



Social contagions on multiplex networks with heterogeneous population

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HIGHLIGHTS

- Proposing a social contagion model on multiplex networks with heterogeneous population.
- An edge-based compartmental approach is developed, and well predicts numerical simulations.
- The system exhibits a continuous or hybrid phase transition.

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ABSTRACT

In this paper, we study the effects of heterogeneous population on the dynamics of social contagions on multiplex networks. We assume a fraction of f nodes with a higher adoption threshold $T > 1$, and the remaining fraction of $1 - f$ nodes with adoption threshold 1. A social contagion model is proposed to describe the social contagions, in which a susceptible node adopting the contagion only when its received accumulated information is larger than the adoption threshold in either subnetwork. With an edge-based compartmental approach and extensive numerical simulations, we find that the system exhibits a continuous phase transition for small values of f , while shows a hybrid phase transition for relatively large values of f and T . For homogeneous multiplex networks the hybrid phase transition occurs, while there is only a continuous phase transition for heterogeneous multiplex networks. Our theoretical predictions agree well with numerical simulations.

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1. Introduction

The dynamics of social contagions on complex networks is a hot topic, which has attracted much attention from the field of network science and social science [1–4]. Through analysis many empirical data, researchers found that the social reinforcement effect is an important character of social contagions. Specifically, social reinforcement means that an infection between neighbors should be triggered by multiple contacts, since the social risks exist. While in biology contagions, such

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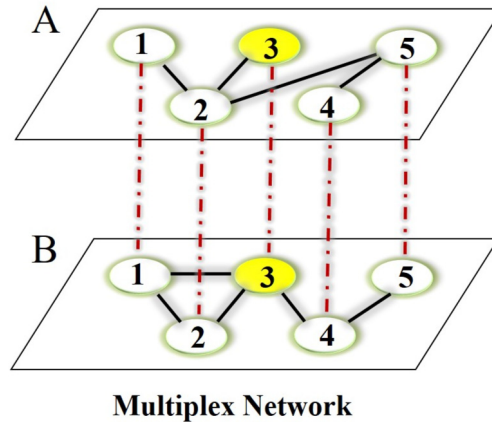


Fig. 1. Illustration of multiplex networks with heterogeneous adoption threshold. There are 5 nodes in subnetworks A and B. Node 3 has adoption threshold $T = 3$, while the remaining nodes with adoption threshold 1.

as epidemic spreading, a single contact between neighbors is enough to trigger the infection [5–11]. To model the spreading dynamics of social contagions, researchers proposed some outstanding models [12–15]. Using the threshold model to investigate the social contagions on complex networks was first proposed by Watts in 2002 [12]. For the threshold model, each node can be in one of active and inactive states. A node in the inactive state means that it has not infected by the social contagion, and may be infected by neighbors. A node in the active state represents that it has been infected by the contagion. An inactive node becoming active only when the fraction of active neighbors in the current step is larger than a given threshold. Through extensive numerical simulations and theoretical analysis, Watts found that the social reinforcement effect induces the emergence of discontinuous growth, and the heterogeneity of degree distribution also affects the outbreak threshold and final size. Along this line, many scholars investigated the effects of seeds size [16], cluster [17], community [18,19], and temporality [20–22] on social contagions.

Multiplexity is another important character of social networks, which indicates that a node belongs to several social networks, such as Facebook, Twitter, and LinkedIn [23–34]. Recently, scholars revealed that multiplexity of complex networks markedly alter the dynamics of social contagions, such as the type of phase transition, final size, and spreading speed [35–38]. Brummitt et al. assumed that a susceptible node becomes infected if the fraction of infected neighbor in either subnetwork is larger than a given threshold [35], and revealed that multiplexity promoting the spreading. Lee et al. [36] further assumed that some nodes becoming infected if a given fraction of neighbors is infected in at least one subnetwork, while the other nodes becoming infected if a given fraction of neighbors is infected in all subnetworks. They found that the spreading dynamic will be facilitated or inhibited by varying the fraction of nodes following two different roles. Wang et al. studied the effects of communication channel character on the social contagions, i.e., nodes only transmit the information on one subnetwork at a given time step [39]. They found that the communication channel alteration character can change the growth of the final size versus information transmission probability on ER–SF networks.

