Characterising spatial dependence on epidemic thresholds in networks

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Abstract: Epidemic processes are an important security research topic for both the internet and social networks. The epidemic threshold is a fundamental metric used to evaluate epidemic spread in networks. Previous work has shown that the epidemic threshold of a network is $1/\lambda_{max}(A)$, i.e., the inverse of the largest eigenvalue of its adjacency matrix. In this work, however, we indicate that such a theoretical threshold ignores spatial dependence among nodes and hence underestimates the actual epidemic threshold. Moreover, inspired by the Markov random field, we analytically derive a more accurate epidemic threshold based on a spatial Markov dependence assumption. Our model shows that the epidemic threshold is indeed $1/\lambda_{max}(A)(1-\rho)$, where ρ is the average spatial correlation coefficient between neighbouring nodes. We then apply simulations to compare the performance of these two theoretical epidemic thresholds in different networks, including regular graphs, synthesised irregular graphs, and a real topology. We find that our proposed epidemic threshold incorporates a certain spatial dependence and thus achieves greater accuracy in characterising the actual epidemic threshold in networks.

Keywords: epidemic thresholds; susceptible-infected-susceptible; SIS model; spatial dependence; Markov random field; MRF; Markov model; mean-field approach.

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1 Introduction

Epidemic processes are an active interdisciplinary research area among physics, mathematics, epidemiology, social science, computer engineering, and computer science (Daley and Gani, 2001; Guille et al., 2013; Mahdizadehaghdam et al., 2016; Nowzari et al., 2016; Pastor-Satorras et al., 2015; Tang and Li, 2011). An epidemic process is a process that an item (such as news, topic, disease, or worm) self-propagates across networks, representing an important security research topic for both the internet and social networks. For example, internet malware, such as worms, botnets, and ransomware, can infect many computers in a short time (Chen and Ji, 2009). In 2017, WannaCry ransomware malware was reported to have infected more than 230,000 computers within 24 hours (Wikipedia, 2017). Moreover, in social networks, both good information (e.g., products, news, topics, and innovations) and unwanted information (e.g., viruses, misinformation, and rumours) can spread from people to people or from friends to friends. On 23 April 2013, a rumour on two explosions in White House and the injury of President Barack Obama was spread over Twitter by some hackers. Due to this rumour, both the Standard & Poor's 500 Index and the DOW Jones industrial average fell 1% (Foster, 2013). It is therefore of great importance to characterise epidemic dynamics in networks, which can help us design network structures, protocols, and policies to facilitate the spread of good information and counteract the propagation of malware and unwanted information.

The epidemic threshold is a fundamental metric used to evaluate epidemic spread in networks (Chakrabarti et al., 2008; Ferreira et al., 2012; Ganesh et al., 2005; Givan et al., 2011; Kephart and White, 1991; Mieghem et al., 2009; Prakash et al., 2011; Wang et al., 2003). Such a threshold reflects the condition on which an infection will either die out or become epidemic. Specifically, in the classic susceptible-infected-susceptible (SIS) model, a node in a network can be either susceptible or infected. If the node is infected, it can be cured and become susceptible with a death rate; otherwise, it can be infected by one of its infected neighbours with a birth rate. When the ratio between the birth rate and the death rate is greater than the epidemic threshold, the infection will become epidemic; otherwise, it will die out.

An important discovery on epidemic spread is that in the SIS model, the epidemic threshold for a network has claimed to be $1/\lambda_{max}(A)$, i.e., the inverse of the largest eigenvalue of its adjacency matrix (Chakrabarti et al., 2008; Mieghem et al., 2009). The process of deriving this threshold, however, assumes that the states of nodes in the network are independent of each other. Such a spatial independence assumption can lead to overestimating the spreading ability of an infection (Chen, 2016; Chen and Ji, 2005; Mieghem et al., 2009). Intuitively, the states of nodes in a network are positively correlated, and two neighbouring nodes tend to be either both infected or both susceptible. Moreover, through simulations and theoretical analysis, Givan et al. (2011) found that the epidemic threshold from Chakrabarti et al. (2008) and Mieghem et al. (2009) cannot accurately reflect the actual epidemic threshold in some types of networks.

The goal of this work is to find a more accurate epidemic threshold in networks. Specifically, we attempt to answer the following questions:

- Can spatial dependence among nodes affect the epidemic threshold? If so, how significantly?
- How can we derive a more accurate epidemic threshold, taking into consideration a certain spatial dependence?
- Can the birth rate and the death rate affect the spatial dependence and thus the epidemic threshold? If so, how?

To answer these questions, we start with a general mathematical framework on modelling the spread of epidemics in networks and point out the difficulty in finding a closed-form expression. We then focus on approximating the complex spatial dependence among nodes in a network. Specifically, we consider two spatial approximation methods: spatial independence and spatial Markov dependence. The spatial Markov dependence approximation is motivated by the Markov random field (MRF) (Wikipedia, 2015), which has been widely applied in image processing. We discover that the spatial independence model leads to the epidemic threshold proposed in the previous work in Chakrabarti et al. (2008) and Mieghem et al. (2009). By applying the mean-field approach, we derive a closed-form expression for the epidemic threshold in an arbitrary network based on the spatial Markov dependence assumption. We then use simulations to evaluate the performance of our derived epidemic threshold. We summarise our discoveries and contributions in the following:

- We find that spatial dependence among nodes affects the epidemic threshold significantly and show that the epidemic threshold in a network depends on not only the largest eigenvalue of its adjacency matrix, but also the spatial correlation coefficient between neighbouring nodes. That is, the epidemic threshold is indeed $1/\lambda_{max}(A)(1-\rho)$, where ρ is the average spatial correlation coefficient between neighbouring nodes.
- Through extensive simulation studies in different networks including regular graphs, synthesised irregular graphs, and a real topology, we show that our proposed threshold better reflects the actual epidemic threshold than the threshold from Chakrabarti et al. (2008) and Mieghem et al. (2009).
- We show, through both analysis and simulations, that the epidemic threshold also depends on both the death rate and the birth rate. It is noted that the death rate is often assumed to be 1 in previous work (Ferreira et al., 2012; Ganesh et al., 2005). However, we find that the epidemic threshold decreases when the death rate increases, whereas the threshold increases when the birth rate increases.
- We also discover that the spatial Markov dependence assumption applied in equation (11) is indeed a maximum entropy estimator.

Although we focus only on the SIS model in this paper, our conclusions on epidemic thresholds can be well extended to other epidemiological models, such as arbitrary cascade models studied in Prakash et al. (2011).

The remainder of this paper is structured as follows. Section 2 introduces the background on the system model, and Section 3 provides a general mathematical framework and spatial approximation models. Section 4 derives epidemic thresholds in regular graphs, whereas Section 5 provides an analysis on the epidemic thresholds in an arbitrary network. Section 6 evaluates the performance of our proposed threshold and compares it with the previous work and simulation results. Section 7 discusses the related work. Finally, Section 8 concludes this paper.

2 System model

We use $G(V, E)$ to represent a network, where V is the set of nodes and E is the set of edges (or links). $|V|$ denotes the number of nodes in the network. In this work, we consider undirected graphs, i.e., if an edge $(i, j) \in E$, then $(j, i) \in$

E. Let $N_i = \{j|(j,i) \in E\}$ be a neighbourhood of node i. $|N_i|$ denotes the number of neighbours of node i.

We study the problem of epidemic spread in a network using the classic SIS model. Specifically, a node or a computer in a network can be either infected or susceptible. A susceptible node can be infected by one of its already infected neighbours with a birth rate (or an infection rate) β, where $0 < \beta \leq 1$. On the other hand, an infected node can be cured and change back to be susceptible with a death rate (or a recovery rate) δ, where $0 < \delta \leq 1$. As applied in Chakrabarti et al. (2008), Chen and Ji (2005), Ganesh et al. (2005) and Mieghem et al. (2009), we assume that the birth rate (or the death rate) is the same for all nodes and does not change with time.

