https://doi.org/10.1016/j.mbs.2016.04.004

Epidemic outbreak for an SIS model in multiplex networks with immunization

Qingchu Wu[a], Yijun Lou[b], and Wenfang Zhu[a]

[a]*College of Mathematics and Information Science, Jiangxi Normal University, Nanchang, Jiangxi* 330022*, P. R. China*
[b]*Department of Applied Mathematics, The Hong Kong Polytechnic University, Hung Hom, Kowloon, Hong Kong*

Abstract

With the aim of understanding epidemic spreading in a general multiplex network and designing optimal immunization strategies, a mathematical model based on multiple degree is built to analyze the threshold condition for epidemic outbreak. Two kinds of strategies, the multiplex node-based immunization and the layer node-based immunization, are examined. Theoretical results show that the general framework proposed here can illustrate the effect of diverse correlations and immunizations on the outbreak condition in multiplex networks. Under a set of conditions on uncorrelated coefficients, the specific epidemic thresholds are shown to be only dependent on the respective degree distribution in each layer.

Keywords: multiplex network, epidemic spreading, threshold condition, immunization.

1. Introduction

In recent years, the study of complex networks has been extended from a single network to a multilayer network with an overlapping fraction q of shared individuals. When $q = 0$, the multilayer network is a disjoint interdependent/interconnected network; while the multilayer network becomes a multiplex/overlay network when $q = 1$. Most recently, multilayer networks have attracted wide attentions due to their novel features, such as complexity [1], diversity [2] and fragility [3]. Diffusion processes over multilayer networks are reviewed in recent work [4].

An susceptible-infected-susceptible (SIS) and an susceptible-infected-recovered (SIR) compartmental structures are two fundamental frameworks in modelling disease spreading. Recently, these compartmental frameworks were incorporated

into multilayer networks and wonderful results were obtained. For example, Dickison et al. [5] studied the spreading of an SIR epidemic model in multilayer networks, where each layer has a random Poissonian degree distribution. Under a certain condition, the model exhibits a mixed phase where an epidemic occurs only in one network, which illustrates the role of the internal layer structure on the spreading process. Almost at the same time, Saumell-Mendiola et al. [6] explored the spreading of an SIS epidemic model in interconnected networks by using the heterogeneous mean-field (HMF) approach [7] and obtained the condition under which an epidemic can spread even though the epidemic is not able to propagate on each network separately. Their results also suggest that the mixed phase does not emerge for the SIS model in multilayer networks. More recently, Salehi et al. [1] proposed a general SIR model in disjoint interdependent networks. By mapping the original network to a colored degree-driven random graph, the authors in [1] obtained analytically exact conditions for epidemic outbreak. They also figured out a multidimensional epidemic threshold, which thoroughly determines the alternative dynamical patterns. Zhu et al. [8] analyzed an SIS epidemic model in a multilayer network with three layers of featured structures and derived the basic reproduction number R_0 [9].

As a general multilayer network, the study of multiplex networks is also important and interesting [10]. Buono et al. [11] studied an SIR model in partially overlapped multiplex networks and found that the epidemic threshold decreases as the overlapped fraction between layers increases. They also concluded that in the limit of a small overlapping fraction, the epidemic threshold is dominated by the most heterogeneous layer. By using the microscopic Markov-chain approximation (MMA) [12], Wu et al. studied the epidemic spreading of SIS models in multiplex networks for both concatenation case and switching case [13]. The MMA approach allows the authors to determine the mutual relationship between the epidemic thresholds of two cases. By a continuous-time MMA approach, Sahneh et al. [14] investigated the dynamic of competitive epidemics in multiplex networks and found that competitive epidemics can coexist under a certain condition.

Several other studies investigated the immunization of multiplex networks, another important topic related to cost-effectiveness evaluation of disease control measures [15]. Buono et al. [16] applied the targeted immunization in one of the layers in partially overlapped multiplex networks and found the targeted immunization is not very efficient because the epidemic threshold is dominated by the most heterogeneous network [11]. In [17], Zuzek et al. studied the random immunization implemented in one layer of a partially overlapped multiplex network, and found that the critical threshold of the epidemic is dominated by the threshold

of the most heterogeneous layer when q is very small. Zhao and coauthors investigated the spreading [18] and immunization [19] of SIR models in multiplex networks (i.e., completely overlapping), where epidemic thresholds for the model with the random immunization and targeted immunization were determined.