The heterogeneity of nodes widely exists in real-world system [40–43]. On the one hand, different nodes have distinct number of connections, e.g., degrees. On the other hand, nodes have different social statuses, education backgrounds. Thus, for a given social contagion, nodes should have different adoption thresholds [44,45]. Wang et al. investigated the roles of heterogeneous adoption threshold on single complex networks, and revealed the system has discontinuous, continuous, and hybrid phase transition [45]. However, the effect of heterogeneous population on the social contagions on multiplex networks is still lacking. In this paper, we propose a social contagion model on multiplex networks with heterogeneous population. Through a generalized edge-based compartmental theory and extensive numerical simulations, we investigate the final outbreak size and phase transition of the system.

2. Model descriptions

In this paper, we assume the social contagions on multiplex networks with degree distribution $P(k_A, k_B)$, where k_A and k_B respectively represents the degrees of a randomly selected node in subnetworks A and B. If there is no degree–degree correlations between two subnetworks, we have $P(k_A, k_B) = P_A(k_A)P_B(k_B)$, where $P_A(k_A)$ and $P_B(k_B)$ are the degree distributions of subnetworks A and B respectively. Each subnetwork is built according to the uncorrelated configuration model with the given degree distribution [46]. A node in two subnetworks represents that it joins into two distinct social platforms, as illustrated in Fig. 1. For the sake of simplicity, we assume all nodes join into the two platforms, i.e., the number of nodes in both subnetworks are the same $N_A = N_B = N$.

The social contagion is described by using the susceptible–adopted–recovered model described in Ref. [38]. Specifically, the susceptible node has not adopted the behavior, the adopted node has adopted the behavior and willing to share the