Let $\tau = \beta/\delta$ be the ratio between the birth rate and the death rate. The epidemic threshold, τ_c, is defined as when $\tau \leq \tau_c$, the epidemic dies out, and no node is infected; and when $\tau > \tau_c$, a nonzero fraction of nodes remain infected for a long time. In previous work (Chakrabarti et al., 2008; Mieghem et al., 2009), it has been shown that the epidemic threshold is

$$\tau_{c,ind} = \frac{1}{\lambda_{max}(A)}, \tag{1}$$

where $\lambda_{max}(A)$ is the largest eigenvalue of the adjacency matrix A of the network. However, this threshold is derived based on the assumption of independence among nodes and has been shown to be unable to accurately capture the actual epidemic threshold (Givan et al., 2011).

A network can be classified into two categories: regular graphs and irregular graphs. For a regular graph, the size of the neighbourhood is the same for all nodes. That is, $|N_i| = k$, for $\forall i \in V$, where k denotes the average nodal degree. Typical regular graphs include ring, lattice, and complete graphs, where k = 2, 4, and $|V| - 1$, respectively. For a regular graph, $\lambda_{max}(A) = k$, and thus equation (1) becomes

$$\tau_{c,ind} = \frac{1}{k}. \tag{2}$$

For an irregular graph, different nodes can have a different number of neighbours. Typical synthesised irregular graphs include ER random graphs, exponential random graphs, and power-law topologies. In an ER random graph, each pair of nodes is connected with a predefined probability p (Erdös and Rényi, 1960). As a result, the probability distribution of the nodal degree is a binomial distribution, as shown in Figure 5(a). A synthesised exponential random graph is formed by adding new nodes into the graph. Each newly added node connects to existing nodes with an equal likelihood (i.e., uniform attachment) (Barabási and Albert, 1999; Jackson and Rogers, 2007). The probability distribution of the nodal degree is an exponential function of the nodal degree, as shown in Figure 5(b). A synthesised power-law topology is formed in a way similar to the synthesised exponential random graph, by adding new nodes into the topology. But the probability that a newly added node is connected to an existing node is proportional to the nodal degree of this existing node (i.e., preferential attachment) (Barabási and Albert, 1999; Barabási et al., 1999). Thus, the probability distribution of the nodal degree shows a scale-free property, i.e., a linear relationship in the log-log plot, as shown in Figure 5(c).

Most real topologies are irregular graphs. Some real topologies can be found online, such as Pajek datasets (Batagelj and Mrvar, 2006) and SNAP (2014).

3 Mathematical framework

In this section, we first present a general mathematical framework on modelling the spread of epidemics in networks and point out the difficulty in finding a closed-form expression. We then introduce two spatial approximation models.

We consider a discrete-time system and refer to the model presented in our previous work (Chen and Ji, 2005) as the starting point. Specifically, we assume that the time interval between time steps is 1, so that the birth rate and the death rate are the probabilities in our study. Let $X_i(t)$ be the state of node i at time t ($t \geq 0$), i.e.,

$$X_i(t) = \begin{cases} 0, \text{if node } i \text{ is susceptible at time } t; \\ 1, \text{if node } i \text{ is infected at time } t. \end{cases} \tag{3}$$

If node i is infected at time t, it will become susceptible with probability δ at time $t+1$, i.e.,

$$P(X_i(t+1) = 0 | X_i(t) = 1) = \delta. \tag{4}$$

This probability is also called the death rate. On the other hand, if node i is susceptible at time t, it will be infected by its infected neighbours with probability

$$I_i(t) = P(X_i(t+1) = 1 | X_i(t) = 0). \tag{5}$$

Thus, the state of node i at time $t+1$ can be derived based on its state at time t and $I_i(t)$, i.e.,

$$\begin{aligned} P(X_i(t+1) = 1) = {} & P(X_i(t) = 1)(1-\delta) \\ & + P(X_i(t) = 0) I_i(t). \end{aligned} \tag{6}$$

Since an infected node will infect its susceptible neighbour with birth rate β, the probability that susceptible node i is *not* infected by its neighbour j at time $t+1$ is $(1-\beta)^{x_j(t)}$, where $x_j(t) \in \{0,1\}$ is the realisation of $X_j(t)$. Note that infected neighbours will attempt to compromise node i independently. Hence, given node i is susceptible at time t and the states of its neighbours, the probability that it becomes infected at time $t+1$ is $1 - \prod_{j \in N_i} (1-\beta)^{x_j(t)}$. Let $\mathbf{X}_{N_i}(t) = \{X_j(t) | j \in N_i\}$ and $\mathbf{x}_{N_i}(t) = \{x_j(t) | j \in N_i\}$, representing the (random) states and their realisation of the neighbours of node i at time t. Then,

$$\begin{aligned} & I_i(t) \\ & = \sum_{\mathbf{x}_{N_i}(t)} P(X_i(t+1) = 1, \mathbf{X}_{N_i}(t) = \mathbf{x}_{N_i}(t) | X_i(t) = 0) \\ & = \sum_{\mathbf{x}_{N_i}(t)} P(\mathbf{X}_{N_i}(t) = \mathbf{x}_{N_i}(t) | X_i(t) = 0)[1 \end{aligned}$$

$$- \prod_{j \in N_i} (1-\beta)^{x_j(t)} \Bigg]$$
$$= 1 - E\left[\prod_{j \in N_i} (1-\beta)^{X_j(t)} \middle| X_i(t) = 0 \right], \quad (7)$$

where $E[|]$ denotes the conditional expectation.

Note that equation (7) can be applied to arbitrary topologies, including both regular and irregular graphs. The difficulty of finding a closed-form expression to this equation lies in the spatial dependence between nodes, i.e., computing $P(\mathbf{X}_{N_i}(t) = \mathbf{x}_{N_i}(t)|X_i(t) = 0)$. Intuitively, the state of node i depends on its neighbours. That is, $X_i(t)$ and $X_j(t)$ (where $j \in N_i$) are *not* independent. Indeed, they are positively correlated (Chen and Ji, 2005; Mieghem et al., 2009). Moreover, the state of node j depends on its own neighbours. In such a way, all nodes in a connected network are *not* independent. The assumption of independence among nodes, applied in the previous work (Chakrabarti et al., 2008; Mieghem et al., 2009), is clearly not accurate.

On the other hand, if node i has k neighbours (where k is usually not a small number), it has 2^k possible combinations for calculating $P(\mathbf{X}_{N_i}(t) = \mathbf{x}_{N_i}(t)|X_i(t) = 0)$, which is too expensive to compute. Therefore, to find $P(\mathbf{X}_{N_i}(t) = \mathbf{x}_{N_i}(t)|X_i(t) = 0)$ analytically, we have to consider some approximation. Here, we study two spatial approximation methods: spatial independence and spatial Markov dependence.

3.1 Independent model

In the independent model, we assume spatial independence between nodes, i.e., the states of all nodes are independent, as applied in the previous work (Chakrabarti et al., 2008; Mieghem et al., 2009). Then, we have

$$P(\mathbf{X}_{N_i}(t) = \mathbf{x}_{N_i}(t)|X_i(t) = 0) = \prod_{j \in N_i} P(X_j(t) = x_j(t)). \quad (8)$$

Applying such a spatial independence assumption to equation (7), we find

$$I_i(t) = 1 - \prod_{j \in N_i} E\left[(1-\beta)^{X_j(t)}\right] = 1 - \prod_{j \in N_i} \left[1 - \beta P(X_j(t) = 1)\right]. \quad (9)$$

Set $p_{i,t} = P(X_i(t) = 1)$. Putting equation (9) into equation (6), we have

$$p_{i,t+1} = 1 - \delta p_{i,t} - (1 - p_{i,t}) \prod_{j \in N_i} (1 - \beta p_{j,t}). \quad (10)$$

Note that equation (10) can be applied to both regular and irregular graphs.