With the aim of designing an optimal immunization scheme in a complicated social network, in this paper, we are going to investigate a general immunization strategy for SIS epidemic models in multiplex networks. In particular, we will develop a novel heterogeneous mean-field (HMF) formulation that allows us to analyze several different kinds of the immunization schemes. Based on the developed formulation, we then analyze the epidemic spreading in multiplex networks without (and with) immunization through novel applications of the generalized HMF theory [7].

2. The epidemic spreading in multiplex networks

2.1. The model

We assume the infectious disease in this study, for example the common cold, obeys the SIS epidemiological transmission structure where infected nodes can be recovered, but may be infected again [7, 20]. In this modelling framework, each node may stay in either susceptible (S) or infected (I) state. At each time step, every infected node may transmit the pathogen to its susceptible neighbors with rate λ (i.e., the infection rate) and meanwhile get recovered and become susceptible again with rate μ (i.e., the recovery rate). In what follows, we are going to embed the SIS structure to a multiplex network by the HMF approach.

A multiplex network is a network with multiple links connecting the same nodes. The multiplex network accounts for two typical scenarios: (i) the links between two individuals may be determined by many different kinds of interactions [21]; (ii) various pathogens spread in several routers separately [22]. For simplicity, we consider the multiplex network with two layers, denoted by A and B. It is natural to assume that an infectious disease spreads along different layer with its specific infection rate. To incorporate this heterogeneity, we assume that layer A (B) has the infection rate λ_a (λ_b resp.). For the convenience of mathematical analysis and in accordance to realistic cases, we also assume that the whole network has a finite size N [23], which implies the existence of a maximal degree M_a for A and M_b for B, respectively.

Recently, Sanz et al. [24] studied the dynamics of two interacting pathogens with the successful application of the HMF approach to the analysis of epidemic spreading in multiplex networks. The work of Saumell-Mendiola et al. [6] in

the interdependent network also illustrates the effectiveness of HMF approach in analyzing SIS epidemic models in a multiplex network. Motived by these studies [6, 24], we are going to employ the HMF approach to our study. It is worth to highlight that although the following HMF model can be derived in a similar way as previous investigations, the analysis performed here is different. In order to obtain the mean-field rate equations, we divide all the nodes into many classes based on their degrees and epidemiological states. We use a vector degree $\vec{k} = (k_a, k_b)$ to denote a class of nodes with degree k_a in layer A and degree k_b in layer B [6], following the joint probability distribution $p(k_a, k_b)$. The respective marginal probability distributions of node with degree $\vec{k}$ can be computed as

$$p(k_a) = \sum_{k_b} p(k_a, k_b) \text{ and } p(k_b) = \sum_{k_a} p(k_a, k_b).$$

Moreover, the n order moment of the joint probability $p(k_a, k_b)$ can be written as

$$\langle k_a^n \rangle = \sum_{k_a, k_b} k_a^n p(k_a, k_b) = \sum_{k_a} k_a^n p(k_a),$$

and

$$\langle k_b^n \rangle = \sum_{k_a, k_b} k_b^n p(k_a, k_b) = \sum_{k_b} k_b^n p(k_b).$$

Let $N_{\vec{k}}$ denote the number of nodes in class with degree $\vec{k}$, and $I_{\vec{k}}(t)$ represent the number of infected nodes at time t in class with degree $\vec{k}$. Clearly, $N_{\vec{k}}$=$N \times p(k_a, k_b)$, where N is the size of whole network. Then the HMF version for an SIS epidemic model in a multiplex network can be described as the following ordinary differential equations:

$$\frac{dI_{\vec{k}}}{dt} = -I_{\vec{k}} + (N_{\vec{k}} - I_{\vec{k}})(\lambda_a k_a \theta_a + \lambda_b k_b \theta_b),$$

