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Solvable epidemic model on degree-correlated networks

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Disease and information spread over social and information networks. Understanding the spread phenomena in networks requires paying attention not only to the degree distribution but also to the degree correlation. However, it is considered difficult to analytically deal with the effect of degree correlation on spread phenomena. Here, we introduce degree correlation using a simple method and present the theoretical formulas of the outbreak threshold and basic reproduction number. We theoretically clarify the effect of the degree correlation.

INTRODUCTION

With the development of transportation and information transmission technology, diffusion processes on complex networks are attracting attention in many fields [1–3]. Outbreak of new infectious diseases that spread over human contact networks have threatened our lives, and computer viruses have caused severe economic damage worldwide through the internet. In considering the spread phenomena in networks, one of the essential structures of the networks is the heterogeneity of degree k, which is the number of connections each node has with other nodes [1–7]. It is well known that many real networks have a scale-free property, whereby the degree distribution follows a power law for large values of k [5], expressed as follows:

$$p_k \sim k^{-\gamma}. \tag{1}$$

A remarkable feature of the scale-free networks is that the second moment $\langle k^2 \rangle = \sum_k k^2 p_k$ diverges when $\gamma \leq 3$. However, some studies argue that many real networks are not strictly scale-free [8–10]. Even so, in most social networks, $\langle k^2 \rangle$ is much larger than $\langle k \rangle^2$. Such networks are collectively called fat-tailed networks [7].

Another important structure is the degree correlation between two nodes connected by links. The degree correlation is described using the degree correlation matrix $e_{kk'}$, which is the probability that one of the two ends of a randomly selected link has a node with degree k and the other has a node with degree k' [4, 7, 11]. This matrix is symmetric as follows:

$$e_{kk'} = e_{k'k}, \tag{2}$$

and since $e_{kk'}$ is a probability, it is normalized as follows:

$$\sum_{k,k'} e_{kk'} = 1. \tag{3}$$

Since the probability that the node at the end of a randomly selected link has degree k is always expressed as

$$q_k = \frac{k p_k}{\langle k \rangle}, \tag{4}$$

the following relationship must be satisfied:

$$q_k = \sum_{k'} e_{kk'}. \tag{5}$$

Moreover, the conditional probability that a node of degree k is connected to a node of degree k' is expressed as follows:

$$p(k'|k) = \frac{e_{kk'}}{q_k}. \tag{6}$$

If the network has no degree correlation, we obtain

$$e_{kk'} = q_k q_{k'}, \tag{7}$$

and thus $p(k'|k) = q_{k'}$. The degree correlation coefficient is described using the Pearson correlation coefficient between the degrees of two ends of the same link as follows:

$$r = \frac{\sum_{kk'} kk'(e_{kk'} - q_k q_{k'})}{\sum_k k^2 q_k - (\sum_k k q_k)^2} \tag{8}$$

Networks where $r > 0$ are called assortative, whereas networks where $r < 0$ are called disassortative [4]. Traditional social networks tend to be assortative, whereas online social networks tend to be disassortative [12].

Epidemic models on static networks can be solved analytically using the degree-based mean-field approximation when there is no degree correlation[1, 3, 13–15]. In this case, we obtain mathematical expressions using $\langle k \rangle$ and $\langle k^2 \rangle$ of the outbreak threshold λ_c of the transmission rate, above which prevalence can occur, and the basic reproduction number R_0, which is the average number of secondary infections that a typical infection would directly cause in a completely susceptible population. However, if there is degree correlation, we have no such analytical solution, although there is a formulation based on the largest eigenvalue of the connectivity matrix or next-generation matrix [3, 16, 17]. Therefore, the effect of correlations on the spread of infection remains unclear. In this study, we introduce a simple degree correlation matrix e_{kh} and we present an analytical solution for the degree-based mean-field approximation. We theoretically clarify that the basic reproduction number R_0 increases with the degree correlation. As an extension, we consider the case of a bipartite population.

