insights into the transmission dynamics [1].

In the conventional models of epidemic spreading, one of the common assumptions is that all edges are equally capable of transmitting infection. Clearly, it is not the case for realistic diseases [2]. In disease transmission, one could imagine the heterogeneous infection rates [3] and multiple connections between individuals marking differing levels of intimacy [4]. In addition, there exist different contact frequencies among individuals [5]. These factors can be characterized by the weight of the edge connecting node i and j, denoted by w_{ij}. In general, the weight structure corresponds to the weight matrix $W = (w_{ij})$ [6] or weight distribution $g(w)$ [5].

Over this time, the study of epidemic spreading in weighted networks has attracted much attention. Yang et al. [7] developed the edge-based Markov chain equations to analyze the contact process of an SIS model in weighted homogeneous

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networks. They found that the more homogeneous weight distribution can lead to the higher epidemic prevalence. In their work, the weight w_{ij} and transmission rate β_{ij} are two separate notions.

However, many researches also assume that the infection rate depends on the edge weight. In an early work [8], Yan et al. considered

$$\beta_w = \left(\frac{w}{w_M}\right)^{\alpha}, \quad \alpha > 0,$$

where w_M is the largest value of w (here we neglect the indices i and j) in the network. Through simulations, they also find that an infectious disease spreads more quickly on unweighted scale-free networks than that on weighted scale-free networks under the same conditions.

By deriving pairwise-type approximation models coupled with individual-based simulations, Rattana et al. [9] studied the SIR epidemic model on weighted networks, where they used a linear transmission rate

$$\beta_w = \tau w, \tag{1}$$

and τ is called the infection rate. They theoretically showed that the heterogeneity of weight distribution can lead to a fall in the basic reproduction number R_0. Compared to the previous simulation approach, their analytic results are important for the study of epidemic spreading in weighted networks. They also further extended their work into the heterogeneous network, and obtain the similar results [10].

Almost simultaneously, Wang et al. [11] developed an edge-based technique for an SIR epidemic model in heterogeneous networks (its degree distribution is $p(k)$). They introduced a nonlinear transmission rate

$$\beta_w = 1 - (1-\tau)^w, \quad 0 \le \tau \le 1, \tag{2}$$

where $w = w_{ij}$ also denotes multiple relation between node i and j [12]. They derived a general epidemic threshold

$$\langle \beta_w \rangle = \frac{\langle k \rangle}{\langle k^2 \rangle - \langle k \rangle}, \tag{3}$$

where $\langle \beta_w \rangle = \sum_w \beta_w g(w)$ and $\langle k^s \rangle = \sum_k k^s p(k)$, $s = 1, 2$. They also found that increasing the heterogeneity of weight distribution can enhance the threshold of epidemic outbreak. Kamp et al. [13] investigated the SIR epidemic model on weighted networks where each node has k contacts and l interaction events and derived early epidemic growth rate and the basic reproduction number in terms of the probability generating functions of the degree distributions. Deijfen et al. [14] considered the SIR epidemic model on configuration networks where each edge (i, j) in the graph is assigned two weights $w_{(i,j)}$ and $w_{(j,i)}$ that are assumed to take values in [0, 1]. They took the branching process approximations and established the basic reproduction number $R_0 = \langle w \rangle (\langle k^2 \rangle - \langle k \rangle)/\langle k \rangle$, which is basically the same with Eq. (3).

Although Rattana et al. [9] also gave the pairwise approximate equations for SIS epidemic model, the epidemic threshold of this model is not theoretically derived and analyzed yet. In this paper, we will fill this gap. Our results show that the SIS model displays a different threshold behavior compared to the SIR model. For the linear transmission rate, the epidemic threshold is not related to the heterogeneity of weight distribution; while for the nonlinear transmission rate, the epidemic threshold is affected by the heterogeneity of weight distribution.

2. The model

We consider the SIS epidemic model on the random and regular network with a general weight distribution. The contact network is a random and regular network (RRN) with a uniform degree $k_i = n$ for each i [15]. A set of weight w_l $(l = 1, \ldots, M)$ is randomly assigned to each edge in the whole network according to a given distribution $g(w)$. For the sake of the following analysis, we first give some useful notations [9]: $[A]$ is the number of nodes in state A over the whole network; $[AB]_w$ is the number of edges connecting a node in state A with a node in state B; $[ABC]_{ww'}$ is the number of triples where a node in state B connects nodes in states A and C via edges of weight w and w', respectively.

In the weighted SIS model, each node may stay in either susceptible (S) state or infected (I) state. At each time step, each infectious node transmits the infection to its each susceptible neighbor across the weighted edge of weight w with rate β_w (i.e., the transmission rate) and meanwhile is recovered and become susceptible again with rate γ (i.e., the recovery rate).

According to the previous researches [16,9], the pairwise model for the SIS dynamics can be written in the form

$$\begin{aligned}
[\dot{S}] &= \gamma[I] - \sum_w \beta_w [SI]_w \\
[\dot{I}] &= -\gamma[I] + \sum_w \beta_w [SI]_w \\
[\dot{SS}]_w &= 2\gamma[SI]_w - 2\sum_{w'} \beta_{w'} [SSI]_{ww'} \\
[\dot{II}]_w &= -2\gamma[II]_w + 2\beta_w[SI]_w + 2\sum_{w'} \beta_{w'} [ISI]_{ww'} \\
[\dot{SI}]_w &= -\gamma[SI]_w + \gamma[II]_w - \beta_w[SI]_w - \sum_{w'} \beta_{w'} [ISI]_{w'w} + \sum_{w'} \beta_{w'} [SSI]_{ww'},
\end{aligned}$$