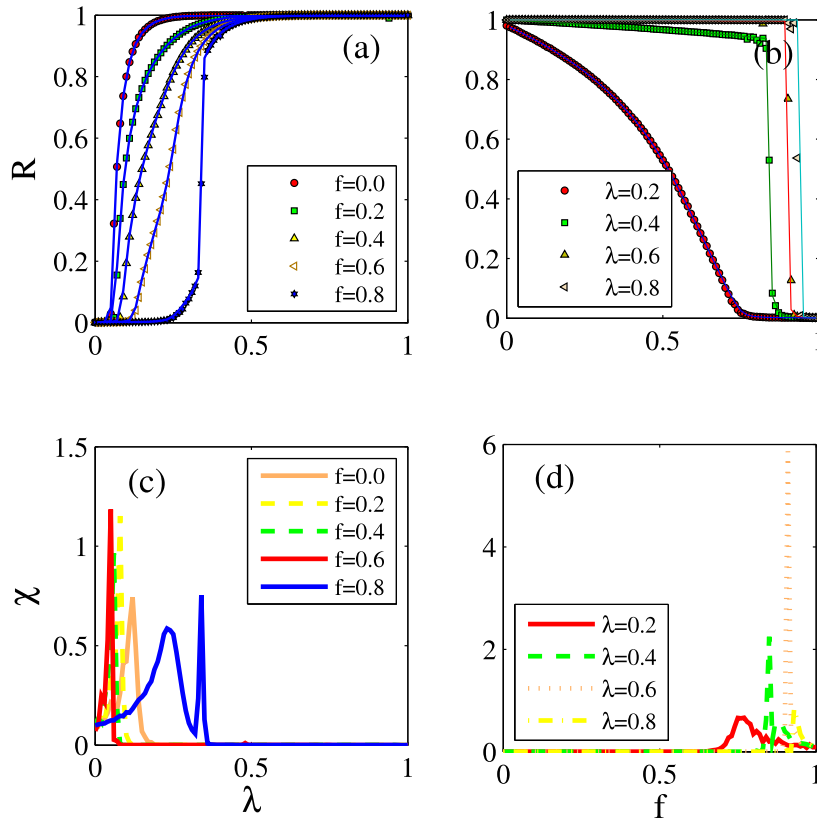


Fig. 2. Social contagions on ER-ER networks. (a) The final outbreak size R , and (c) relative variance χ versus information transmission probability λ with different values of f . (b) R and (d) χ versus f with different values of λ . In (a) and (b), the symbols and lines respectively stand for the numerical and theoretical predictions. In (c) and (d), lines are the simulation results. The network size is $N = 10^4$, and the adoption threshold is $T = 3$.

behavioral information to susceptible neighbors, the recovered node has lost interest in the behavior. For each node, the willingness in adopting the behavior can be determined by the values of adoption thresholds T_A and T_B in subnetworks A and B respectively. The larger value of the adoption threshold, the less willingness of the node. In this paper, we set $T_A = T_B = T$ for a given node. To describe the heterogeneous of population, we assume that a fraction of f nodes with a higher adoption threshold $T > 1$, and the remaining $1 - f$ nodes with a lower threshold $T = 1$ (see Fig. 1).

To trigger the spreading of social contagions, we randomly select a vanishingly small fraction of nodes as the seed. We adopt the synchronous update method to renew the states of nodes. At each time step, each adopted node tries to transmit the behavioral information to each susceptible node with probability $\lambda_A = \lambda_B = \lambda$ in the two subnetworks. If the susceptible node received a piece of information successfully in subnetwork A (B), its accumulated received information m_A (m_B) plus one in subnetwork A (B). Then we compare m_A (m_B) in subnetwork A (B) with the adoption threshold. If $m_A > T$ or $m_B > T$, the susceptible node becomes adopted in subnetworks A and B simultaneously. The adopted node may lose interest in the behavior with probability $\gamma = 1.0$. The spreading dynamics terminates when there is no nodes in the adopted state.

3. Theoretical analysis

To describe the model proposed in Section 2, we develop a generalized edge-based compartmental (EBC) theory which is inspired by Refs. [47,13,48,49]. Assuming that the network is large, local-tree like, and without degree-degree correlations between nodes. Denoting $\theta_A(t)$ ($\theta_B(t)$) as the probability that an edge of a test node v in subnetworks A (B) has not transmitted the behavioral information to it by time t . According to the descriptions of the social contagions, node v is susceptible only when its accumulated received behavioral information is less than its adoption threshold in both subnetworks. Thus, the probability of node v with degree (k_A, k_B) is susceptible as

$$s(k_A, k_B, t) = (1 - f)\theta_A^{k_A}\theta_B^{k_B} + f \sum_{m_A=0}^{T-1} \sum_{m_B=0}^{T-1} \phi_{m_A}^A(k_A, t)\phi_{m_B}^B(k_B, t). \quad (1)$$

On the right hand of Eq. (1), the first term is the probability that node v is susceptible if its adoption threshold is $T = 1$, and the second term is the probability that node v is in the susceptible state if its adoption threshold is $T > 1$. The expression