MODEL

Here, to understand the effect of degree correlation, we use a simple formulation of $e_{kk'}$ that satisfies the above constraints (Eqs. (2), (3) and (5)) as follows:

$$e_{kk'} = q_k q_{k'} + \varepsilon p_k p_{k'} \left(\frac{k}{\langle k \rangle} - 1 \right) \left(\frac{k'}{\langle k \rangle} - 1 \right). \quad (9)$$

Since all $e_{kk'}$ must be greater or equal to zero, the tuning parameter ε must be within the following range

$$- \min \left[\frac{k_{\max}^2}{(k_{\max} - \langle k \rangle)^2}, \frac{k_{\min}^2}{(k_{\min} - \langle k \rangle)^2} \right] \\ < \varepsilon < \frac{k_{\max} k_{\min}}{(k_{\max} - \langle k \rangle)(\langle k \rangle - k_{\min})}. \quad (10)$$

In the case of $\varepsilon > 0$, the two nodes tend to connect ($e_{kk'} > q_k q_{k'}$) when their degrees k and k' are both greater or lesser than the mean $\langle k \rangle$. Therefore, if $\varepsilon > 0$, the network is assortative, whereas if $\varepsilon < 0$, the network is disassortative. Indeed, the degree correlation coefficient r is calculated as follows:

$$r = \varepsilon \frac{(\langle k^2 \rangle - \langle k \rangle^2)^2}{\langle k^3 \rangle \langle k \rangle - \langle k^2 \rangle^2}. \quad (11)$$

As it can be easily proved, because $\langle k^3 \rangle \langle k \rangle > \langle k^2 \rangle^2$, $r > 0$ when $\varepsilon > 0$, and $r < 0$ when $\varepsilon < 0$. From Eq. (6), the conditional probability is given as follows:

$$p(k'|k) = q_{k'} + \varepsilon p_{k'} \left(\frac{k'}{\langle k \rangle} - 1 \right) \left(1 - \frac{\langle k \rangle}{k} \right), \quad (12)$$

and the average nearest-neighbors' degree of nodes with degree k is calculated as

$$k_{nn}(k) = \sum_{k'} k' p(k'|k) \\ = \frac{\langle k^2 \rangle}{\langle k \rangle} + \varepsilon \frac{\langle k^2 \rangle - \langle k \rangle^2}{\langle k \rangle} \left(1 - \frac{\langle k \rangle}{k} \right), \quad (13)$$

which is an increasing function of k when $\varepsilon > 0$.

RESULT

Simple epidemic model

In this section, we consider an epidemic model presented in the works of Boguna et al. and Moreno et al. [16–18], which is expressed as follows:

$$\frac{di_k(t)}{dt} = -i_k(t) + \lambda k [1 - i_k(t)] \sum_{k'} p(k'|k) i_{k'}(t), \quad (14)$$

where $i_k(t)$ represents the density of infected nodes within each degree class k. This model corresponds to the degree-based mean-field approximation for the susceptible-infected-susceptible (SIS) model on fat-tailed networks. The first term on the right-hand side of Eq. (14) represents the recovery. The second term represents the infection, which is proportional to the infection rate (λ) times the density of susceptible nodes $(1 - i_k(t))$, the number of neighboring nodes (k), and the probability that any neighbor is infected $(\sum_{k'} p(k'|k) i_{k'}(t))$. Substituting Eq. (9) into Eq. (14), we obtain

$$\frac{di_k(t)}{dt} = -i_k(t) + \lambda(1 - i_k(t)) \\ [k\Theta(t) + \varepsilon (k - \langle k \rangle) (\Theta(t) - I(t))], \quad (15)$$

where $\Theta(t)$ represents the probability that an end of a randomly chosen link is infected, which is expressed as follows:

$$\Theta(t) = \sum_k q_k i_k(t). \quad (16)$$

$I(t)$ represents the fraction of infected nodes and is expressed as follows:

$$I(t) = \sum_k p_k i_k(t). \quad (17)$$

The equilibrium condition for Eq. (15) results in

$$i_k^* = \frac{k\Theta^* + \varepsilon(k - \langle k \rangle)(\Theta^* - I^*)}{1/\lambda + k\Theta^* + \varepsilon(k - \langle k \rangle)(\Theta^* - I^*)}. \quad (18)$$