3.2 Markov model

Inspired by the local Markov property of MRF (Wikipedia, 2015), we assume spatial Markov dependence, i.e., $X_j(t)$'s (where $j \in N_i$) are independent given $X_i(t) = 0$. Then, we have

$$P(\mathbf{X}_{N_i}(t) = \mathbf{x}_{N_i}(t)|X_i(t) = 0) = \prod_{j \in N_i} P(X_j(t) = x_j(t)|X_i(t) = 0). \quad (11)$$

Such a conditional independence assumption considers a certain dependence between node i and its neighbours and better characterises the spatial dependence among nodes than the spatial independence assumption. Moreover, equation (11) is indeed a *maximum entropy* estimator of the conditional joint distribution (Cover and Thomas, 1991; Good, 1963). In Appendix, we show this interesting result.

We apply the spatial Markov dependence assumption to equation (7) and find

$$I_i(t) = 1 - \prod_{j \in N_i} E\left[(1-\beta)^{X_j(t)} \middle| X_i(t) = 0\right] = 1 - \prod_{j \in N_i} \left[1 - \beta P(X_j(t) = 1|X_i(t) = 0)\right]. \quad (12)$$

Set $p_{i,t} = P(X_i(t) = 1)$ and $p_{j|i,t} = P(X_j(t) = 1|X_i(t) = 0)$. Putting equation (12) into equation (6), we have

$$p_{i,t+1} = 1 - \delta p_{i,t} - (1 - p_{i,t}) \prod_{j \in N_i} (1 - \beta p_{j|i,t}). \quad (13)$$

Note that equation (13) can be applied to both regular and irregular graphs.

4 Epidemic thresholds in regular graphs

In this section, we apply two different spatial approximation methods to derive closed-form expressions for the epidemic threshold in regular graphs: the independent model and the Markov model. We then use the symmetric property of regular graphs to analyse the spatial correlation in regular graphs.

4.1 Independent model

In equation (10), we consider the steady state. Set $p_i = \lim_{t \to \infty} p_{i,t}$, so equation (10) becomes

$$p_i = 1 - \delta p_i - (1 - p_i) \prod_{j \in N_i} (1 - \beta p_j). \quad (14)$$

When a regular graph is considered, due to its symmetric property, we have $p_i = p_j = p$, for $\forall i, j$. That is,

$$p = 1 - \delta p - (1 - p)(1 - \beta p)^k, \quad (15)$$

which leads to

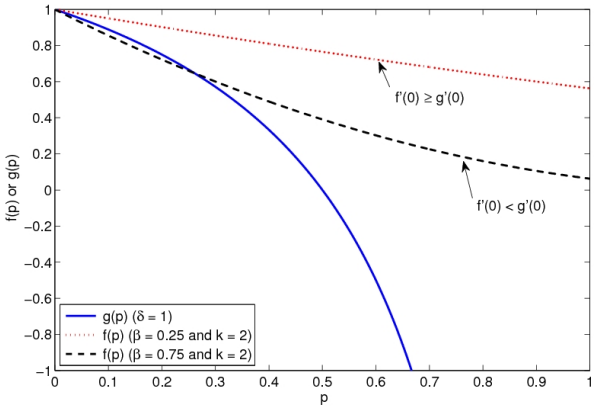
$$(1 - \beta p)^k = \frac{1 - (\delta + 1)p}{1 - p}. \quad (16)$$

Set $f(p) = (1-\beta p)^k$ and $g(p) = \frac{1-(\delta+1)p}{1-p}$. Then the solutions to the above equation are the intersection points between curves $f(p)$ and $g(p)$. Note that $f(0) = g(0) = 1$, $f(1) \geq 0$, and $\lim_{p\to 1} g(p) \to -\infty$. Moreover, $f'(p) = -\beta k(1-\beta p)^{k-1} < 0$, and $g'(p) = -\frac{\delta}{(1-p)^2} < 0$. Thus, whether equation (16) has a non-zero solution depends on the slopes of $f(p)$ and $g(p)$ at $p = 0$. Figure 1 demonstrates two examples of $f(p)$ and how the slopes at $p = 0$ affect the intersection points between $f(p)$ and $g(p)$. Hence, to get a non-zero solution for equation (16), $f'(0)$ needs to be smaller than $g'(0)$. That is, $\frac{\beta}{\delta} > \frac{1}{k}$. Hence,

$$\tau_{c,ind} = \frac{1}{k}, \tag{17}$$

which is identical to equation (2) and has been shown in Chakrabarti et al. (2008) and Mieghem et al. (2009) for the epidemic threshold in regular graphs. Here, we apply a different approach to obtain the same result.

Figure 1 Demonstration of the functions of $f(p)$ and $g(p)$ (see online version for colours)



4.2 Markov model

Similar to the independent model, we consider the steady state in the Markov dependent model. Set $p_i = \lim_{t\to\infty} p_{i,t}$ and $p_{j|i} = \lim_{t\to\infty} p_{j|i,t}$, so equation (13) becomes

$$p_i = 1 - \delta p_i - (1-p_i)\prod_{j\in N_i}(1-\beta p_{j|i}). \tag{18}$$

Consider the regular graph with an average nodal degree of k. Due to the symmetric property of regular graphs, we can set $p = p_i$ for $\forall i$, and $q = p_{j|i}$ for $\forall (i,j) \in E$. Then,

$$p = 1 - \delta p - (1-p)(1-\beta q)^k. \tag{19}$$

Define ρ as the spatial correlation coefficient between neighbouring nodes i and j (i.e., $\forall (i,j) \in E$) in the steady state. Setting $X_i = \lim_{t\to\infty} X_i(t)$, $\forall i \in V$, we have

$$\begin{aligned}\rho &= \frac{E[X_iX_j] - E[X_i]E[X_j]}{\sqrt{Var[X_i]Var[X_j]}} \\ &= \frac{P(X_i=1, X_j=1) - p^2}{p(1-p)}.\end{aligned} \tag{20}$$

Thus,

$$E[X_iX_j] = P(X_i=1, X_j=1) = p(1-p)\rho + p^2, \tag{21}$$

and

$$\begin{aligned}q &= \frac{P(X_j=1) - P(X_j=1, X_i=1)}{P(X_i=0)} \\ &= (1-\rho)p.\end{aligned} \tag{22}$$

Therefore, equation (19) becomes

$$p = 1 - \delta p - (1-p)[1-\beta(1-\rho)p]^k. \tag{23}$$

That is,

$$[1-\beta(1-\rho)p]^k = \frac{1-(\delta+1)p}{1-p}. \tag{24}$$

Note that when $\rho = 0$, which means that neighbouring nodes are independent, equation (24) is reduced to equation (16).

Set $h(p) = [1-\beta(1-\rho)p]^k$ and $g(p) = \frac{1-(\delta+1)p}{1-p}$. Then the solutions to equation (24) are the intersection points between curves $h(p)$ and $g(p)$. Note that $h(0) = g(0) = 1$, $h(1) \geq 0$, and $\lim_{p\to 1} g(p) \to -\infty$. Moreover, $h'(p) = -\beta k(1-\rho)[1-\beta(1-\rho)p]^{k-1} < 0$, and $g'(p) = -\frac{\delta}{(1-p)^2} < 0$. Thus, whether equation (24) has a non-zero solution depends on the slopes of $h(p)$ and $g(p)$ at $p = 0$. That is, $h'(0)$ has to be smaller than $g'(0)$ to get a non-zero solution for equation (24). That is,

$$\frac{\beta}{\delta} > \frac{1}{k(1-\rho)}. \tag{25}$$

Hence, the epidemic threshold is

$$\tau_{c,cor} = \frac{1}{k(1-\rho)}. \tag{26}$$

when $\rho > 0$, $\tau_{c,cor} > \tau_{c,ind}$ for the same regular graph. That is, ignoring the spatial dependence among nodes, $\tau_{c,ind}$ underestimates the actual epidemic threshold. On the other hand, $\tau_{c,cor}$ incorporates a certain spatial dependence and depends on the correlation coefficient between neighbouring nodes.