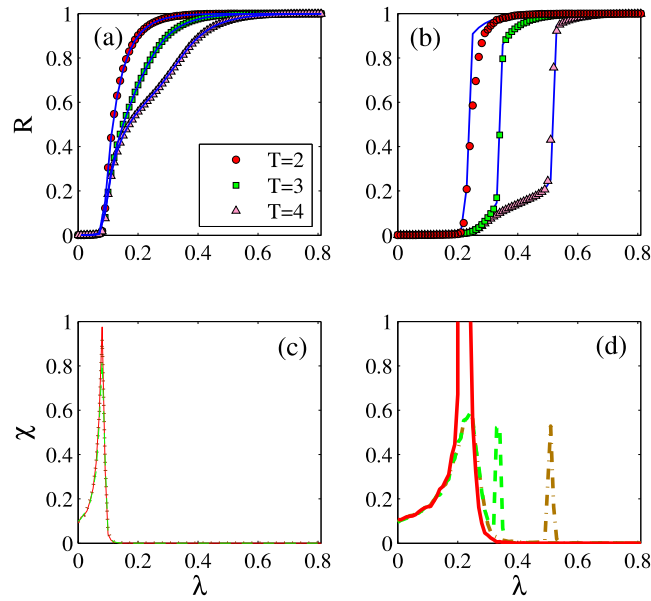


Fig. 3. Social contagions on ER-ER networks with different values of adoption threshold. (a) R and (c) χ versus λ with $f = 0.4$. (b) R and (d) χ versus λ with $f = 0.8$. In (a) and (b), the symbols and lines respectively stand for the numerical and theoretical predictions. In (c) and (d), lines are the simulation results. The network size is $N = 10^4$, and the adoption threshold is $T = 3$.

$\phi_{m_A}^A(k_A, t)$ is the probability the node v has received accumulated m_A piece of information in subnetwork A by time t , which is

$$\phi_{m_A}^A(k_A, t) = \binom{k_A}{m_A} \theta_A^{k_A - m_A} (1 - \theta_A)^{m_A}. \quad (2)$$

Similarly, the term $\phi_{m_B}^B(k_B, t)$ stands for the probability that node v has received accumulated m_B piece of information in subnetwork B by time t , which is

$$\phi_{m_A}^A(k_A, t) = \binom{k_A}{m_A} \theta_A^{k_A - m_A} (1 - \theta_A)^{m_A}. \quad (3)$$

Considering the degree distribution of the system, the probability that a randomly selected node is susceptible is

$$S(t) = \sum_{k_A} \sum_{k_B} P(k_A) P(k_B) s(k_A, k_B, t). \quad (4)$$

To get the value of $S(t)$, we should further compute the expressions of $\theta_A(t)$ and $\theta_B(t)$.

In subnetwork A , an edge of node v can connect to a susceptible, adopted and recovered node. Thus, $\theta_A(t)$ can be further expressed as

$$\theta_A(t) = \xi_S^A(t) + \xi_A^A(t) + \xi_R^A(t), \quad (5)$$

where $\xi_S^A(t)$, $\xi_A^A(t)$ and $\xi_R^A(t)$ respectively represents the probability that node v connects to a susceptible, adopted, and recovered neighbor in subnetwork A , and has not transmitted the information to v by time t . Similarly, we get the expressions of $\theta_B(t)$ as

$$\theta_B(t) = \xi_S^B(t) + \xi_A^B(t) + \xi_R^B(t), \quad (6)$$

where $\xi_S^B(t)$, $\xi_A^B(t)$ and $\xi_R^B(t)$ have the similar meaning with $\xi_S^A(t)$, $\xi_A^A(t)$ and $\xi_R^A(t)$. The only difference is that the definition is for subnetwork B .

In subnetwork A , if an edge of v connects to a susceptible neighbor u . Node u is in the susceptible state only when its received pieces of information from neighbors except v is less than the adoption threshold in two subnetworks. Thus, the

