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Different methods for the threshold of epidemic on heterogeneous networks

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Abstract

The study of the spread of epidemic on different social networks has attracted many attentions from researchers in different fields. One main topical problem is the threshold of transmission rate or the basic reproductive number on different social networks. Recently, several efficient methods on solving the threshold of epidemic on heterogeneous networks were proposed. In this paper, we summarize several methods and compare their advantages or disadvantages systematically.

Keywords: Epidemic, Threshold of transmission rate, Mean field method, Percolation method, Markov method, Matrix method

1. Introduction

How will an infectious disease(computer viruses) propagate in population (Internet)? This is an important question in mathematical epidemiology [1]. Since the human contact patterns or the topology of Internet can be regarded as complex networks [2, 3]. More and more researchers are attributed to investigate the spread of epidemic on complex networks, and a vast amount of work has been produced in the field of network-based models [4, 5, 6, 7, 8, 9, 10]. From viewpoint of epidemiology, at the first step, we are more care about the threshold of transmission rate or the basic reproductive number on different complex networks. Recently, many methods were proposed to answer such problem. To compare the advantage or disadvantage of these methods, we summarize several methods systematically and compare the advantage or disadvantage of these methods.

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We focus on the SIS-like epidemic model on scale-free networks. For the SIS model, each susceptible (S) node is infected with probability β at each time step if it is connected to an infected (I) node. Meanwhile, the infected agent recovers and returns to the susceptible state again with probability μ.

In following sections, we give several typical methods on obtaining the thresholds of epidemics of SIS-like model on heterogenous networks. Including mean-field method [5, 6, 7, 8], percolation method [3, 4, 11], Markov process method [12, 13, 14], and matrix method [1, 15, 16], respectively.

2. Mean field method

Mean field method has been applied to the description of the Ising model, evolutionary game, dynamics of epidemic, and so on.

Recently, Pastor Satorras and Vespignani used the mean field method to the spread of epidemic on heterogeneous networks [5, 6, 7, 8].

In order to include the heterogeneous of complex networks, denoting $\rho_k \in [0, 1]$ is the density of infected nodes with k neighbors, and $1 - \rho_k$ is the density of the susceptible nodes with k neighbors. Then the dynamical equation is described as:

$$\frac{d\rho_k}{dt} = k(1 - \rho_k)\beta\Theta(t, k) - \rho_k, \tag{1}$$

where we have, without loss of generality, set the recovery rate $\mu = 1$. $\Theta(t, k)$ gives the probability that a randomly chosen link emanating from a node of connectivity k leads to infected nodes and has the following form

$$\Theta(t, k) = \sum_{k'} p(k'|k)\rho_{k'}, \tag{2}$$

here the conditional probability $p(k'|k)$ means that a randomly chosen link emanating from a node of connectivity k leads to a node of connectivity k'. By using the assumption $p(k'|k) = k'p(k')/\langle k\rangle$ for uncorrelated networks, we find

$$\Theta = \frac{\sum_{k'} p(k')k'\rho_{k'}}{\langle k\rangle}, \tag{3}$$

here $\langle k\rangle = \sum_k p(k)k$ is the mean degree of network.

Looking for stationary solutions, we have

$$\rho_k = \frac{k\beta\Theta}{1 + k\beta\Theta}. \tag{4}$$

By combining Eq.3 and Eq.4, we get a self-consistency equation

$$\Theta = \frac{\beta}{\langle k\rangle} \sum_k \frac{p(k)k^2\Theta}{1 + k\beta\Theta}. \tag{5}$$

The solution $\Theta = 0$ always satisfies the consistency Eq. 5. A non-zero stationary prevalence can be obtained when the right-hand side and the left-hand side of Eq. 5, expressed as function of

Θ, cross in the interval $0 < \Theta \leq 1$, allowing a nontrivial solution. It is easy to know that this corresponds to the following inequality

$$\frac{d}{d\Theta}(\frac{\beta}{\langle k\rangle}\sum_k \frac{p(k)k^2\Theta}{1+k\beta\Theta})|_{\Theta=0} \geq 1 \tag{6}$$

being satisfied. As a result, the threshold for β_c is obtained

$$\beta_c = \frac{\langle k\rangle}{\langle k^2\rangle}. \tag{7}$$

For heterogeneous networks, if their degree distribution satisfies $p(k) \sim k^{-\gamma}$ with $2 < \gamma \leq 3$, the threshold $\beta_c \to 0$ when the size of network is sufficiently large. Such method can also be generalized to other models, such as SIR, SI_iR, S_iI_iR, and so on [17, 18].

