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Mean-field level analysis of epidemics in directed networks

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Abstract

The susceptible–infected–removed spreading model in a directed graph is studied. The mean-field level rate equations are built with the degree–degree connectivity correlation element and the (in, out)-degree distribution. And the outbreak threshold is obtained analytically—it is determined by the combination of connectivity probability and the degree distribution. Furthermore, the methods of calculating the degree–degree correlations in directed networks are presented. The numerical results of the discrete epidemic processes in networks verify our analyses.

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1. Introduction

Mathematical models of epidemic spreading are important tools in understanding the dynamics of spreading (such as diseases, information and states). Many features such as the age and the social structure of the population, the contact pattern among individuals and the stages of infection are critical to epidemic evolution ([1, 2] and references therein).

Among all these critical features, the contact pattern of individuals has long been acknowledged in determining the properties of epidemic spreading ([1, 3] and references therein). According to the network-based perspective, many social, biological and technological systems are described by complex networks, whose nodes represent agents and links mimic the interaction among them.

There are several reasons why we must understand how directed networks affect the epidemic processes on them. The incidence of asymmetry in disease transmission may be

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described properly by a directed network [8]. The transmission of computer viruses is based on the World Wide Web, which is confirmed to be intrinsically directed [4, 5]. And metabolic networks are also directed ([6, 7] and references therein).

Several works have presented studies of epidemics in directed networks. In [8] the generating functions are used to study the epidemic probabilities in directed and semi-directed networks. In this mathematical model, nodes have in edges, out edges and undirected edges. The theoretical results show that epidemics in directed and semi-directed networks are very different from those in undirected networks.

In [9], the percolation properties in directed networks are analyzed. It has long been recognized that the susceptible–infected–removed model can be mapped to bond percolation [10, 11]. So this result provides knowledge of epidemics also. Furthermore there are numerical works concerning epidemics on directed networks in [12]. But the treatment therein is relatively simple, they just use the in-degree distribution to substitute the common degree distribution in undirected networks.

It has been recognized that there are two kinds of degree–degree correlations in social and technological networks, which are called ‘assortative’ and ‘disassortative’ [13, 14]. According to the numerical measures in [14], both undirected and directed networks show the property of degree–degree correlations. In the case of undirected networks, the effects of this correlation property on epidemic processes are concerned and analyzed in mathematical models [15–17]. There is no such work in the case of directed networks. In this paper, we built a detailed analyzing model for epidemics in directed networks, which contains the effects of the degree–degree correlations and the degree distributions. Through these equations, we give the critical elements that determine the epidemic outbreak threshold.

In [14], some methods are introduced to measure the degree–degree correlations in directed networks, but we think those are relatively simple and are not enough. It is complex to define and measure these properties in directed networks; here we present our methods to calculate different kinds of correlations based on the connectivity matrix and the degree distribution of the directed network.

The last subject of this paper is to introduce our numerical works, including how to connect individual nodes into a simply connected network, the discrete Monte Carlo methods to simulate the epidemic process, and so on. The results show the difference between epidemics in directed and undirected networks very clearly, and verify the theoretical results in the paper.

The paper is organized as follows. In section 2, we classify the nodes in networks according to their degrees; in section 3, we build the mean-field rate equations and get the theoretical result of the threshold; in section 4, we introduce the methods to measure the degree–degree correlations in directed networks and section 5 contains our numerical works.

2. Classifying the nodes in a network

The structure of a directed graph has been characterized in [4, 5, 7]. In this paper, it is supposed that the whole graph consists of only a giant weakly connected component (GWCC) (see figure 9 in [4]). In other words, every site in the graph is reachable from every other, provided that the links are treated as bidirectional.