4.3 Spatial correlation

The epidemic threshold in equation (26) depends on the correlation coefficient ρ. In this section, we will show that in a regular graph, under the spatial Markov assumption, ρ is determined by the birth rate β and the death rate δ. Specifically, set $P_{uv}(t) = P(X_i(t) = u, X_j(t) = v)$, where $u, v \in \{0,1\}$, and $q_{uv}(t) = P(X_i(t+1) = 1, X_j(t+1) = 1 | X_i(t) = u, X_j(t) = v)$ for simplifying the notation. Thus,

$$P_{11}(t+1) = \sum_{u,v\in\{0,1\}} [P_{uv}(t)q_{uv}(t)], \tag{27}$$

where

$$q_{11}(t) = (1-\delta)^2$$
$$q_{10}(t) = (1-\delta)\left[1-(1-\beta)\prod_{l\in N_j-\{i\}}(1-\beta p_{l|j,t})\right]$$
$$q_{01}(t) = (1-\delta)\left[1-(1-\beta)\prod_{l\in N_i-\{j\}}(1-\beta p_{l|i,t})\right]$$
$$q_{00}(t) = \left[1-\prod_{l\in N_j-\{i\}}(1-\beta p_{l|j,t})\right]\left[1-\prod_{l\in N_i-\{j\}}(1-\beta p_{l|i,t})\right].$$

The derivation of $q_{uv}(t)$'s is based on the spatial Markov assumption (Chen and Ji, 2005) and follows the same spirit of deriving $I_i(t)$ in equation (12). By setting $P_{uv} = \lim_{t\to\infty} P_{uv}(t)$ and considering $t \to \infty$ and regular graphs, equation (27) turns into

$$P_{11} = P_{11}(1-\delta)^2 + P_{00}\left[1-(1-\beta q)^{k-1}\right]^2 + (P_{10}+P_{01})(1-\delta)\left[1-(1-\beta)(1-\beta q)^{k-1}\right]. \quad (28)$$

Note that $P_{01} = P_{10} = p - P_{11}$, $P_{00} = 1 - 2p + P_{11}$, and $q = (1-\rho)p$. Thus, setting $r = (1-\beta q)^{k-1} = [1-\beta(1-\rho)p]^{k-1}$, we have

$$P_{11} = P_{11}(1-\delta)^2 + (1-2p+P_{11})(1-r)^2 + 2(p-P_{11})(1-\delta)[1-(1-\beta)r]. \quad (29)$$

Since we are interested in the epidemic threshold, we focus on the case when p is very small and approaches 0 from the right. When $p \to 0^+$, by ignoring the higher order of p, in equation (21), $P_{11} \to \rho p$. Similarly, $r \to 1-(k-1)(1-\rho)\beta p$. Thus, when $p \to 0^+$, the item $(1-2p+P_{11})(1-r)^2$ in equation (29) is in the order of p^2 and does not contain constant or p term, and can be safely ignored. Moreover, the item $1-(1-\beta)r$ becomes β. Therefore, when $p \to 0^+$, equation (29) becomes

$$(2\delta - \delta^2)P_{11} = 2\beta(1-\delta)(p-P_{11}). \quad (30)$$

Putting $P_{11} = \rho p$ into the above equation, we have

$$\rho = \frac{2\beta(1-\delta)}{(2\delta-\delta^2)+2\beta(1-\delta)}, \text{when } p \to 0^+. \quad (31)$$

It is noted that from equation (31), $0 \le \rho < 1$. Specifically, when $\delta = 1$, $\rho = 0$. That is, if we assume that the death rate is 1 as proposed in previous work such as Ferreira et al. (2012) and Ganesh et al. (2005), there is no spatial dependence from our analysis. On the other hand, however, if $\delta < 1$, $\rho > 0$, i.e., the spatial correlations between neighbouring nodes can affect the epidemic threshold. Since $\frac{\partial\rho}{\partial\delta} < 0$ and $\frac{\partial\rho}{\partial\beta} > 0$, ρ increases when δ decrease or β increases. Another observation is that our derived ρ is independent of the number of neighbours, i.e., k.

Putting equation (31) into equation (26), we find the epidemic threshold in regular graphs:

$$\tau_{c,mar} = \frac{2-\delta}{2(k-1)-(k-2)\delta}. \quad (32)$$

It can be seen that if $\delta = 1$, $\tau_{c,mar} = \tau_{c,ind}$. If $\delta < 1$, however, $\tau_{c,mar} > \tau_{c,ind}$. Moreover, since $\frac{d\tau_{c,mar}}{d\delta} < 0$, $\tau_{c,mar}$ increases as δ decreases. Thus, $0 < \delta \le 1$ leads to

$$\frac{1}{k} \le \tau_{c,mar} < \frac{1}{k-1}. \quad (33)$$

That is, the epidemic threshold in regular graphs is in $[\frac{1}{k}, \frac{1}{k-1})$. Moreover, although β does not appear in equation (32), $\tau_{c,mar}$ does depend on β. This can be shown in equations (26) and (31): when β increases, ρ increases, and therefore, $\tau_{c,mar}$ increases.

Note that the deviation of $\tau_{c,mar}$ is based on the spatial Markov dependence assumption and does not consider all spatial dependence among nodes. As we will show in Subsection 6.2, although $\tau_{c,mar}$ performs much better than $\tau_{c,ind}$, it does not closely follow the actual epidemic threshold.

5 Epidemic thresholds in arbitrary networks

In this section, we extend our analysis on epidemic thresholds from regular graphs to arbitrary networks. Similar to the analysis for regular graphs, here we study two spatial approximation methods for arbitrary networks: spatial independence and spatial Markov dependence.

5.1 Independent model

In an independent model, the states of all nodes in a network are assumed to be independent, as shown in equations (8) and (9). Note that equation (10) can be also applied to an arbitrary network. We find that equation (10) is similar to equation (7) in Chakrabarti et al. (2008). The only difference between these two equations is that the second term on the right hand side of equation (10) does not include $\prod_{j\in N_i}(1-\beta p_{j,t})$ [i.e., $\zeta_{i,t+1}$ in Chakrabarti et al. (2008)]. However, as pointed out by both Chakrabarti et al. (2008) and Givan et al. (2011), both equations lead to the same result on the epidemic threshold:

$$\tau_{c,ind} = \frac{1}{\lambda_{max}(A)}, \quad (34)$$

where $\lambda_{max}(A)$ is the largest eigenvalue of the adjacency matrix A of the network. Please refer to Chakrabarti et al. (2008) for the detailed derivation from equation (10) to equation (34). Comparing with the previous work (Chakrabarti et al., 2008), here we derive it under the general mathematical framework to understand the effect of spatial dependence.

5.2 Markov model

In a Markov model, given node i is susceptible, the states of all neighbours of node i are assumed to be independent, as shown in equations (11) and (12). Note that equation (13) can be also applied to an arbitrary network.

To simplify $p_{j|i,t}$ in equation (13), we define $\rho_{i,j,t}$ as the spatial correlation coefficient between neighbouring nodes i and j at time t for $\forall(i,j) \in E$. That is,

$$\begin{aligned}\rho_{i,j,t} &= \frac{E[X_i(t)X_j(t)] - E[X_i(t)]E[X_j(t)]}{\sqrt{Var[X_i(t)]Var[X_j(t)]}} \\ &= \frac{P(X_i(t)=1, X_j(t)=1) - p_{i,t}p_{j,t}}{\sqrt{p_{i,t}(1-p_{i,t})p_{j,t}(1-p_{j,t})}}. \end{aligned} \tag{35}$$

Since we are considering the epidemic threshold, i.e., the condition at which the epidemic will die out, it is safe to say that when t becomes large, both $p_{i,t}$ and $p_{j,t}$ become small and approach to 0, which allows us to simplify the equation. That is, when $t \to \infty$, $1 - p_{i,t} \to 1$, and $1 - p_{j,t} \to 1$. Then

$$\begin{aligned}P(X_i(t)=1, X_j(t)=1) &\approx \rho_{i,j,t}\sqrt{p_{i,t}p_{j,t}} + p_{i,t}p_{j,t} \\ &\approx \rho_{i,j,t}\sqrt{p_{i,t}p_{j,t}}. \end{aligned} \tag{36}$$

The second approximation comes from the observations that $-1 \le \rho_{i,j,t} \le 1$ and $p_{i,t}p_{j,t}$ is a higher order term than $\sqrt{p_{i,t}p_{j,t}}$ when t is very large.