Though the mean field method is easy and can be generalized to other cases, its shortcomings is obvious: first, such method holds for the thermodynamic limit case, so the obtained results are approximate; second, a premise that network is uncorrelated is set in advance to obtain the threshold of epidemic. However, many real networks are correlated (for example, scientists collaboration network, Internet, World-Wide Web, food web and so on), as a result, mean field method isn't good at dealing with correlated networks.

3. Percolation method

A percolation process is one in which nodes or edges on a network are randomly designated either "occupied" or "unoccupied" and asks about various properties of the resulting patterns of nodes. Because spread of epidemic on networks is a contact process, its process can be viewed as the example of "bond percolation". M. E. J.Newman used the percolation ideas and generating function methods to the spread of epidemic on networks [3, 4, 11].

At first, another distribution is denoted as $q(k)$- the degree of the node we reach by following a randomly chosen edge on the network, which is different to degree distribution $p(k)$. Since the degree distribution of the node at the end of a randomly chosen edge is proportional to $kp(k)$, as a result, distribution $q(k)$ is given as:

$$q(k) = \frac{(k+1)p(k+1)}{\sum_k p(k)k} = \frac{(k+1)p(k+1)}{\langle k\rangle}. \tag{8}$$

Defining two generating functions for the $p(k)$ and $q(k)$:

$$G_0(x) = \sum_{k=0}^{\infty} p(k)x^k, \qquad G_1(x) = \sum_{k=0}^{\infty} q(k)x^k. \tag{9}$$

The generation function $H_1(x)$ for the total number of nodes by following an randomly chosen edges, which satisfied

$$H_1(x) = xq(0) + xq(1)H_1(x) + xq(2)H_1^2(x) + \cdots = xG_1(H_1(x)). \tag{10}$$

Similarly, The total number of nodes reachable from a randomly chosen node is generated by $H_0(x)$

$$H_0(x) = xp(0) + xp(1)H_1(x) + xp(2)H_1^2(x) + \cdots = xG_0(H_1(x)). \tag{11}$$

When the transmission rate is β, the distribution of the sizes of clusters (i.e., disease outbreaks size) is generalized as:

$$H_0(x) = xG_0(H_1(x)), \qquad H_1(x) = 1 - \beta + \beta x G_1(H_1(x)). \tag{12}$$

The epidemic outbreaks take place means the emergence of "giant cluster" , which is given:

$$\langle s \rangle = 1 + \frac{\beta G_0'(1)}{1 - \beta G_1'(1)}. \tag{13}$$

We note the Eq.13 diverges when $\beta G_1'(1) = 1$, i.e., the outbreak of epidemic on networks. Thus,

$$\beta_c = \frac{1}{\beta G_1'(1)} = \frac{G_0'(1)}{G_0''(1)} = \frac{\sum_k p(k)k}{\sum_k p(k)k(k-1)} \doteq \frac{\langle k \rangle}{\langle k^2 \rangle}. \tag{14}$$

Percolation method can been generalized to different cases-assortative networks, disassortative networks, hierarchy networks, and so on, yet, such method is somewhat esoteric to many researchers.

4. Markov process method

Denoting the probability that a node i is infected at time t as $\rho_{i,t}$, and let $\zeta_{i,t}$ be the probability that a node i does not infected from its infectious neighbors at time t, which is given as [12, 13, 14],

$$\begin{aligned} \zeta_{i,t} = & \prod_{j \in \wedge_i} (\rho_{j,t-1}(1-\beta) + (1 - \rho_{j,t-1}) \\ = & \prod_{j \in \wedge_i} (1 - \beta \rho_{j,t-1}). \end{aligned} \tag{15}$$

here $\wedge_i$ means the immediate neighbors of i. A node i can guarantee at time step t if it was not infected at time step $t-1$ and did not receive infection from its neighbors at t, i.e., $(1-\rho_{i,t-1})\zeta_{i,t}$, or was infected at time step $t-1$ but cured at t again, i.e., $\mu\rho_{i,t-1}\zeta_{i,t}$.