For a directed graph of N nodes, all nodes can be divided into K_{in} classes according to their in-degree, the numbers being denoted as $N_{(k,\cdot)}$ for $k = 1, 2, \dots, K_{\text{in}}$; equivalently they can be divided into K_{out} classes according to their out-degree, the numbers being denoted as $N_{(\cdot,l)}$ for $l = 1, 2, \dots, K_{\text{out}}$; or they can be divided into $K_{\text{in}} \times K_{\text{out}}$ classes according to

their (in, out)-degree, the numbers being denoted as $N_{(k,l)}$. Here we have the relationships $N_{(k,\cdot)} = \sum_{l=1}^{K_{out}} N_{(k,l)}$, $N_{(\cdot,l)} = \sum_{k=1}^{K_{in}} N_{(k,l)}$ and $N = \sum_{k=1}^{K_{in}} N_{(k,\cdot)} = \sum_{l=1}^{K_{out}} N_{(\cdot,l)}$.

Suppose here that the degree distribution $P(k, l)$ is known. Here the first element $1 \leq k \leq K_{in}$ denotes in-degree and the second element $1 \leq l \leq K_{out}$ denotes out-degree. One can calculate two marginal degree distributions:

$$P(k, \cdot) = \sum_{j=1}^{K_{out}} P(k, j) \tag{2.1}$$

and

$$P(\cdot, l) = \sum_{i=1}^{K_{in}} P(i, l). \tag{2.2}$$

Besides the degree distribution, another critical factor that characterizes a directed graph is the connectivity probability. Here we denote $P((i, j)|(k, l))$ as the detailed connectivity probability that ‘a link that points to a node with (k, l) -degree comes from a node with (i, j) -degree’. Based on it one can calculate all kinds of marginal connectivity probabilities such as $P((i, \cdot)|(k, \cdot))$ which means the probability that ‘a link that points to nodes with k in-degree comes from nodes with i in-degree’; or $P((\cdot, j)|(k, \cdot))$ which means the probability that ‘a link that points to nodes with k in-degree comes from nodes with j out-degree’.

In the standard compartment model, a population with N individuals is categorized according to its infection states: susceptible (S), infected (I), or recovered and immune (R). There are two basic models: susceptible–infected–susceptible (SIS) and susceptible–infected–removed (SIR). In this paper, we take the SIR model to present the analyzing framework. The model is based on two parameters, the transmission rate λ and the recovery rate μ which is normalized to one. The infection process is via neighbors: $S(i) + I(j) \xrightarrow{\lambda} I(i) + I(j)$, where i and j are two neighbors, and by recovery with rate μ : $I(i) \xrightarrow{\mu} R(i)$.

3. The model and the threshold

Denote $s_{(k,l)}(t)$, $\rho_{(k,l)}(t)$ and $r_{(k,l)}(t)$ as the density of susceptible, infected and removed nodes in a class that has (k, l) -degree at time t , respectively. The normalization condition, valid at each time t , is

$$s_{(k,l)}(t) + \rho_{(k,l)}(t) + r_{(k,l)}(t) = 1 \tag{3.1}$$

for each (k, l) . Global quantities, such as the epidemic incidence, are expressed by an average over the various (in, out)-degree classes: $r_\infty = \lim_{t \rightarrow \infty} r(t)$, with $r(t) = \sum_{(k,l)} P(k, l)r_{(k,l)}(t)$.

Similarly, we can denote $s_{(k,\cdot)}(t)$, $\rho_{(k,\cdot)}(t)$ and $r_{(k,\cdot)}(t)$ for a class with in-degree k and denote $s_{(\cdot,l)}(t)$, $\rho_{(\cdot,l)}(t)$ and $r_{(\cdot,l)}(t)$ for a class with out-degree l .

