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Mean field theory of epidemic spreading with effective contacts on networks

Qingchu Wu [a,*], Shufang Chen [b]

[a] College of Mathematics and Information Science, Jiangxi Normal University, Nanchang, Jiangxi 330022, P R China
[b] College of Physics and Communication Electronics, Jiangxi Normal University, Nanchang, Jiangxi 330022, P R China

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ABSTRACT

We present a general approach to the analysis of the susceptible-infected-susceptible model with effective contacts on networks, where each susceptible node will be infected with a certain probability only for effective contacts. In the network, each node has a given effective contact number. By using the one-vertex heterogenous mean-field (HMF) approximation and the pair HMF approximation, we obtain conditions for epidemic outbreak on degree-uncorrelated networks. Our results suggest that the epidemic threshold is closely related to the effective contact and its distribution. However, when the effective contact is only dependent of node degree, the epidemic threshold can be established by the degree distribution of networks.

1. Introduction

The study of epidemic spreading through networks has drawn a wide attention of researchers in mathematical, physical and biological communities. In order to understand how the structure of interactions influences the spread of an infectious disease, Pastor-Satorras and Vespignani [1] developed a heterogenous mean-field approximation (HMF) approach. According to the HMF theory, many dynamical transmission processes can be mapped into a coupled ordinary differential equations. For instance, the susceptible-infected-susceptible (SIS) model on degree-uncorrelated network with the degree distribution $p(k)$ is given by

$$\frac{d\rho_k}{dt} = -\rho_k(t) + \beta k(1-\rho_k(t))\frac{\sum_{k'} k' p(k')\rho_{k'}(t)}{\langle k \rangle}.$$

Here, $\rho_k(t)$ represent the densities of infected nodes at time t in the population with degree k, β is the infection rate and the notation $\langle f(k)\rangle$ means the expectation of f with respect to the degree distribution.

Considering the limited activity of infected nodes, Zhou et al. [2] proposed a constant infectivity m for each individual, that means each infected individual will generate m contacts at each time step. Furthermore, Yang et al. [3] studied the susceptible-infected-removed (SIR) model with identical infectivity. They found that the epidemic threshold $\beta_c = 1/m$. Along this way, Fu et al. [4] analyzed an SIS model with piecewise linear infectivity $\phi(k)$ as a piecewise linear function of node degree k. At this time, $\beta_c = \frac{\langle k \rangle}{\langle k\phi(k)\rangle}$.

On the other hand, considering the contact effectiveness of susceptible nodes, Li et al. [5] studied an SIR model with effective contacts in homogeneous or heterogeneous networks. They introduced an effective contact function $\varphi(k)$ with respect to degree k, and obtained $\beta_c = \frac{\langle k \rangle}{\langle k\varphi(k)\rangle}$ with the same form as the model with saturated infectivity.

Regardless of introducing $\phi(k)$ and $\varphi(k)$, all these researches stress the potential existence of the epidemic threshold even in the scale-free network. This point improves our understanding of epidemic dynamics in complex networks. However, we should consider the infectivity and effective contact together for all the nodes. As a unified viewpoint, the infectivity or effective contact is referred to here as the *effective* degree (this is different from Refs.[6–8]),

* Corresponding author. Tel.: +86 015270881015.
E-mail address: wqingchu5@163.com (Q. Wu).

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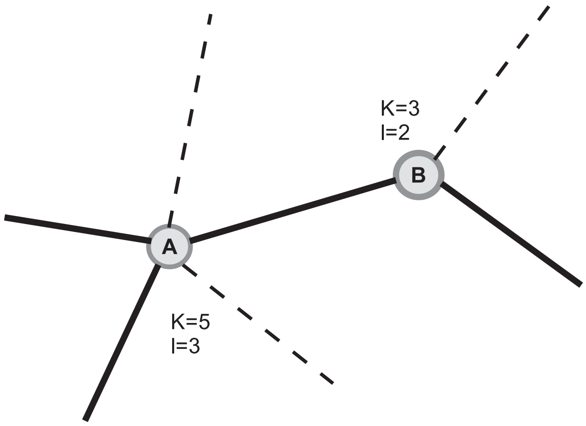

Fig. 1. Effective contact between two nodes. Node A (B) has k original contacts where only l contacts (solid and thick) are effective and other $k-l$ contacts (dashed and thin) are ineffective.

denoted by l. While, the usual degree is also called the *original* degree, denoted by k. In Fig. 1, we illustrate an effective link between two nodes. In this sense, $0 \le l \le k$. Taking the SIS model as an example, not only each susceptible node has its effective contact, but also each infected node has its effective contact. When l is degree-dependent, $l = \varphi(k)$ for susceptible nodes and $l = \phi(k)$ for infected nodes.