where the recovery rate is scaled as unitary. In the above system, θ_a and θ_b represent the probabilities that a randomly-selected link emanating from a node of degree $\vec{k}$ leads to infected nodes in the layer A and B, respectively. Suppose each layer in the network underlying disease transmission is uncorrelated to its degree, then we have the probabilities

$$\theta_a = \frac{\sum_{\vec{k}} k_a I_{\vec{k}}(t)}{\sum_{\vec{k}} k_a N_{\vec{k}}} \text{ and } \theta_b = \frac{\sum_{\vec{k}} k_b I_{\vec{k}}(t)}{\sum_{\vec{k}} k_b N_{\vec{k}}}.$$

Let $\rho_{\vec{k}} = I_{\vec{k}}/N_{\vec{k}}$ be the proportion of nodes with degree $\vec{k}$, then its dynamics are determined by the following system:

$$\frac{d\rho_{\vec{k}}}{dt} = -\rho_{\vec{k}} + (1-\rho_{\vec{k}})(\lambda_a k_a \theta_a + \lambda_b k_b \theta_b), \tag{1}$$

where

$$\theta_a = \frac{\sum_{\vec{k}} k_a p(k_a,k_b)\rho_{\vec{k}}(t)}{\sum_{\vec{k}} k_a p(k_a,k_b)} = \frac{\sum_{\vec{k}} k_a p(k_a,k_b)\rho_{\vec{k}}(t)}{\langle k_a \rangle}, \tag{2}$$

and

$$\theta_b = \frac{\sum_{\vec{k}} k_b p(k_a,k_b)\rho_{\vec{k}}(t)}{\sum_{\vec{k}} k_b p(k_a,k_b)} = \frac{\sum_{\vec{k}} k_b p(k_a,k_b)\rho_{\vec{k}}(t)}{\langle k_b \rangle}. \tag{3}$$

We would like to remark that model (1) is similar to the SIS model in directed networks [25, 26] if we regard k_a as the in-degree and k_b as the out-degree. However, the main difference lies in the additional summation term in system (1).

2.2. The outbreak condition

In theoretical epidemiology, the condition of an epidemic outbreak, such as the value of the basic reproduction number R_0, plays an important role. The epidemic will prevail and persist in a population when the outbreak condition is satisfied; while it is not satisfied, the pathogen will not spread in the population. There are two frequently-used methods (although sometimes not rigorous) to determine the outbreak condition: (i) Analyzing the existence of a positive stationary state, such as performed in Pastor-Satorras and Vespignani [7]; (ii) Determining the linear stability of the disease-free equilibrium or deriving the basic reproduction number R_0 characterized as the spectral radius of the next generation matrix [9]. If we use the second method to our model (1), the basic reproduction number R_0 is equal to the spectral radius of the next generation matrix, $\rho(FV^{-1})$, where F is the matrix describing the rate of new occurring infections and V is the matrix characterising the rate of transferring individuals out of the original group. For model (1), it is easy to see that

$$F = \left(\lambda_a k_a k'_a p(k'_a,k'_b)\langle k_a \rangle^{-1} + \lambda_b k_b k'_b p(k'_a,k'_b)\langle k_b \rangle^{-1}\right)_{(M_a \times M_b)\times(M_a \times M_b)} \tag{4}$$

and $V = I$, an identity matrix. Therefore, $R_0 = \rho(F)$. Note that each entry of F is a summation of two terms, which is different from the matrix form studied in [6, 8], and as a result, it is challenging to obtain an explicit expression directly for R_0, the leading eigenvalue of F.