Let us start with the situation that the detailed connectivity probability $P((i, j)|(k, l))$ is given: in this case we can build the basic coupled equations about these densities, for each (k, l) , $1 \leq k \leq K_{in}$, $1 \leq l \leq K_{out}$ [17, 19]:

$$\begin{cases} \frac{ds_{(k,l)}(t)}{dt} = -\lambda k s_{(k,l)}(t) \Theta(t) \\ \frac{d\rho_{(k,l)}(t)}{dt} = \lambda k s_{(k,l)}(t) \Theta(t) - \rho_{(k,l)}(t) \\ \frac{dr_{(k,l)}(t)}{dt} = \rho_{(k,l)}(t). \end{cases} \tag{3.2}$$

Here $\Theta(t)$ is the probability of the event: ‘a given link comes from an infected node’ and is expressed as

$$\Theta(t) = \sum_{(i,j)} P((i,j)|(k,l))\rho_{(i,j)}(t). \tag{3.3}$$

Set the initial conditions $\rho_{(k,l)}(0) = \epsilon \ll 1$, $s_{(k,l)}(0) = 1 - \epsilon$, and $r_{(k,l)} = 0$. Integrate the first equation of (3.2), yielding

$$s_{(k,l)}(t) = s_{(k,l)}(0) e^{-\lambda k \phi_{(k,l)}(t)} \approx e^{-\lambda k \phi_{(k,l)}(t)} \tag{3.4}$$

with the auxiliary function

$$\phi_{(k,l)}(t) = \int_0^t \sum_{(i,j)} P((i,j)|(k,l))\rho_{(i,j)} dt' = \sum_{(i,j)} P((i,j)|(k,l))r_{(i,j)}(t) \tag{3.5}$$

where $r_{(i,j)}(t) = \mu \int_0^t \rho_{(i,j)}(t') dt'$. The physical meaning of $\phi_{(k,l)}$ is as follows: the probability that a link leads to a node with (k, l) -degree comes from a removed node. Note that the initial seeds are neglected in equality (3.4), so here the removed nodes only include those that would be infected during the spreading process.

As $t \rightarrow \infty$, $1 - r_{(k,l)}(\infty) = s_{(k,l)}(\infty) = \lim_{t \rightarrow \infty} s_{(k,l)}(t)$. And we have the self-consistent equation about $\phi_{(k,l)}(\infty)$:

$$\phi_{(k,l)}(\infty) = \sum_{(i,j)} P((i,j)|(k,l))(1 - s_{(i,j)}(\infty)) = \sum_{(i,j)} P((i,j)|(k,l))(1 - e^{-\lambda i \phi_{(i,j)}(\infty)}). \tag{3.6}$$

Let $\Phi = (\phi_{(1,1)}, \phi_{(1,2)}, \dots, \phi_{(k_{in}, k_{out})})^T$ and equation (3.6) can be written as $\Phi = F(\Phi)$; it has a solution $\Phi = 0$, which means there is no spreading at all.

Now we have the spatial equation (3.6) instead of the temporal equation (3.2) to characterize the system. It is advantageous to understand equation (3.6) from the perspective of classical statistical mechanics. Here Φ may be treated as an order parameter. At the threshold point, there is an equilibrium state which is stable and $\Phi = 0$. The initial infective seeds put into the network are just the perturbation of the system, and the system will stay near the equilibrium state: $\Phi \approx 0$.

As λ becomes bigger than the threshold value, the equilibrium state $\Phi = 0$ will lose stability, and the system will evolve to another stable equilibrium state $\Phi > 0$ eventually under a perturbation.

The stability of the vector function F at the point $\Phi = 0$ is determined by the local derivative of F :

$$\left. \frac{\partial F}{\partial \Phi} \right|_{\Phi=0} = \lambda A. \tag{3.7}$$

Here A is a $(K_{in} \times K_{out}) \times (K_{in} \times K_{out})$ matrix with the form:

$$\begin{pmatrix} 1P((1,1)|(1,1)) & \cdots & iP((i,j)|(1,1)) & \cdots & K_{in}P((K_{in}, K_{out})|(1,1)) \\ 1P((1,1)|(1,2)) & \cdots & iP((i,j)|(1,2)) & \cdots & K_{in}P((K_{in}, K_{out})|(1,2)) \\ \vdots & \vdots & \vdots & \vdots & \vdots \\ 1P((1,1)|(k,l)) & \cdots & iP((i,j)|(k,l)) & \cdots & K_{in}P((K_{in}, K_{out})|(k,l)) \\ \vdots & \vdots & \vdots & \vdots & \vdots \\ 1P((1,1)|(K_{in}, K_{out})) & \cdots & iP((i,j)|(K_{in}, K_{out})) & \cdots & K_{in}P((K_{in}, K_{out})|(K_{in}, K_{out})) \end{pmatrix}. \tag{3.8}$$