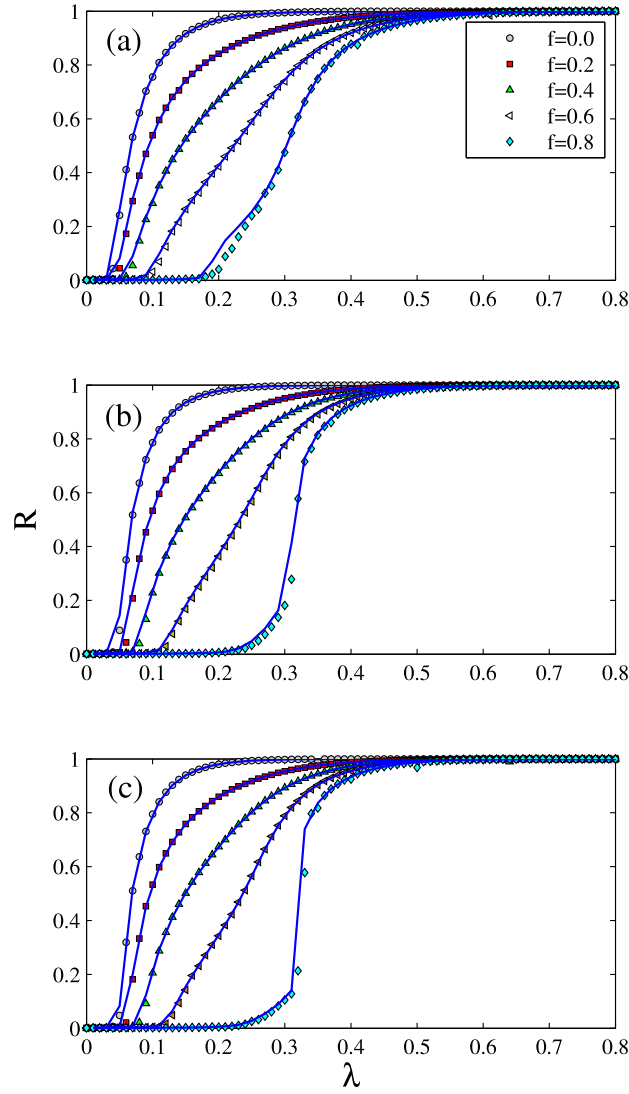


Fig. 4. Social contagions on ER-SF networks. The final behavior adoption size $R(\infty)$ versus λ on ER-SF networks with degree exponent $\gamma_D^B = 2.5$ (a), $\gamma_D^B = 3.5$ (b), and $\gamma_D^B = 4.0$ (d). Symbols and lines respectively represent the numerical and theoretical results. The network size is $N = 10^4$, and the adoption threshold is $T = 3$.

expression of $\xi_S^A(t)$ is

$$\begin{aligned}
 \xi_S^A(t) &= (1-f) \frac{\sum_{k_A} \sum_{k_B} k_A P_A(k_A) P_B(k_B) \theta_A(t)^{k_A-1} \theta_B(t)^{k_B}}{\langle k_A \rangle} \\
 &\quad + f \frac{\sum_{k_A} \sum_{k_B} k_A P_A(k_A) P_B(k_B) \Theta_A(k_A, t)}{\langle k_A \rangle} \\
 &= (1-f) G_{A1}(\theta_A(t)) G_{B0}(\theta_B(t)) \\
 &\quad + \frac{f}{\langle k_A \rangle} \left[\sum_{k_A} \sum_{k_B} k_A P_A(k_A) P_B(k_B) \Theta_A(k_A, t) \right], \tag{7}
 \end{aligned}$$

where $G_{A0}(x)$ is the generating function of degree distribution $P_A(k_A)$, $G_{A1}(x) = G'_{A0}(x)/G'_{A0}(1)$ is the generating function of the excess distribution of subnetwork A, $G_{B0}(x)$ is the generating function of the degree distribution of subnetwork B. The first term of Eq. (7) is the probability that node u is in the susceptible state in subnetwork A when $T = 1$, and the second term represents the probability that node u is susceptible when $T > 1$. The term $\Theta_A(k_A, k_B, t)$ stands for the probability that