Then we have following equation:

$$1 - \rho_{i,t} = (1 - \rho_{i,t-1})\zeta_{i,t} + \mu\rho_{i,t-1}\zeta_{i,t}, \qquad i = 1, \cdots N. \tag{16}$$

$$\Rightarrow \rho_{i,t} = 1 - (1 - \rho_{i,t-1})\zeta_{i,t} - \mu\rho_{i,t-1}\zeta_{i,t}, \qquad i = 1, \cdots N. \tag{17}$$

let $\vec{\boldsymbol{\rho}}(\boldsymbol{t}) = (\rho_{1,t}, \rho_{2,t}, \cdots, \rho_{N,t})'$ and $\mathbf{g}(.) = (g_1(.), g_2(.), \cdots, g_N(.))'$. Where

$$\mathbf{g}(\vec{\boldsymbol{\rho}}(\boldsymbol{t-1})) = 1 - (1 - \rho_{i,t-1})\zeta_{i,t} - \mu\rho_{i,t-1}\zeta_{i,t}. \tag{18}$$

From Eq.17, we obtain

$$\vec{\boldsymbol{\rho}}(\boldsymbol{t}) = \mathbf{g}(\vec{\boldsymbol{\rho}}(\boldsymbol{t-1})). \tag{19}$$

Denote $\nabla\mathbf{g}(\vec{\mathbf{0}})$ be the Jacobian determinant at $\vec{\mathbf{0}}$, where

$$[\nabla\mathbf{g}(\vec{\mathbf{0}})]_{i,j} = \begin{cases} \beta A_{i,j} & for j \neq i \\ 1 - \mu & for j = i \end{cases} \tag{20}$$

here $\mathbf{A} = (A_{i,j})_{N\times N}$ is the adjacency matrix of network. Consequently,

$$\mathbf{S} = \nabla \mathbf{g}(\vec{\mathbf{0}}) = \beta \mathbf{A}' + (1-\mu)\mathbf{I}. \tag{21}$$

Here $\mathbf{S}$ calls the system matrix. Therefore, The ith eigenvalue of $\mathbf{S}$ is of the form $\lambda_{i,\mathbf{S}} = 1-\mu+\beta\lambda_{i,\mathbf{A}}$ ($\lambda_{i,\mathbf{A}}$ is the ith eigenvalue of matrix $\mathbf{A}$) and the eigenvectors of $\mathbf{S}$ are the same as those of $\mathbf{A}$.

For a connected undirected network, the matrix $\mathbf{A}$ is a real, nonnegative, and irreducible square matrix, by using the Perron-Frobenius theorem [20], we can find that the largest eigenvalue is a positive real number and also has the largest magnitude all eigenvalues, i.e.,

$$\lambda_{1,\mathbf{S}} = |\lambda_{1,\mathbf{S}}| \geq |\lambda_{i,\mathbf{S}}|, \qquad i = 2, \cdots, N. \tag{22}$$

In order to the die out of epidemic, All of eigenvalues of $\mathbf{S}$ should satisfy $|\lambda_{i,\mathbf{S}}| < 1$ [19]. Thus,

$$\frac{\beta_c}{\mu} = \frac{1}{\lambda_{1,\mathbf{A}}}. \tag{23}$$

where $\lambda_{1,\mathbf{A}}$ is the largest eigenvalue of matrix $\mathbf{A}$, and by setting $\mu = 1$ we have

$$\beta_c = \frac{1}{\lambda_{1,\mathbf{A}}}. \tag{24}$$

Remark 1: In a heterogeneous network, the first eigenvalue of the adjacency matrix,$\lambda_{1,\mathbf{A}} = \sqrt{d_{max}}$ ($d_{max}$is the largest distance between any two nodes, according to [21]). That is, $\lambda_{1,\mathbf{A}} \to 0$ since $d_{max} \propto ln(N)$ for infinite heterogeneous networks ($2 < \gamma \leq 3$). This result concurs with above results for the threshold of epidemic.