Denote Λ_m as the largest eigenvalue of A . According to equation (3.7), the origin will be unstable whenever $\lambda\Lambda_m > 1$, which defines an epidemic threshold

$$\lambda_c = \frac{1}{\Lambda_m}, \tag{3.9}$$

above which the solution $\Phi = 0$ is unstable, and another solution takes over as the actual steady state—the spreading of the disease.

The next subject is how the largest eigenvalue Λ_m is determined or is affected. First of all, the upper and lower boundary of Λ_m are simple. Considering the row summations of the matrix A , we have

$$D_{in}(k, l) = \sum_i \sum_j iP((i, j)|(k, l)) = \sum_i iP((i, \cdot)|(k, l)). \tag{3.10}$$

The physical meaning of $D_{in}(k, l)$ is clear: it is the average of in-degrees of the nearest upstream nodes of the class with (k, l) -degree. We call node n_1 the nearest upstream neighbor of node n_2 if $n_1 \rightarrow n_2$.

Without loss of generality, we assume that the matrix A is non-negative and irreducible, so there exists the relationship

$$\min_{(k,l)} D_{in}(k, l) \leq \Lambda_m \leq \max_{(k,l)} D_{in}(k, l). \tag{3.11}$$

Now let us consider the case of uncorrelated networks, which means the conditional probability $P((i, j)|(k, l))$ is independent of the (in, out)-degree of the upstream nodes, and it has the form:

$$P((i, j)|(k, l)) = \frac{jP(i, j)}{E(d_{out})}. \tag{3.12}$$

Here $E(d_{out}) = \sum_{(i,j)} jP(i, j) = \sum_j jP(\cdot, j)$ is the average of the out-degrees of the whole network.

Under this condition, we have

$$\Lambda_m = D_{in}(k, l) = \sum_i \sum_j \frac{ijP(i, j)}{E(d_{out})} = \frac{E(d_{in}d_{out})}{E(d_{out})}, \quad \forall (k, l). \tag{3.13}$$

This result coincides with that obtained by percolation theory [9]. In [9], the correlation between the in- and out-degrees of the nodes are presented and analyzed. If the in-degree distribution and out-degree distribution are independent, which means $P(i, j) = P(i, \cdot)P(\cdot, j)$, we have [9] $\Lambda_m = E(d_{in})$.

4. A brief discussion of the degree–degree correlation in directed networks

In realistic networks, nodes do not always select their neighbors at random; they present some kinds of selectivity. So there are kinds of correlations at the network level. Of course, the simplest correlation in the mathematical model is the degree–degree correlation. That is to say, the selective element is the degrees of the nodes. In [13, 14], two kinds of correlations, ‘assortative’ and ‘disassortative’, are named for undirected networks.

In the case of directed networks, there are two kinds of edges for a single node: in edge and out edge. So the situation becomes more complex. We consider that there are three steps to studying this problem. The first step is the theoretical design of the measurement of connectivity correlation in directed networks; in other words, we should know how to design the correlation coefficient. The second step is the empirical study, i.e. we should know what

kinds of correlations exist in different realistic directed networks. The third step is to learn how different kinds of correlations affect the dynamical processes in directed networks.

Here we will discuss the first step briefly and we will give a method to define the correlation coefficients.

Since there are two kinds of degree distributions in directed networks, in-degree and out-degree, the situations one should consider are more complex than those in undirected networks. For example, given a node with big out-degree and little in-degree, how can we find its connection preference—does it prefer to connect to nodes with big out-degree and little in-degree, or to nodes with big in-degree and little out-degree, or to nodes with big total degree? So we consider that we should design a uniform method to calculate all these correlation coefficients.