Considering $p_{j|i,t}$ in equation (13) and approximating $P(X_i(t)=0)$ to be 1, we have

$$\begin{aligned}p_{j|i,t} &= \frac{P(X_j(t)=1) - P(X_i(t)=1, X_j(t)=1)}{P(X_i(t)=0)} \\ &\approx p_{j,t} - \rho_{i,j,t}\sqrt{p_{i,t}p_{j,t}} \\ &= p_{j,t}\left(1 - \rho_{i,j,t}\sqrt{\frac{p_{i,t}}{p_{j,t}}}\right). \end{aligned} \tag{37}$$

It is noted that when regular graphs are considered and $t \to \infty$, $p_{i,\infty} = p_{j,\infty} = p$, and $\rho_{i,j,\infty} = \rho$, where $\rho_{i,j,\infty}$ does not depend on edge (i,j). Therefore, in regular graphs, $p_{j|i,\infty} = (1-\rho)p$, as shown in equation (22). For an irregular graph, on the other hand, due to the fact that different nodes can have a different number of neighbours, $p_{i,\infty}$ and $p_{j,\infty}$ can be different, and $\rho_{i,j,\infty}$ depends on edge (i,j). To obtain a closed-form expression, however, here we consider the first-order mean-field approach (Wikipedia, 2011; Opper and Saad, 2001). The mean-field method approximates and replaces the effect of all interactions with a single average interaction. In our case, we replace $\rho_{i,j,\infty}$ with ρ, which is the average spatial correlation coefficient of neighbouring nodes in a topology at the epidemic threshold. Moreover, note that nodes i and j are neighbours and connect to each other. Thus, when $t \to \infty$, we further assume that $\sqrt{\frac{p_{i,t}}{p_{j,t}}} \approx 1$, which can reduce the complexity of the equation. In such a way, we obtain the following equation for both regular and irregular graphs:

$$p_{j|i,t} = p_{j,t}(1-\rho), \tag{38}$$

when $t \to \infty$ at the epidemic threshold.

Putting equation (38) into equation (13), we find

$$\begin{aligned}&p_{i,t+1} \\ &= 1 - \delta p_{i,t} - (1-p_{i,t}) \prod_{j \in N_i} (1 - \beta p_{j,t}(1-\rho)). \end{aligned} \tag{39}$$

Following the similar procedure of deriving equation (34) from equation (10), we can find that the epidemic threshold based on equation (39) is

$$\tau_{c,cor} = \frac{1}{\lambda_{max}(A)(1-\rho)}. \tag{40}$$

It is noted that when a regular topology is considered, equation (40) is reduced to $\tau_{c,cor}$ in equation (26). Moreover, it can be seen that different from $\tau_{c,ind}$ in equation (34), $\tau_{c,cor}$ considers a certain spatial dependence. If $\rho = 0$, $\tau_{c,cor} = \tau_{c,ind}$. Otherwise, when $\rho > 0$, as shown in previous work (Chen and Ji, 2005; Mieghem et al., 2009), $\tau_{c,cor} > \tau_{c,ind}$. In other words, our analysis shows that $\tau_{c,ind}$ underestimates the actual epidemic threshold by ignoring the spatial dependence among nodes.

6 Simulation results and performance evaluation

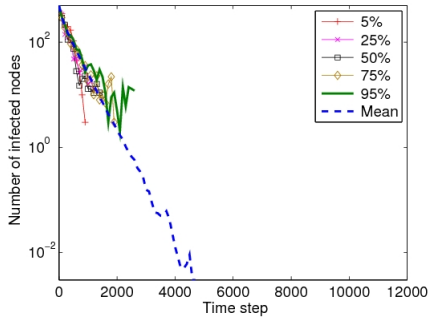
In this section, we evaluate the performance of the estimation of the epidemic threshold through simulations. Specifically, we first describe the setup of our simulations. We then compare different estimators with the simulation results for both regular and synthesised irregular graphs. Finally, we evaluate the performance of our proposed epidemic threshold in a real topology.

6.1 Simulation setup

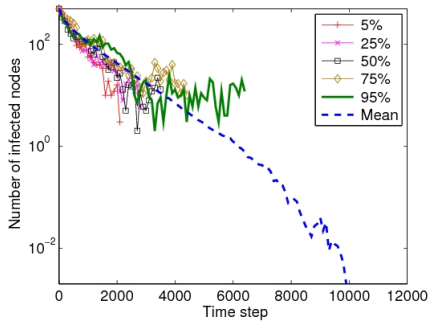
We simulate the spread of epidemics with different birth rates and death rates in different topologies. The simulator is based on discrete time. In each time step, if node i is infected, it will become susceptible with the probability of δ at the next time step; otherwise, it will be infected by its infected neighbour j with the probability of β. Here, probabilities are created by a random number generator. At the beginning of the simulations, we randomly assign half of the nodes to be infected. We run each simulation long enough so that it reaches the steady state. For each scenario, we run 1,000 times using different seeds. Figure 2 shows the sample runs of epidemic spread in a ring graph with a fixed death rate (i.e., $\delta = 0.1$) and different birth rates (i.e., $\beta = 0.13$, 0.14, and 0.15). The figure plots the number of infected nodes over time. In each sub-figure, the '5%' curve indicates that the epidemic spreads no faster than this curve in 50 out of 1,000 simulation runs. The similar definition is applied to the '25%', '50%', '75%', and '95%' curves. Moreover, the 'mean' curve is the average over 1,000 runs. It can be seen that in the 'mean' curve, the number of infected nodes can be under 1 for some time steps. This is because in some runs the infection has already died out in earlier time steps. Note that we use the log scale for the

y-axis to make the spread process more visible. It can be seen that when β is small and thus the ratio between β and δ is below the epidemic threshold, the infection dies out quickly with an exponential rate, as shown in Figure 2(a). When the ratio between β and δ is around the epidemic threshold, the infection still dies out, but with a much slower rate, as indicated in Figure 2(b). When the ratio between β and δ is above the epidemic threshold, a nonzero fraction of nodes are infected, and the infection becomes epidemic, as shown in Figure 2(c).

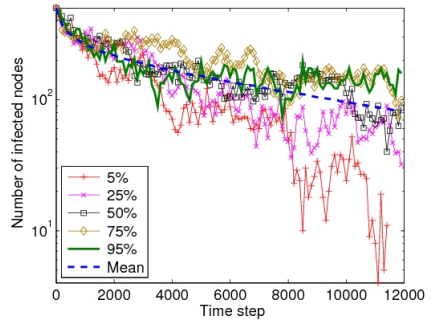
Figure 2 Sample runs of epidemic spread in a ring graph (δ = 0.1 and $|V|$ = 1,000), (a) below threshold (β = 0.13) (b) around threshold (β = 0.14) (c) above threshold (β = 0.15) (see online version for colours)



(a)



(b)



(c)

To find the epidemic threshold (i.e., τ_c) for a given death rate δ, we apply binary search as described in Algorithm 1, where ϵ is a small number (e.g., ϵ = 0.01). Among the inputs of the algorithm, β_{low} is a valid birth rate that causes the epidemic to die out (e.g., β_{low} = 0), whereas β_{high} maps to a case when the epidemic survives (e.g., β_{high} = 1).