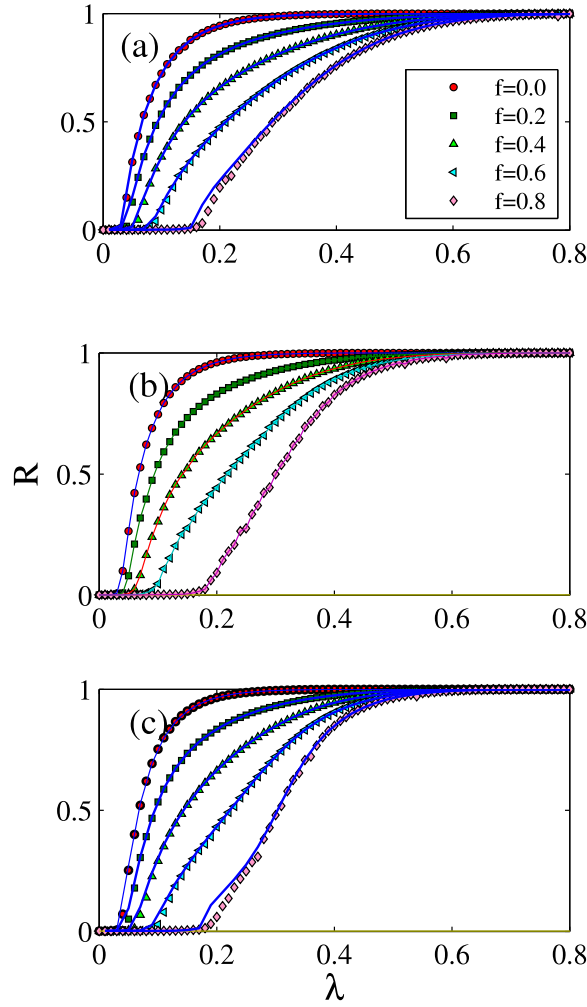


Fig. 5. Social contagions on SF-SF networks. The final behavior adoption size $R(\infty)$ versus λ on ER-SF networks with degree exponents $\gamma_D^A = 2.5$, $\gamma_D^B = 2.5$ (a), $\gamma_D^A = 2.5$, $\gamma_D^B = 3.5$ (b), and $\gamma_D^A = 2.5$, $\gamma_D^B = 4.0$ (d). Symbols and lines respectively represent the numerical and theoretical results. The network size is $N = 10^4$, and the adoption threshold is $T = 3$.

a node with degree (k_A, k_B) is susceptible, and can be expressed as

$$\Theta_A(k_A, k_B, t) = \sum_{m_A=0}^{T-1} \sum_{m_B=0}^{T-1} \tau_{m_A}^A(k_A, t) \phi_{m_B}^B(k_B, t), \quad (8)$$

where $\tau_{m_A}^A(k_A, t)$ is the probability that node v has received m_A pieces of information by time t as

$$\tau_{m_A}^A(k_A, t) = \binom{k_A-1}{m_A} \theta_A^{k_A-m_A-1} (1-\theta_A)^{m_A}. \quad (9)$$

With a similar discussion, we can get the expressions of $\xi_S^B(t)$, $\Theta_B(k_A, k_B, t)$, and $\tau_{m_B}^B(k_B, t)$.

In subnetwork A, the decrease of $\theta_A(t)$ only when the information is transmitted through an edge. Thus we have

$$\frac{d\theta_A(t)}{dt} = -\lambda \xi_A^A. \quad (10)$$

If the adopted node does not transmit the information to the susceptible node before recovering, the value of ξ_R^A increases, the expression is

$$\frac{d\xi_R^A(t)}{dt} = (1-\lambda)\xi_A^A. \quad (11)$$

Combining Eqs. (10)–(11), we get

$$\xi_R^A(t) = [1 - \theta_A(t)] \frac{(1 - \lambda)}{\lambda}. \quad (12)$$

Combining Eqs. (4), (10) and (11), we get the evolutions of nodes in different states. With a similar discussion, we can get the expressions of $\xi_S^B(t)$ and $\xi_R^B(t)$.