By substituting Eq. (18) into Eqs. (16) and (17), we obtain the following self-consistent equations

$$\Theta^* = \sum_k \frac{k}{\langle k \rangle} p_k \frac{k\Theta^* + \varepsilon(k - \langle k \rangle)(\Theta^* - I^*)}{1/\lambda + k\Theta^* + \varepsilon(k - \langle k \rangle)(\Theta^* - I^*)}), \\ I^* = \sum_k p_k \frac{k\Theta^* + \varepsilon(k - \langle k \rangle)(\Theta^* - I^*)}{1/\lambda + k\Theta^* + \varepsilon(k - \langle k \rangle)(\Theta^* - I^*)}. \quad (19)$$

The self-consistent equations always have a zero solution $I^* = \Theta^* = 0$. If the transmission rate λ is above an outbreak threshold λ_c, there is a nonzero solution, which can be obtained through numerical calculation. Fig. 1(a) shows an example of the simulation results, which are similar to those demonstrated by Fig. 1 in the previous study [4].

To calculate the outbreak threshold analytically, we consider the situation that the nonzero solution converges to 0. Expanding Eq. (19) and ignoring the terms of the second or higher order of Θ^* and I^*, we obtain

$$\Theta^* = \lambda_c \left[\beta \Theta^* + \varepsilon \alpha (\Theta^* - I^*) \right], \\ I^* = \lambda_c \langle k \rangle \Theta^*, \quad (20)$$

where we set

$$\alpha = \frac{\langle k^2 \rangle - \langle k \rangle^2}{\langle k \rangle}, \ \beta = \frac{\langle k^2 \rangle}{\langle k \rangle}. \quad (21)$$
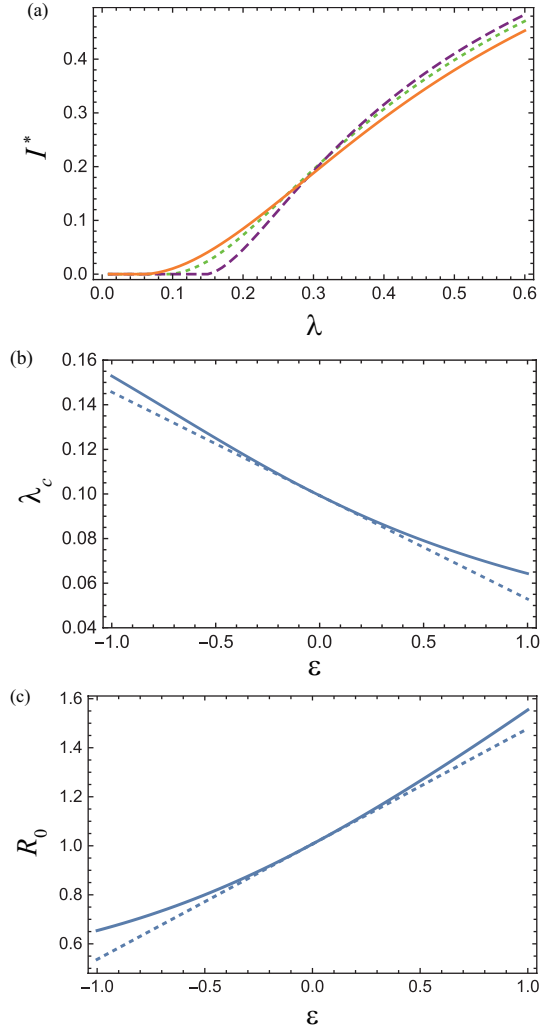
satisfies $\lambda_c = \langle k \rangle / \langle k^2 \rangle$ for $\varepsilon = 0$

$$\lambda_c = \frac{\varepsilon\alpha + \beta - \sqrt{(\varepsilon\alpha + \beta)^2 - 4\varepsilon\alpha\langle k \rangle}}{2\varepsilon\alpha\langle k \rangle}. \qquad (23)$$

By expanding Eq. (23) around $\varepsilon = 0$, we obtain

$$\lambda_c = \frac{\langle k \rangle}{\langle k^2 \rangle}\left[1 - \varepsilon\left(1 - \frac{\langle k \rangle^2}{\langle k^2 \rangle}\right)^2\right] + O(\varepsilon^2). \qquad (24)$$

Therefore, it is clear that the outbreak threshold λ_c decreases when ε increases (see Fig. 1(b)). The other solution of Eq. (22) is positive when $\varepsilon > 0$, and diverges infinitely when $\varepsilon \to 0$. This solution appears to corresponds to an unstable solution of Eq. (15), but it could not be proved here. Considering R_0 as follows, it can be seen that this solution is irrelevant to the outbreak threshold.