Algorithm 1 Finding epidemic threshold τ_c

Input: δ, β_{low}, β_{high}, ϵ
Output: τ_c
while $(\beta_{high} - \beta_{low}) > \epsilon * \beta_{low}$ **do**
  $\beta = (\beta_{high} + \beta_{low})/2$
  Simulate epidemic spread using β and δ
  Average the number of final infections over 1,000 runs and get avg_inf_num
  if $avg\_inf\_num > 0$ **then**
    $\beta_{high} = \beta$
  else
    $\beta_{low} = \beta$
  end if
end while
$\tau_c = \beta_{low}/\delta$

To obtain $\tau_{c,cor}$ in equation (40), we need to find the average spatial correlation coefficient ρ at the epidemic threshold through simulations. It is noted that at the epidemic threshold, the epidemic dies out, and thus we cannot calculate the spatial correlation coefficient from simulations. Moreover, when β/δ is just above the epidemic threshold and the average number of final infections is close to 0, there are few samples of infected nodes, which makes the estimated correlation coefficient inaccurate. On the other hand, when the average number of final infections is large, the calculated coefficient is accurate, but may be very different from ρ in equation (40). To obtain a reasonable estimate of ρ, we apply the value of the average correlation coefficient when the average number of final infections is between 1 and 10. The details of finding spatial correlation coefficient ρ are given in Algorithm 2, where τ_c is the epidemic threshold when the death rate is δ, ϵ_β is a small value used for increasing the birth rate (e.g., ϵ_β = 0.001), and ϵ_n is the threshold value used to determine when to stop searching for the correlation coefficient and is between 1 and 10.

Algorithm 2 Finding spatial correlation coefficient ρ

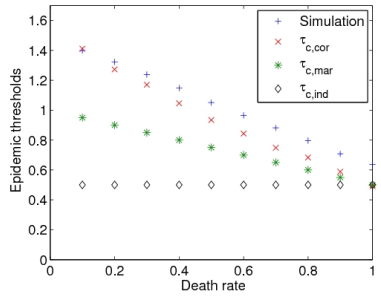
Input: δ, τ_c, ϵ_β, ϵ_n
Output: ρ
Set $\beta = \tau_c \times \delta$, $\beta_s = \epsilon_\beta * \beta$, and $found = 0$
while $found = 0$ **do**
  $\beta = \beta + \beta_s$
  Simulate epidemic spread using β and δ
  Average the number of final infections over 1,000 runs and get avg_inf_num
  if $avg\_inf\_num \geq \epsilon_n$ **then**
    Average the correlation coefficient over 1,000 runs and get the empirical correlation coefficient ρ_e
    $\rho = \rho_e$
    $found = 1$
  end if
end while

6.2 Regular graphs

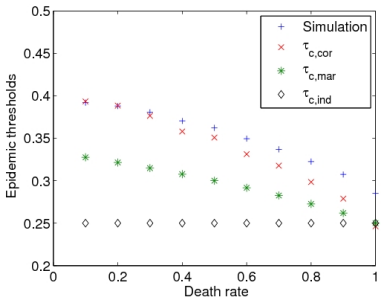
We compare the performance of three estimators of the epidemic threshold [i.e., $\tau_{c,ind}$ in equations (17), $\tau_{c,mar}$ in equation (32), and $\tau_{c,cor}$ in equation (40)] in regular graphs

with simulation results. Figure 3 shows epidemic thresholds with different death rates ($0 < \delta \leq 1$) for ring ($k = 2$), lattice ($k = 4$), and complete graphs ($k = |V| - 1 = 99$). It can be seen that $\tau_{c,mar}$ is a more accurate estimator than $\tau_{c,ind}$, whereas $\tau_{c,cor}$ has the best performance among three estimators. For example, in ring graphs, when $\delta = 0.1$, the actual epidemic threshold is 1.4, whereas $\tau_{c,ind} = 0.5$, $\tau_{c,mar} = 0.95$, and $\tau_{c,cor} = 1.41$. There is about 50% performance improvement from the independence model (i.e., $\tau_{c,ind}$) to the Markov model (i.e., $\tau_{c,mar}$), and $\tau_{c,cor}$ is the most accurate estimate of the actual epidemic threshold. Therefore, the spatial independence assumption, which has been widely applied in previous work (Chakrabarti et al., 2008; Mieghem et al., 2009), significantly underestimates the epidemic threshold, whereas our proposed Markov model can incorporate a certain spatial dependence and predict the threshold more accurately. Moreover, while $\tau_{c,ind}$ is independent of δ, our model is able to catch the tendency changes with δ. For example, as indicated by Figures 3(a) and 3(b), both simulation results and our model show that the epidemic threshold decreases when the death rate increases.

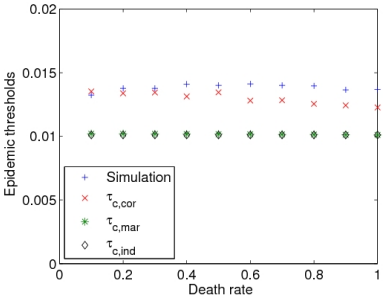
Figure 3 Epidemic thresholds in regular graphs, (a) ring ($|V| = 1{,}000$) (b) lattice ($|V| = 2{,}500$) (c) complete ($|V| = 100$) (see online version for colours)



(a)



(b)



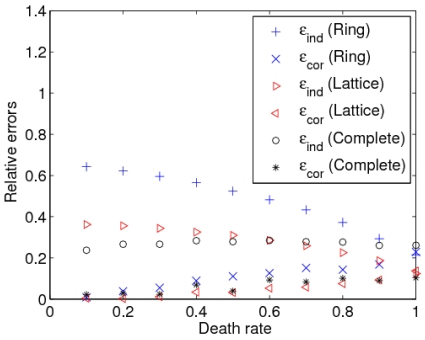
(c)

We further define the relative errors of the estimation for $\tau_{c,ind}$ as

$$\epsilon_{ind} = \frac{|\tau_{c,ind} - \tau_c|}{\tau_c}, \tag{41}$$

where τ_c is the epidemic threshold from the simulation. Similarly, we can define ϵ_{cor} for $\tau_{c,cor}$. Figure 4 shows how relative errors change with the death rate for three regular graphs. We can see that for all cases, $\epsilon_{cor} < \epsilon_{ind}$ when $\delta < 1$. When δ is small and less than 0.5, ϵ_{cor} is less than 0.1 for all cases, whereas ϵ_{ind} is greater than 0.2. On the other hand, when δ is large and closes to 1, ϵ_{cor} is slightly better than ϵ_{ind}. Our evaluation shows that the epidemic threshold depends heavily on the spatial correlation between neighbouring nodes.

Figure 4 Relative errors of epidemic thresholds in regular graphs (see online version for colours)



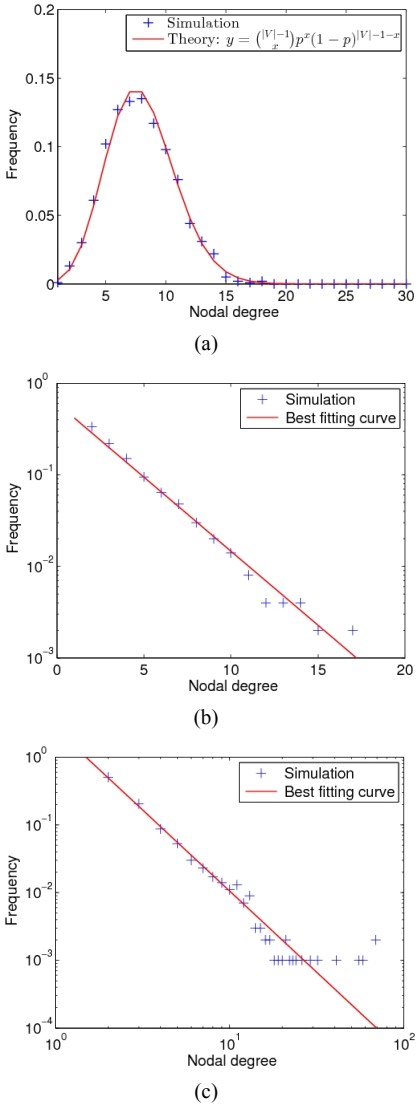
6.3 *Synthesised irregular graphs*

Next, we compare the performance of two estimators of the epidemic threshold [i.e., $\tau_{c,ind}$ in equation (34) and $\tau_{c,cor}$ in equation (40)] for synthesised irregular graphs. Specifically, we simulate the spread of epidemics in three representative irregular graphs: an ER random graph, an exponential random graph, and a power-law topology. The power-law topology was generated by BRITE (2001). The nodal degree distributions of these three topologies are plotted in Figure 5. It can be seen that the nodal degree distribution of the synthesised ER random graph closely follows a binomial distribution, whereas the nodal degree distribution of the exponential random graph is exponential, and that of the power-law topology is scale-free.