Markov process method is so simple that many researchers can understand it, what's more, as author of Refs.[12, 13, 14] stated: "irrespective of the virus propagation model, the effect of the underlying topology can be captured by just one parameter: the first eigenvalue λ_1 of the adjacency matrix A". Of course, for an arbitrary and large networks, how to get the first eigenvalue of the adjacent matrix is a difficult thing.

5. Matrix method

Combining Eq. 1 and Eq. 3, Eq. 1 can be rewritten as [1, 15, 16]:

$$\frac{d\vec{\boldsymbol{\rho}}}{dt} = \mathbf{B}\vec{\boldsymbol{\rho}} + N(\vec{\boldsymbol{\rho}}, t). \tag{25}$$

Where in which a linear $\mathbf{B}\vec{\boldsymbol{\rho}}$ and a non-linear parts $N(\vec{\boldsymbol{\rho}}, t)$ are given as follows:

$$B_{kk'} = -\delta_{kk'} + \frac{\beta k k' p(k')}{\langle k \rangle}, \qquad (k, k' = 1, 2, \cdots, k_{max}). \tag{26}$$

$$N_k(\vec{\boldsymbol{\rho}}, t) = -\frac{k\rho_k}{\langle k \rangle}\beta \sum_{k'=1}^{k_{max}} k'\rho_{k'} < 0, \qquad (k, k' = 1, 2, \cdots, k_{max}). \tag{27}$$

where $\delta_{kk'}$ is the Kroenecher symbol and k_{max} is the largest degree of network.

By setting $\mathbf{v} = (1, 2, \cdots, k_{max})'$, we can rewrite matrix $\mathbf{B}$ in compact form

$$\mathbf{B} = -\mathbf{I} + \frac{1}{\langle k \rangle}(\beta p(1)\mathbf{v}, 2\beta p(2)\mathbf{v}, \cdots, k_{max}\beta p(k_{max})\mathbf{v})' \tag{28}$$

whose structure implies that the matrix $\mathbf{B}$ has $k_{max} - 1$ eigenvalues equal to -1: $\lambda_{1,\mathbf{B}} = \cdots = \lambda_{k_{max}-1,\mathbf{B}} = -1$. To find the k_{max}th it is enough to note that

$$\mathbf{Bv} = (-1 + \frac{\beta}{\langle k \rangle}\sum_{k=1}^{k_{max}} k^2 p(k))\mathbf{v} = (-1 + \beta\frac{\langle k^2 \rangle}{\langle k \rangle})\mathbf{v}. \tag{29}$$

i.e., the last eigenvalue of $\mathbf{B}$ is

$$\lambda_{k_{max},\mathbf{B}} = -1 + \beta\frac{\langle k^2 \rangle}{\langle k \rangle}. \tag{30}$$

Due to Eq.1 can be viewed as a special case of following equation

$$y'_k = -\alpha_k(t)y_k + (c_k - y_k)\sum_{k'=1}^{k'=N} \beta_{kk'}(t)y_{k'}. \tag{31}$$

which is the model of multi-group Gonorrhea established by Lajmanovich and Yorke [16].

According to the result of [16], if all of eigenvalues of matrix $\mathbf{B}$ are less than zero, then the null solution $\vec{\boldsymbol{\rho}} = \vec{\mathbf{0}}$ is globally asymptotically stable, otherwise the unique endemic solution $\vec{\boldsymbol{\rho}} = (\rho_1^*, \rho_2^*, \cdots, \rho_{k_{max}}^*)' \neq \vec{\mathbf{0}}$ is globally asymptotically stable. Therefore, from Eq.30, $\beta_c = \frac{\langle k \rangle}{\langle k^2 \rangle}$ (Eq.7) is obtained again.

This method not only gives the threshold of epidemic on network but also proves the global asymptotically stable of null solution. However, such method is difficult to generalized to more complex epidemic models or other type of networks.

6. Conclusion

In summary, we summarized several methods on giving the threshold of SIS-like epidemic model on heterogeneous networks. According to our above description, researchers can compare the advantage or disadvantage of different methods, and use these methods to analysis the spread of epidemic on heterogeneous network under certain conditions.

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