Next, we calculate the basic reproduction number R_0. The Jacobi matrix $J_{kk'}$ of Eq. (14) at the disease-free equilibrium $(i_k(t) = 0)$ is expressed as follows:

$$J_{kk'} = -\delta_{kk'} + \lambda k \sum_{k'} p(k'|k), \qquad (25)$$

where $\delta_{kk'}$ is the Kronecker delta or identity matrix. The second term of the right hand side of Eq. (25) represents the transmission part. In this case, the next-generation matrix of Eq. (14) is calculated as follows [19]:

$$\begin{aligned} A_{kk'} &= \lambda k p(k'|k) \\ &= \lambda p_{k'}\frac{kk' + \varepsilon(k' - \langle k \rangle)(k - \langle k \rangle)}{\langle k \rangle}. \end{aligned} \qquad (26)$$

The basic reproduction number R_0 is determined by the spectral radius of the next-generation matrix A. Focusing on the following relations

$$\begin{aligned} \sum_{k'} q_{k'}A_{k'k} &= \lambda(\beta + \varepsilon\alpha)q_k - \lambda\varepsilon\alpha p_k, \\ \sum_{k'} p_{k'}A_{k'k} &= \lambda\langle k \rangle q_k, \end{aligned} \qquad (27)$$

we see that the following vectors are the eigenvectors of A:

$$2\langle k \rangle q_k - \left[\beta + \varepsilon\alpha \pm \sqrt{(\beta + \varepsilon\alpha)^2 - 4\varepsilon\alpha\langle k \rangle}\right]p_k. \qquad (28)$$

The corresponding eigenvalues are calculated as follows:

$$\lambda\langle k \rangle\frac{\beta + \varepsilon\alpha \mp \sqrt{(\beta + \varepsilon\alpha)^2 - 4\varepsilon\alpha\langle k \rangle}}{2}. \qquad (29)$$

Since A is a positive matrix, the Perron–Frobenius theorem shows that the solution of the positive branch in Eq. (29) is the dominant eigenvalue. Therefore,

$$R_0 = \lambda\langle k \rangle\frac{\beta + \varepsilon\alpha + \sqrt{(\beta + \varepsilon\alpha)^2 - 4\varepsilon\alpha\langle k \rangle}}{2}. \qquad (30)$$

FIG. 1. (a) The fraction of infected nodes I^* is plotted as a function of the transmission rate λ for some values of ε. The curves are obtained by solving Eq. (19) numerically. The orange (solid), green (dotted), and purple (dashed) curves correspond to an assortative network ($\varepsilon = 1$), an uncorrelated network ($\varepsilon = 0$), and a disassortative network ($\varepsilon = -1$), respectively. (b) The dependency of the outbreak threshold λ_c on ε. The solid curve is given by Eq. (23). The dotted curve is obtained from an approximate expression (i.e., Eq. (24)) that considers the first-order term of ε. (c) The dependency of the basic reproduction number R_0 on ε, when $\lambda = 0.1$. The solid and dotted curves represent Eqs. (30) and (31), respectively. Here, the degree distribution is $p_k \propto k^{-3}$ for $2 \le k \le 1000$.