Based on the degree distribution $P(k, l)$ and the detailed connectivity probability $P((i, j)|(k, l))$, here we present the method to calculate the correlation coefficient of in-degree in the network. It can serve as a template for other kinds of correlation coefficients.

According to (3.10), $D_{\text{in}}(k, l)$ is the average of in-degrees of the nearest upstream nodes of the class with (k, l) -degree. Thus, we can get the average of in-degrees of the nearest upstream nodes of the class with (k, \cdot) -degree:

$$D_{\text{in}}(k, \cdot) = \sum_l \frac{P(k, l)}{P(k, \cdot)} D_{\text{in}}(k, l). \quad (4.1)$$

Then we can define its average over the whole network $\langle \cdot \rangle_1$:

$$\langle D_{\text{in}} \rangle_1 = \sum_k \frac{kP(k, \cdot)}{E(d_{\text{in}})} D_{\text{in}}(k, \cdot). \quad (4.2)$$

Here $\frac{kP(k, \cdot)}{E(d_{\text{in}})}$ is a probability measure. Accordingly, the average of in-degree over the whole network is as follows:

$$\langle k \rangle_1 = \sum_k \frac{kP(k, \cdot)}{E(d_{\text{in}})} k. \quad (4.3)$$

The covariance of the in-degree k and the average of in-degrees of the nearest upstream nodes of the class with (k, \cdot) -degree D_{in} is

$$\text{Cov}(D_{\text{in}}, k) = \sum_k \frac{kP(k, \cdot)}{E(d_{\text{in}})} (D_{\text{in}}(k, \cdot) - \langle D_{\text{in}} \rangle_1)(k - \langle k \rangle_1). \quad (4.4)$$

The correlation coefficient of the in-degrees of directly connected nodes is

$$R_{(\text{in}, \text{in})} = \frac{\text{Cov}(D_{\text{in}}, k)}{\sqrt{\text{Var}(D_{\text{in}})}\sqrt{\text{Var}(k)}}. \quad (4.5)$$

Here the variance $\text{Var}(\cdot) = \text{Cov}(\cdot, \cdot)$.

Thus, we define a method to measure the correlation of (in-degree)–(in-degree) in directed networks. Note that here only the degree distribution $P(k, l)$ and the connectivity probability $P((i, j)|(k, l))$ are used; we can say that just these two variables determine the connection structure and the epidemic processes in directed networks.

The measurements of other kinds of correlations can be designed in this way.

5. Numerical works

In order to characterize the epidemic processes in directed networks more clearly, we design a series of numerical works and construct three types of networks. The first directed network

has a power-law in-degree distribution and an approximately normal out-degree distribution, the two marginal distributions are independent; the second directed network is obtained by inverting the direction of the edges in the first network. The purpose is to show the role of two marginal distributions. The third network is an undirected network which is constructed using the in-degree distribution of the first network as its own distribution; the purpose is to compare the effects of directed edges and undirected ones. The steps are as follows:

- (A) Generate a simple connected directed network with the desired degree distribution. This includes the following steps:
- set the in-degree marginal distribution $P(k, \cdot) \propto k^{-\gamma}$ as a template, assign randomly each node a set of 'inward half-edges';
 - calculate the total number of inward half-edges, then assign the same number of outward half-edges to all nodes; each half-edge is assigned to a node chosen at random, so the marginal out-degree approximates to the normal distribution and is independent of in-degree;
 - select a node randomly, denoted as Node_A ; search all the nodes that can be its potential neighbors, these nodes must satisfy two conditions: they have outward half-edges that are not connected and they are not the nearest neighbors of Node_A . According to the number of inward half-edges of Node_A , we select randomly the same number of nodes and connect one of their outward half-edges with an inward half-edge of Node_A . Thus we have a connected group; as it grows, it becomes the target network eventually;
 - select a node randomly from the group that has inward half-edges that do not connect, repeat the steps as mentioned in (c). As each node in the connected group has used up its inward half-edges, we get a simple connected network that has no self-loops and parallel edges.