In this paper, we focus on the impact of effective contact on epidemic spreading. Since the infection can arise only along the effective contact, the previous approach based on the original degree k is not plausible. Here we introduce an effective approach to this problem which allows for a straightforward generalization of traditional HMF approach on degree-uncorrelated networks. In addition, the epidemic thresholds are explicitly obtained by one-vertex and pair HMF approximation.

2. An analysis framework

The epidemic model used here is SIS. The SIS epidemic model can be adapted for a class of infectious diseases such as gonorrhea, in which infected individuals can be recovered, but may be infected again [1,4]. In the SIS model, each node may stay in either susceptible (S) state or infected (I) state. At each time step, each infected node transmits the infection to its each susceptible neighbor with rate β (i.e., the infection rate) and meanwhile is recovered and become susceptible again with rate μ (i.e., the recovery rate). Without less of generality, we set $\mu = 1$.

For the convenience of mathematical analysis and in accordance to realistic cases, we assume that the network has a finite size N [9], which determines a maximal degree M. We still denote the degree distribution of the original network by $p(k)$, the probability that a node chosen uniformly at random has degree k. The notation $p(k'|k)$ represents the probability of a given node of degree k pointing to a node of degree k'.

In order to build the mean-field rate equations, we divide all the nodes into many classes according to their degrees and their epidemiological states. Unlike the classic heterogenous mean-field model, the degree class consists of not only the original degree but also the effective degree. Here, we use notation (k, l) to denote a class of nodes with the original degree k and the effective degree l $(0 \le l \le k)$ and call it the node degree for simplicity, which follows the joint probability distribution $p(k, l)$. Then, the respective marginal probability distribution of the original degree and effective degree reads as

$$p(k,\cdot) = \sum_{l=0}^{k} p(k,l), \quad p(\cdot,l) = \sum_{k=l}^{M} p(k,l).$$

Clearly, we have $p(k,\cdot) = p(k)$. Moreover, the n order moment of the joint probability $p(k, l)$ can be written as

$$\langle k^n \rangle = \sum_{k,l} k^n p(k,l) = \sum_{k=1}^{M} k^n \sum_{l=0}^{k} p(k,l) = \sum_{k=1}^{M} k^n p(k,\cdot),$$

and

$$\langle l^n \rangle = \sum_{k,l} l^n p(k,l) = \sum_{l=0}^{M} l^n \sum_{k=l}^{M} p(k,l) = \sum_{l=0}^{M} l^n p(\cdot,l).$$

We also define some conditional probabilities. $p(l|k)$ denotes the probability that a given node of degree k has l effective contacts. Similarly, $p(k|l)$ stands for the probability that a given node with l effective contacts is of degree k. And $p(k', l'|k, l)$ means the probability that a randomly chosen link emanated from a given node of degree (k, l) leads to a node of degree (k', l').

Let $\rho_{k,l}(t)$ represents the probability that a node with degree (k, l) is in the infected state. Then the SIS model with effective contacts on networks can be described by the following ordinary differential equations [10]:

$$\frac{d\rho_{(k,l)}}{dt} = -\rho_{(k,l)} + \beta l \sum_{k',l'} \phi_{(k,l)(k',l')} p(k',l'|k,l), \tag{1}$$

where $\phi_{(k,l)(k',l')}$ denotes the probability that a node of degree (k, l) is connected to a node of degree (k', l'). It is easy to get that $\phi_{(k,l)(k',l')} = 0$ for $l = 0$ or $l' = 0$.

Model (1) is not a closed system and cannot be directly analyzed. However, one can close it by some approximation techniques [10,11]. For the sake of the following analysis, we first give some useful notations [10]: $[A_{(k,l)}]$ is the probability that a node with degree (k, l) is in state A; $[A_{(k,l)}B_{(k',l')}]$ is the probability that a node of degree (k, l) in state A is connected by the effective link to a node of degree (k', l') in state B; $[A_{(k,l)}B_{(k',l')}C_{(k'',l'')}]$ is the generalization to three nodes such that the pairs $[A_{(k,l)}B_{(k',l')}]$ and $[B_{(k',l')}C_{(k'',l'')}]$ are connected through a node of degree (k', l') and so forth.

Furthermore, an infected state is represented by 1 and a susceptible one by 0. So, $[1_{(k,l)}] = \rho_{(k,l)}$ and $\phi_{(k,l)(k',l')} = [0_{(k,l)}1_{(k',l')}]$.

3. The one-vertex HMF approximation

3.1. The model

We firstly consider the one-vertex mean-field approximation, i.e., $\phi_{(k,l)(k',l')} = (1-\rho_{(k,l)})\rho_{(k',l')}$, then model (1) becomes

$$\frac{d\rho_{(k,l)}}{dt} = -\rho_{(k,l)} + \beta l (1-\rho_{(k,l)}) \sum_{k',l'} \rho_{(k',l')} p(k',l'|k,l) \tag{2}$$