By combining Eq. (20) and eliminating I^* and Θ^*, we obtain

$$1 = \lambda_c\left[\beta + \varepsilon\alpha(1 - \lambda_c\langle k \rangle)\right]. \qquad (22)$$

If there is no degree correlation ($\varepsilon = 0$), we obtain $\lambda_c = 1/\beta = \langle k \rangle / \langle k^2 \rangle$ as in previous studies [13, 14]. Eq. (22) has two solutions. However, we select a solution that

If we expand Eq. (30) around $\varepsilon = 0$, we obtain

$$R_0 = \lambda \frac{\langle k^2 \rangle}{\langle k \rangle} \left[1 + \varepsilon \left(1 - \frac{\langle k \rangle^2}{\langle k^2 \rangle} \right)^2 \right] + O(\varepsilon^2). \qquad (31)$$

Therefore, R_0 increases with the increase in ε (see Fig. 1(c)). By solving $R_0 = 1$ for Eq. (30) and (31), we obtain Eq. (23) and (24), respectively. Using Eq. (11), we rewrite Eq. (31) as follows:

$$R_0 \simeq \lambda \left(\frac{\langle k^2 \rangle}{\langle k \rangle} + r \frac{\langle k^3 \rangle \langle k \rangle - \langle k^2 \rangle^2}{\langle k^2 \rangle \langle k \rangle} \right). \qquad (32)$$

Eq. (32) coincides with the approximation formula derived by Goltsev et al. [20].

Bipartite population

We then consider a population represented by a bipartite graph. A possible example is a sexually transmitted disease between men and women, who have the degree distributions $p_k^{(0)}$ and $p_k^{(1)}$, respectively [21, 22]. We use the following expressions:

$$\begin{aligned} \langle k \rangle_{(i)} &= \sum_k k p_k^{(i)} \\ q_k^{(i)} &= \frac{k}{\langle k \rangle_{(i)}} p_k^{(i)}, \end{aligned} \qquad (33)$$

for $i \in \{0, 1\}$. To consider the degree correlation, we expand Eq. (9) as follows:

$$e_{kk'} = q_k^{(0)} q_{k'}^{(1)} + \varepsilon p_k^{(0)} p_{k'}^{(1)} \left(\frac{k}{\langle k \rangle_{(0)}} - 1 \right) \left(\frac{k'}{\langle k \rangle_{(1)}} - 1 \right). \qquad (34)$$

Note that $e_{kk'}$ is not symmetric generally, because the first subscript corresponds to men, and the second corresponds to women. If $i_k^{(0)}(t)$ and $i_k^{(1)}(t)$ are the densities of infected nodes within each degree class k for men and women, respectively, Eq. (14) is expanded as follows:

$$\begin{aligned} \frac{di_k^{(0)}(t)}{dt} &= -i_k^{(0)}(t) + \lambda^{(0)} k [1 - i_k^{(0)}(t)] \sum_{k'} p^{(1)}(k'|k) i_{k'}^{(1)}(t), \\ \frac{di_k^{(1)}(t)}{dt} &= -i_k^{(1)}(t) + \lambda^{(1)} k [1 - i_k^{(1)}(t)] \sum_{k'} p^{(0)}(k'|k) i_{k'}^{(0)}(t), \end{aligned} \qquad (35)$$

where $\lambda^{(0)}$ represents the transmission rate from women to men, and $\lambda^{(1)}$ represents the inverse transmission rate. Here, the conditional probability is expressed as follows:

$$\begin{aligned} p^{(0)}(k'|k) &= q_{k'}^{(0)} + \varepsilon p_{k'}^{(0)} \left(\frac{k'}{\langle k \rangle_{(0)}} - 1 \right) \left(1 - \frac{\langle k \rangle_{(1)}}{k} \right), \\ p^{(1)}(k'|k) &= q_{k'}^{(1)} + \varepsilon p_{k'}^{(1)} \left(\frac{k'}{\langle k \rangle_{(1)}} - 1 \right) \left(1 - \frac{\langle k \rangle_{(0)}}{k} \right). \end{aligned} \qquad (36)$$

In this case, the next-generation matrix is expressed as follows:

$$\begin{pmatrix} 0 & A^{(01)} \\ A^{(10)} & 0 \end{pmatrix}, \qquad (37)$$

where the matrices $A^{(01)}$ and $A^{(10)}$ correspond to the transmissions from women to men and vice versa, respectively, and are given as

$$\begin{aligned} A_{kk'}^{(01)} &= \lambda^{(0)} k p^{(1)}(k'|k), \\ A_{kk'}^{(10)} &= \lambda^{(1)} k p^{(0)}(k'|k). \end{aligned} \qquad (38)$$