We compare the performance of $\tau_{c,ind}$ and $\tau_{c,cor}$ with simulation results in Figure 6 for these three irregular graphs. It can be seen that $\tau_{c,cor}$ fits much closer to the actual epidemic threshold than $\tau_{c,ind}$, especially when the death rate is not large. Moreover, $\tau_{c,cor}$ can catch the tendency changes with the death rate, i.e., the actual epidemic threshold decreases when δ increases. We further compare the relative errors of two estimators (i.e., ϵ_{ind} and ϵ_{cor}) in Figure 7. It is shown that for all cases, $\epsilon_{cor} < \epsilon_{ind}$. Moreover, when $\delta < 0.5$, $\epsilon_{ind}/\epsilon_{cor} > 3$, and $\epsilon_{cor} < 0.16$. It is apparent that the theoretical epidemic threshold considering the spatial correlation (i.e., $\tau_{c,cor}$)

performs much better than the estimator based on the spatial independence assumption (i.e., $\tau_{c,ind}$).

Figure 5 Nodal degree distributions of irregular graphs ($|V|$ = 1,000), (a) ER random graph ($p = \frac{8}{999}$) (b) exponential random graph (c) power-law topology (exponent $\approx$ 2.4) (see online version for colours)



6.4 *A real topology*

We further evaluate the performance of two estimators (i.e., $\tau_{c,ind}$ and $\tau_{c,cor}$) in a real topology. Specifically, we study the spread of epidemics in a co-authorship network (Collaboration Network in Science of Networks, 2007). This real topology is a collaboration network of scientists working on network experiment and theory. We find that the topology given by Collaboration Network in Science of Networks (2007) is not connected. Hence, we only consider the giant component of the topology, which contains 379 nodes and 914 edges. The nodal degree distribution of this giant component is shown in Figure 8(a).

Figure 6 Epidemic thresholds in irregular graphs ($|V|$ = 1,000), (a) ER random graph ($\lambda_{max}(A)$ = 9.03) (b) exponential random graph ($\lambda_{max}(A)$ = 6.84) (c) power-law topology ($\lambda_{max}(A)$ = 10.77) (see online version for colours)

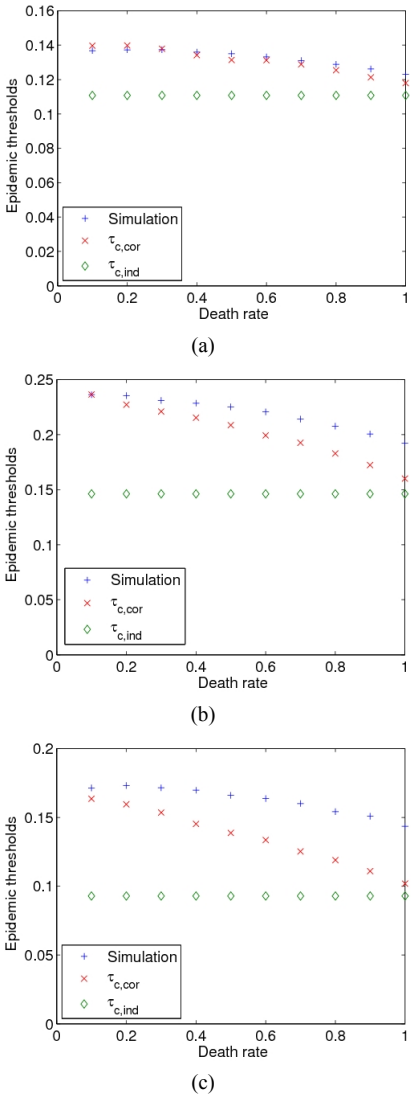
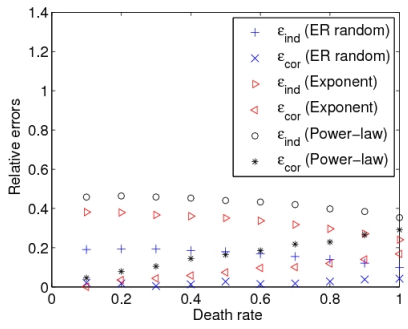


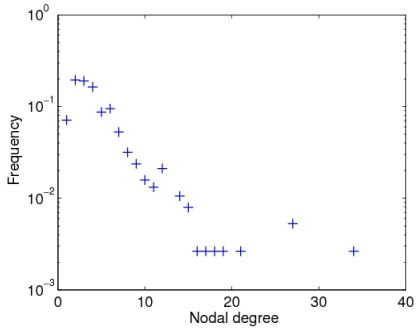
Figure 7 Relative errors of epidemic thresholds in arbitrary networks (see online version for colours)



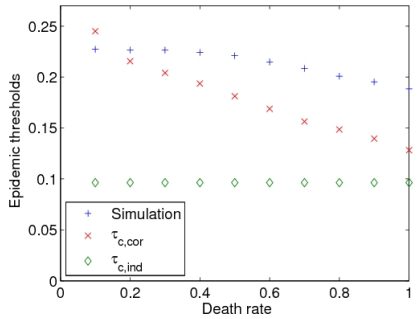
We compare the performance of $\tau_{c,ind}$ and $\tau_{c,cor}$ with simulation results in Figure 8(b). It can be seen that with reference to the actual epidemic threshold, $\tau_{c,cor}$ is much

more accurate than $\tau_{c,ind}$. Figure 8(c) further plots ϵ_{ind} and ϵ_{cor}. It shows that for all cases, $\epsilon_{cor} < 0.32$, whereas $\epsilon_{ind} > 0.48$. Moreover, when $\delta \leq 0.5$, $\epsilon_{cor} < 0.18$. As a result, it is evident that the epidemic threshold depends strongly on the spatial correlation among nodes.

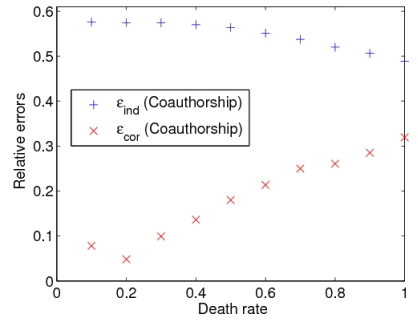
Figure 8 Epidemic thresholds in a co-authorship network ($|V| = 379$), (a) nodal degree distribution (b) epidemic thresholds (c) relative errors (see online version for colours)



(a)



(b)



(c)

7 Related work

It has been a long history of applying mathematical modelling to study epidemic thresholds in networks (Daley and Gani, 2001; Pastor-Satorras et al., 2015). After the emergence of the internet, Kephart and White (1991) were the first one to consider the spread of computer viruses in the 'homogeneous mixing' topology and found that the epidemic threshold is the reciprocal of the average nodal degree. In their seminal papers, Pastor-Satorras and Vespignani (2001, 2002) discovered that the epidemic threshold is 0 in a power-law topology with an infinite size and an exponent that ranges between 2 and 3, and further considered the case when the size of the power-law topology is finite. Moreover, Boguna et al. unraveled the root cause of the absence of the epidemic threshold in heterogenous networks in Boguna et al. (2013).