Here we set the number of nodes $N = 5000$, the maximum of in-degree is $K_{\text{in}} = 50$, and the template power-law distribution has exponent $\gamma = 2.1$. After the network has been connected, we measure that the realistic exponent is $\gamma = 2.0346$, the first- and second-order averages of the in-degree are $E(d_{\text{in}}) = 2.5454$ and $E(d_{\text{in}}^2) = 26.1430$. The first- and second-order averages of the out-degree are $E(d_{\text{out}}) = 2.5454$ and $E(d_{\text{out}}^2) = 9.0046$. In another aspect, $E(d_{\text{in}}d_{\text{out}}) = 6.4164$. Figure 1 shows the two marginal distributions.

- (B) Using the network constructed in step (A), we simulate the epidemic processes. At the beginning, one node is selected randomly to be infective. At every discrete time period, an infective node transmits disease to its downstream susceptible neighbors through directed edges. The transmission is parallel among infective nodes, and edges are independent of each other. At the end of the time period, infective nodes become removed. The epidemic process ends as there is no infective node in the whole network.

As the parameter λ increases from 0 to 1, we get a prevalence of removed nodes among the whole population. Figure 3 shows the dependence of prevalence on λ , where the data are averaged over 10^3 independent runs.

- (C) Using the network obtained in step (A), we invert the direction of each edge. Thus we get a new network which has approximately normal in-degree distribution and power-law out-degree distribution. And we perform a simulation in this network just as in step (B).
- (D) We use the in-degree sequence in step (A) as the degree distribution of the undirected network and construct a simple connected network. The essential idea of the algorithm is similar to that mentioned above, the detailed description of it can be found in [22]. The shortcoming of this method is that one can hardly connect all nodes to the network. The sample that we use here has $N = 4028$ nodes; the first and second averages of the

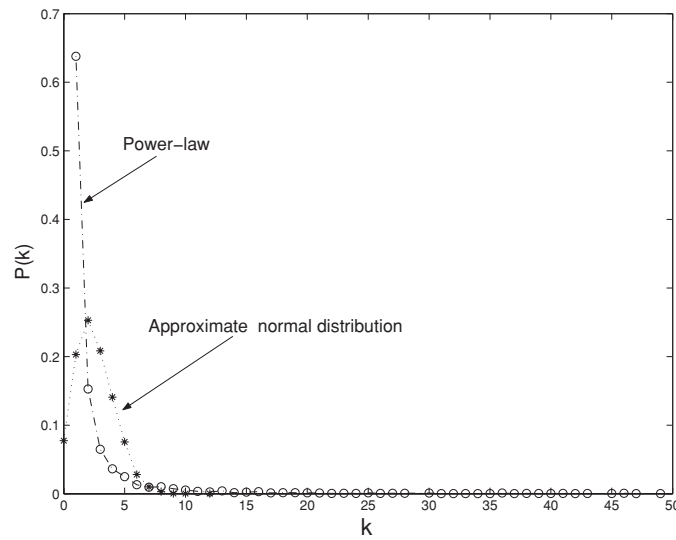


Figure 1. The two marginal degree distributions of the directed network.