When there is no nodes in the adopted state, the system reaches its final state, we have $d\theta_A(t)/dt = d\theta_B(t)/dt = 0$. Denoting $\theta_A(\infty) = \theta_A$, and $\theta_B(\infty) = \theta_B$. Therefore, we get

$$\begin{aligned} \theta_A = & (1 - f)G_{A1}(\theta_A)G_{B0}(\theta_B) + \frac{f}{\langle k_A \rangle} \left[\sum_{k_A} \sum_{k_B} k_A P_A(k_A) P_B(k_B) \Theta_A(k_A, \infty) \right] \\ & + (1 - \theta_A) \frac{1 - \lambda}{\lambda}. \end{aligned} \quad (13)$$

Similarly, we obtain

$$\begin{aligned} \theta_B = & (1 - f)G_{B1}(\theta_B)G_{A0}(\theta_A) + \frac{f}{\langle k_B \rangle} \left[\sum_{k_A} \sum_{k_B} k_B P_A(k_A) P_B(k_B) \Theta_B(k_B, \infty) \right] \\ & + (1 - \theta_B) \frac{1 - \lambda}{\lambda}, \end{aligned} \quad (14)$$

where $G_{B1}(x) = G'_{B0}(x)/G'_{B0}(1)$ is the generating function of the excess distribution of subnetwork B . From Eqs. (13) and (14), we know that $\theta_A = \theta_B = 1$ is a trivial solution. If the social contagion outbreaks, the nontrivial solutions of $\theta_A < 1$ and $\theta_B < 1$ exist. To compute the critical points of the system, we first denote the right hand of Eqs. (13) and (14) as $H_1(\theta_A, \theta_B)$ and $H_2(\theta_A, \theta_B)$ respectively. At the critical point, the Jacobian matrix M of $H_1(\theta_A, \theta_B)$ and $H_2(\theta_A, \theta_B)$ is

$$M = \begin{pmatrix} \frac{\partial H_1(\theta_A, \theta_B)}{\partial \theta_A} & \frac{\partial H_1(\theta_A, \theta_B)}{\partial \theta_B} \\ \frac{\partial H_2(\theta_A, \theta_B)}{\partial \theta_A} & \frac{\partial H_2(\theta_A, \theta_B)}{\partial \theta_B} \end{pmatrix}. \quad (15)$$

At the critical points, the maximum eigenvalue of M equals 1. By using the bifurcation theory [50], we can verify the growth pattern of the final outbreak size R versus the information transmission probability λ .

4. Numerical simulations

We study social contagions on uncorrelated artificial networks in this section. In Fig. 2, we show the final outbreak size R versus information transmission probability λ and the fraction f of nodes with large adoption threshold on ER–ER multiplex networks, i.e., homogeneous multiplex networks. The degree distribution is $P(k_A, k_B) = e^{-(k_A)} \frac{\langle k_A \rangle^{k_A}}{k_A!} e^{-(k_B)} \frac{\langle k_B \rangle^{k_B}}{k_B!}$, where the average degree of networks A and B are $\langle k_A \rangle$ and $\langle k_B \rangle$ respectively. In simulations, we set $\langle k_A \rangle = \langle k_B \rangle = 10$, and the network size is $N = 10^4$. We perform at least 5000 times of simulations to get the average numerical results. In Fig. 2(a), we find that R increases continuously with λ for small values of f , such as $f = 0.0$ and 0.2 . With the increase of f , R first increases continuously and then discontinuously with λ . From the view of statistical mechanics, the phenomenon is called as hybrid phase transition [45]. For instance, when $f = 0.8$ the phenomenon is observed. The type of phase transition can be verified by using the bifurcation theory to analyze Eqs. (13) and (14). Numerically, we can study the relative variance

$$\chi = \frac{\langle R(\infty) - \langle R(\infty) \rangle \rangle^2}{\langle R(\infty) \rangle^2}, \quad (16)$$

where $\langle \cdot \rangle$ is the average value. The value of χ exhibits a peak [51] at the threshold point. As shown in Fig. 2(c), χ exhibits a peak for small values of f (e.g., $f = 0.0$ and 0.2), and shows two peaks for large values of $f = 0.8$. Obviously, our theoretical predictions agree well with numerical simulations. For a given values of λ , we find that R decreases with f . For small values of f , R decreases continuously with λ , while for large values of λ , R exhibits an abrupt decrease. By studying the values of χ , we can locate the numerical threshold points (see Fig. 2(d)), at which χ exhibits a peak.