By using the following relation:

$$\begin{aligned} \sum_{k'} q_{k'}^{(0)} A_{k'k}^{(01)} &= \lambda^{(0)} (\beta^{(0)} + \varepsilon \alpha^{(0)}) q_k^{(1)} - \lambda^{(0)} \varepsilon \alpha^{(0)} p_k^{(1)}, \\ \sum_{k'} p_{k'}^{(0)} A_{k'k}^{(01)} &= \lambda^{(0)} \langle k \rangle_{(0)} q_k^{(1)}, \\ \sum_{k'} q_{k'}^{(1)} A_{k'k}^{(10)} &= \lambda^{(1)} (\beta^{(1)} + \varepsilon \alpha^{(1)}) q_k^{(0)} - \lambda^{(1)} \varepsilon \alpha^{(1)} p_k^{(0)}, \\ \sum_{k'} p_{k'}^{(1)} A_{k'k}^{(10)} &= \lambda^{(1)} \langle k \rangle_{(1)} q_k^{(0)}, \end{aligned} \qquad (39)$$

we can calculate the dominant eigenvalue of the next-generation matrix given by Eq. (37). When expanded to the first order, the basic reproduction number is written as follows:

$$\begin{aligned} R_0 = & \sqrt{\lambda^{(0)} \lambda^{(1)} \frac{\langle k^2 \rangle_{(0)}}{\langle k \rangle_{(0)}} \frac{\langle k^2 \rangle_{(1)}}{\langle k \rangle_{(1)}}} \\ & \left[1 + \varepsilon \left(1 - \frac{\langle k \rangle_{(0)}^2}{\langle k^2 \rangle_{(0)}} \right) \left(1 - \frac{\langle k \rangle_{(1)}^2}{\langle k^2 \rangle_{(1)}} \right) \right] \\ & + O(\varepsilon^2). \end{aligned} \qquad (40)$$

When $\varepsilon = 0$, Eq. (40) reproduces the well-known result demonstrated by May et al. [21]. Note that when the network composition is the same for men and women, Eq. (40) coincides with Eq. (31)

CONCLUSION

In this study, we introduce an explicit expression for the degree correlation matrix e_{kh} in Eq. (9) and apply it to degree-based mean-field approximation [16–18] for an SIS model on a fat-tailed network. As a result, we succeed in expressing the outbreak threshold λ_c and basic reproduction number R_0 using relatively simple mathematical formulas. We theoretically clarify the effect of the degree correlation on λ_c and R_0. The parameter ε introduced here is useful because it is proportional to the degree correlation coefficient, r (Eq. (11)). In our model, if $\langle k^2 \rangle$ diverges to infinity, R_0 diverges to infinity and λ_c converges to 0, regardless of the degree correlation. Note that the degree correlation introduced here is just one

of the possible correlation structures. The degree correlation exhibited in actual networks is more complicated, as shown by reports that it exhibits power law behavior $k_{\mathrm{nn}}(k) \sim k^{\mu}$ in many real networks [7]. In contrast, according to Eq. (13) it approaches constancy when k increases. Moreover, note that networks containing nodes with a very high degree, such as scale-free networks, cause structural disassortativity due to structural limitation on e_{kh} [7]. There have been many studies on epidemic models on correlated networks [4, 16, 17, 20, 23, 24], but none have reported such a simple mathematical treatment as this study. Eq. (9) can be expanded in various ways, for example, the following extension may be considered:

$$e_{kk'} = q_k q_{k'} + \varepsilon q_k q_{k'} \left(\frac{k}{\langle k^2 \rangle} - 1 \right) \left(\frac{k'}{\langle k^2 \rangle} - 1 \right). \quad (41)$$

However, the calculations performed here are too complicated to achieve analytical solutions. We would like to emphasize that Eq. (9) is immensely useful in that it enables analytical handling. We expect our simple formulations to be effective, especially in the case where the maximum of degree k in the network is not large because of some restrictions. In real social networks, the links can change adaptively depending on the social conditions. The method adopted in this study is expected to be useful when considering such dynamical networks.

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