An important discovery on the epidemic threshold is that the threshold for a network has shown to be the inverse of the largest eigenvalue of its adjacency matrix, which was first found by Chakrabarti et al. (2008) and Wang et al. (2003). Mieghem et al. also showed this epidemic threshold condition in networks through Markov chain modelling and mean field theory in Mieghem et al. (2009). Ganesh et al. (2005) rigorously pointed out that the inverse of the largest eigenvalue of its adjacency matrix is the lower-bound of the epidemic threshold through stochastic modelling and graph theory. On the other hand, Givan et al. pointed out, through simulations and theoretical analysis in Givan et al. (2011), that the epidemic threshold from Chakrabarti et al. (2008), Wang et al. (2003) and Mieghem et al. (2009) is not accurate in many cases. In this work, we attempt to derive a more accurate epidemic threshold in networks by considering the spatial correlation among nodes. Although our proposed epidemic threshold is still an approximation to the actual threshold, we show that, through both analysis and simulations, our estimator performs much better than the threshold proposed in previous works (Chakrabarti et al., 2008; Wang et al., 2003; Mieghem et al., 2009) in various topologies.

It is noted that pairwise approximation for epidemic thresholds has been studied in Cator and Mieghem (2012) and Mata and Ferreira (2013), considering the interactions between neighbouring nodes. However, our work is fundamentally different from these works. First, the deviation in Cator and Mieghem (2012) and Mata and Ferreira (2013) is based on a continuous-time model, whereas our analysis relies on discrete-time. We consider that the actual epidemic process is a discrete-time event. A detailed discussion of comparing the discrete-time epidemic model with the continuous-time model can be found in Chen et al. (2003). Second, whereas the previous works provide neither a simple, clear physical meaning to the results nor a closed-form expression, we do point out an intuitive observation that the epidemic threshold is directly affected by the spatial correlation coefficient between neighbouring nodes and provide a closed-form solution.

Moreover, different from the previous work (Chen, 2016), this paper derives analytically the epidemic threshold in arbitrary networks by using the general mathematical framework and the mean-field approach, as well as showing that equation (11) is a maximum entropy estimator. Furthermore, we add the simulation results and performance evaluation on epidemic thresholds in an exponential random graph and a real topology (i.e., a co-authorship network).

Many works have studied the epidemic process and the epidemic threshold in different types of networks. For example, Chakrabarti et al. (2007) studied the epidemic threshold in sensor and P2P networks, whereas Valler et al. (2011) derived it in mobile ad hoc networks. Ogura

and Preciado (2016) extended the study to time-varying large-scale networks. Wei et al. (2013) investigated the propagation of two competing memes in a composite network. Moreover, Sahneh et al. (2013) used the generalised epidemic mean-field model to predict epidemic spread over multilayer complex networks, whereas Sanatkar et al. (2016) analysed the epidemic threshold in dynamic switching networks. None of these works have considered the effect of spatial dependence on the epidemic threshold.

Information diffusion and influence spread in online social networks (OSNs) bear resemblance to the epidemic process in networks. Many scenarios of information cascading in OSNs have been modeled through epidemiological models. For example, the popular independent cascade model on social influence, studied in Kempe et al. (2003), can be described as a special *susceptible-infected-recovered* (SIR) model (Prakash et al., 2011). The cascading behaviour in large blog graphs has been characterised by the classic *SIS* model in Leskovec et al. (2007). Moreover, the *susceptible-infected-cured* (SIC) model is proposed in Wang and Wang (2016) to study the propagation of conflict information (e.g., rumour and anti-rumour) in OSNs.

8 Conclusions

In this work, we have proposed a new epidemic threshold by taking into consideration a certain spatial dependence. Specifically, we have exploited the assumption of Markov spatial dependence and shown analytically that the epidemic threshold in networks indeed depends on the correlation coefficient between neighbouring nodes. Through extensive simulations, we have demonstrated that our proposed epidemic threshold better characterises the actual threshold than the threshold from Chakrabarti et al. (2008) and Mieghem et al. (2009) in arbitrary networks such as lattice, ER random graphs, power-law topologies, and a real co-authorship network. To the best of our knowledge, this is the first attempt in quantitatively understanding the effect of spatial dependence on epidemic thresholds in networks.

Our discoveries on epidemic thresholds have important implications and applications for predicting and controlling the dynamics of the epidemic spreading process. Compared with the previous work, our proposed epidemic threshold provides a more accurate prediction on whether an infection will die out or become epidemic. Especially, when β/δ is between $1/\lambda_{max}(A)$ and $1/\lambda_{max}(A)(1-\rho)$ in a network, it is predicted in previous work (Chakrabarti et al., 2008; Mieghem et al., 2009) that the infection will become epidemic; however, we show that the infection actually dies out. Moreover, an objective function for controlling epidemic spread should consider both the largest eigenvalue of the topology and the spatial correlation between neighbouring nodes (Nowzari et al., 2016).

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Appendix

Maximum entropy estimator

In this appendix, we show that equation (11) is a maximum entropy estimator (Cover and Thomas, 1991; Good, 1963). Without loss of generality, we assume that node i has m neighbours and name these neighbours from 1 to m. That is, $m = |N_i|$, and j = 1, 2, ..., m for $X_j(t)$ in equation (11). We use i_j to denote the state of the neighbour j of node i at time t, i.e., $i_j = x_j(t)$ (note that i_j = 0 or 1). We apply the simplified notation

$$p_{i_1,i_2,\cdots,i_m} = P(\mathbf{X}_{N_i}(t) = \mathbf{x}_{N_i}(t) | X_i(t) = 0) \tag{42}$$

to denote the conditional joint distribution, and

$$p_{i_j} = P(X_j(t) = x_j(t)|X_i(t) = 0) \tag{43}$$

to denote the conditional marginal distribution.

The entropy of the conditional joint distribution is

$$J = -\sum_{i_1,i_2,\cdots,i_m} p_{i_1,i_2,\cdots,i_m} \log p_{i_1,i_2,\cdots,i_m}, \tag{44}$$

and the restraints are

$$p_{i_k} = \sum_{i_1,\cdots,i_{k-1},i_{k+1},\cdots,i_m} p_{i_1,i_2,\cdots,i_m}, \tag{45}$$

where k = 1, 2, ..., m.

To maximise the entropy J, we apply the Lagrange's method. That is, construct the Lagrangian function

$$\mathcal{L}(p_{i_1,i_2,\cdots,i_m}; \alpha_{i_k}^{(k)}, \forall k) = J - \sum_{k=1}^{m} \alpha_{i_k}^{(k)} (p_{i_k} - \sum_{i_1,\cdots,i_{k-1},i_{k+1},\cdots,i_m} p_{i_1,i_2,\cdots,i_m} \Bigg). \tag{46}$$

Using the theorem of Lagrange, we differentiate function $\mathcal{L}(p_{i_1,i_2,\cdots,i_m}; \alpha_{i_k}^{(k)}, \forall k)$ with respect to $p_{i_1,i_2,\cdots,i_m}$, set the result to zero, and then find

$$1 + \log p_{i_1,i_2,\cdots,i_m} = \sum_{k=1}^{m} \alpha_{i_k}^{(k)}. \tag{47}$$

Note that

$$\log p_{0,i_2,\cdots,i_m} - \log p_{1,i_2,\cdots,i_m} = \alpha_0^{(1)} - \alpha_1^{(1)}. \tag{48}$$

Since $p_{0,i_2,\cdots,i_m} + p_{1,i_2,\cdots,i_m} = p_{i_2,\cdots,i_m}$, we find that

$$p_{i_1,i_2,\cdots,i_m} = f_1(i_1) p_{i_2,\cdots,i_m}. \tag{49}$$

By induction,

$$p_{i_1,i_2,\cdots,i_m} = f_1(i_1) f_2(i_2) \cdots f_m(i_m). \tag{50}$$

Applying the restraints (45), we find that $f_k(i_k) = p_{i_k}$, where k = 1, 2, ..., m. Therefore,

$$p_{i_1,i_2,\cdots,i_m} = \prod_{k=1}^{m} p_{i_k}. \tag{51}$$

In other words, equation (11) is a maximum entropy estimator.