We further study the effects of adoption threshold T on the social contagions for a given f in Fig. 3. For a relatively small value of $f = 0.4$, we find that R always increases continuously for any values of T in Fig. 3(a), and χ exhibits only one peak as shown in Fig. 3(c). With the increase of $f = 0.8$, we find that R increases sharply with λ when $T = 2$, and χ shows only one peak. For large values of $T = 3$ and 4 , the system has a hybrid phase transition, i.e., R first increases continuously and the increases discontinuously with λ , as shown in Fig. 3(b). In this situation χ shows two peaks as a function of λ in Fig. 3(d). Our theory can well predict the numerical simulations.

In Fig. 4, we investigate social contagions on ER–SF networks. By adopting the uncorrelated configuration model to generate scale-free networks with power-law degree distribution $P(k_A, k_B) = e^{-(k_A)} \frac{\langle k_A \rangle^{k_A}}{k_A!} \zeta_B k_B^{-\gamma_D^B}$, where $\zeta_B = 1/\sum_k k_B^{-\gamma_D^B}$, $\zeta_B = 1/\sum_k k_B^{-\gamma_D^B}$, and γ_D^B is the degree exponent of subnetwork B . In simulations, we set the minimum and maximum degrees

of subnetwork as $k_{\min}^B \sim 3$ and $k_{\max}^B \sim \sqrt{N}$, respectively. In this case, subnetwork B is a heterogeneous network, while subnetwork A is a homogeneous network. The average degrees of subnetworks A and B are the same, i.e., $\langle k_A \rangle = \langle k_B \rangle = 10$. From Fig. 4, we find that R increases with f and λ . Interestingly, with the increase of γ_D^B the system has the hybrid phase transition. In other words, decreasing the degree heterogeneity of subnetwork B , the hybrid phase transition emerges. Again, the theoretical predictions and the numerical results agree well with each other.

We finally study the social contagions on SF–SF networks in Fig. 5. Specifically, the degree distributions of the two subnetworks follow the power-law degree distribution, i.e., $P(k_A, k_B) = \zeta_A k_A^{-\gamma_D^A} \zeta_B k_B^{-\gamma_D^B}$, where $\zeta_A = 1/\sum_k k_A^{-\gamma_D^A}$, $\zeta_B = 1/\sum_k k_B^{-\gamma_D^B}$, and γ_D^A is the degree exponent of subnetwork A . In simulations, we set the average degrees of subnetworks A and B are the same, i.e., $\langle k_A \rangle = \langle k_B \rangle = 10$. We find that R always increases with λ continuously. Combining the phenomena obtained in Fig. 4, we concluded that the hybrid phase transition occurs only on multiplex networks with homogeneous degree distributions.

5. Discussions

In this paper, we theoretically studied the dynamics of social contagions on multiplex networks with heterogeneous populations. To describe the heterogeneous population, we divided the population into two types. One type has a relatively large adoption threshold $T > 1$ with probability f , while the other type has adoption threshold 1 with probability $1 - f$. We used a social contagion model to describe the dynamics of social contagions, in which assumed that a susceptible node adopting the contagion only when its received behavioral information is large than the adoption threshold in either subnetwork. We developed a generalized edge-based compartmental approach to describe the model, and agreed well with numerical simulations. On ER–ER networks, the system exhibited a continuous phase transition for small values of f , and shows a hybrid phase transition for large values of f . On ER–SF networks, the final outbreak size always grows continuously for small values of degree exponent (i.e., heterogeneous networks), and shown a hybrid phase transition for large values of degree exponent (i.e., homogeneous networks). On SF–SF networks, we found that the system always exhibits a continuous phase transition. Our findings may shed some light into studying the dynamics of social contagions on multiplex networks, such as how the inter-layer and intra-layer clustering and degree–degree correlations. In addition, the effects of the distribution of adoption threshold on social contagions need to be further addressed.

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