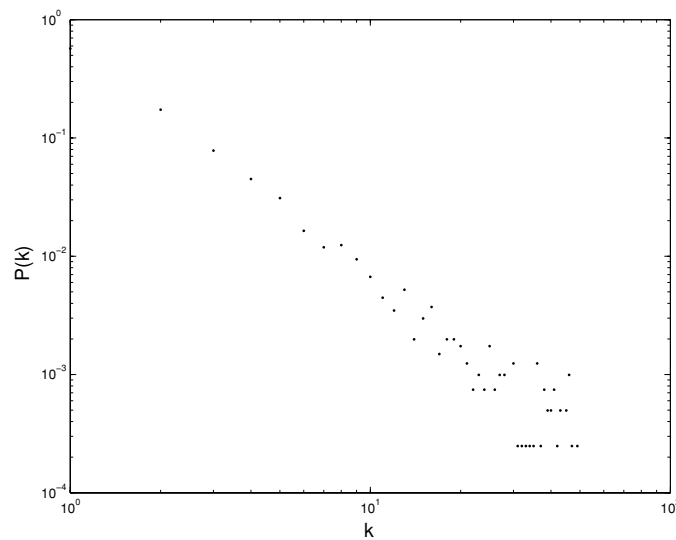


Figure 2. The degree distribution of the realistic undirected network, the two coordinates are logarithmic.

degree distribution are $\langle k \rangle = 2.8972$ and $\langle k^2 \rangle = 32.1445$, and the power-law exponent $\gamma = 2.0013$. Figure 2 shows the degree distribution.

Then we simulate the epidemic process in the undirected network. The results are shown in figure 3.

Three curves in figure 3 show the threshold phenomenon very clearly. We can estimate roughly that the epidemic threshold in the undirected network is about 0.1; according to the theoretical result, the threshold is $\lambda_c = \frac{\langle k \rangle}{\langle k^2 \rangle}$ [17, 19], which takes value $\frac{\langle k \rangle}{\langle k^2 \rangle} = \frac{2.8972}{32.1445} = 0.09$

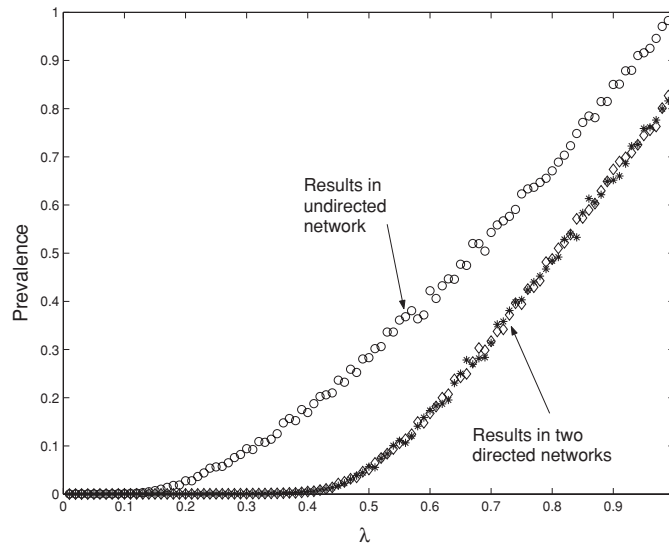


Figure 3. Prevalence measured as the fraction of removed nodes as a function of the transmission rate λ , for an undirected network (\circ) and two directed networks.

here. In this paper, we get the threshold in the directed network $\lambda_c = \frac{1}{E(d_{in})} = \frac{1}{2.5454} = 0.39$, and the estimated value from figure 3 is about 0.4.

The two curves produced from two directed networks are almost coincident, but this is not fortuitous. Note that the only difference between these two networks is that their edge direction is inverse. According to the self-duality of the contact process [23], suppose A and B are two sub-networks, then the probability that the contact process that starts from A will reach B in the first network is the same as the probability that the contact process that starts from B will reach A in the second network.

6. Conclusion

In summary, we build the mean-field rate equation models for SIR epidemics in directed networks and find out the form of the connectivity matrix that decides the properties of epidemic spreading. We find the boundaries of the epidemic threshold using the average of in-degrees of the nearest upstream nodes.

Under the special condition that the connectivity of the network is uncorrelated, the epidemic threshold is determined only by the degree distribution $P(k, l)$: $\Lambda_m = \frac{E(d_{in}d_{out})}{E(d_{out})}$; with a further condition that the in-degree and out-degree distributions are independent, we have $\Lambda_m = E(d_{in})$.

It is easy to check that the methods used in this paper combined with the framework in [19–21] can be used to solve the SIS epidemic model in directed networks, and the results are similar.

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