Now, we turn to the first method, by analysing the existence of a positive steady state, to identify an outbreak condition. Following Pastor-Satorras and Vespignani [7], we utilize the stationarity condition $\frac{d\rho_{\vec{k}}}{dt} = 0$ in (1) and obtain

$$\rho_{\vec{k}} = \frac{\lambda_a k_a \theta_a + \lambda_b k_b \theta_b}{1 + \lambda_a k_a \theta_a + \lambda_b k_b \theta_b}. \tag{5}$$

Substituting (5) into (2) and (3) leads to the following equalities

$$\theta_a = \frac{1}{\langle k_a \rangle} \sum_{k_a, k_b} k_a p(k_a, k_b) \frac{\lambda_a k_a \theta_a + \lambda_b k_b \theta_b}{1 + \lambda_a k_a \theta_a + \lambda_b k_b \theta_b} := G_a(\theta_a, \theta_b), \tag{6}$$

and

$$\theta_b = \frac{1}{\langle k_b \rangle} \sum_{k_a, k_b} k_b p(k_a, k_b) \frac{\lambda_a k_a \theta_a + \lambda_b k_b \theta_b}{1 + \lambda_a k_a \theta_a + \lambda_b k_b \theta_b} := G_b(\theta_a, \theta_b). \tag{7}$$

According to the implicit function theorem, Eq. (6) defines a function $\theta_a = h(\theta_b)$ when the following inequality holds:

$$\frac{\partial G_a}{\partial \theta_a} = \frac{1}{\langle k_a \rangle} \sum_{k_a, k_b} \frac{\lambda_a k_a^2 p(k_a, k_b)}{(1 + \lambda_a k_a \theta_a + \lambda_b k_b \theta_b)^2} \neq 1. \tag{8}$$

This inequality implies that $\frac{\partial G_a}{\partial \theta_a}(0,0) \neq 1$, which is equivalent to $\lambda_a \frac{\langle k_a^2 \rangle}{\langle k_a \rangle} \neq 1$.

Let us regard model (1) as a system of parameter λ_b. Denote the matrix F defined in (4), with parameter λ_b, as F_{λ_b}. According to the monotonicity of spectral radius of nonnegative matrix, $\rho(F_{\lambda_b})$ is a monotonically increasing function of λ_b, which implies that $R_0 = \rho(F_{\lambda_b})$ increases as λ_b increases.

When $\lambda_b = 0$, the system is reduced to the standard SIS model in a single network [7]. In the case $\lambda_a \frac{\langle k_a^2 \rangle}{\langle k_a \rangle} > 1$, it is well known that $\lambda_a \frac{\langle k_a^2 \rangle}{\langle k_a \rangle} > 1$ implies $\rho(F_0) > 1$. Therefore,

$$R_0 = \rho(F_{\lambda_b}) > \rho(F_0)$$

for each positive λ_b. In this case, the epidemic spreads certainly.

Now we consider the case where $\lambda_a \frac{\langle k_a^2 \rangle}{\langle k_a \rangle} \leq 1$. Since $\lambda_a \frac{\langle k_a^2 \rangle}{\langle k_a \rangle} \neq 1$ implies the existence of h, we firstly consider $\lambda_a \frac{\langle k_a^2 \rangle}{\langle k_a \rangle} < 1$. In this scenario, $\frac{\partial G_a}{\partial \theta_a} < \lambda_a \frac{\langle k_a^2 \rangle}{\langle k_a \rangle}$ and inequality (8) holds. Hence a unique function $\theta_a = h(\theta_b)$ can be defined by Eq. (6). Substituting the implicit function $\theta_a = h(\theta_b)$ into (7), one can obtain a scalar self-consistency equation

$$\theta_b = G_b[h(\theta_b), \theta_b]. \tag{9}$$

Define $H(\theta_a,\theta_b) = \theta_a - G_a(\theta_a,\theta_b) = \theta_a + \frac{1}{\langle k\rangle}\sum_{k_a,k_b}\frac{k_a p(k_a,k_b)}{1+\lambda_a k_a\theta_a+\lambda_b k_b\theta_b} - 1$. The first and second derivatives of the right hand side of Eq. (9) with respect to θ_b are given by

$$\frac{d}{d\theta_b}G_b[h(\theta_b),\theta_b] = \frac{\partial G_b}{\partial\theta_a}h'(\theta_b) + \frac{\partial G_b}{\partial\theta_b} = -\frac{\partial G_b}{\partial\theta_a}\frac{\partial H}{\partial\theta_b}\Big/\frac{\partial H}{\partial\theta_a} + \frac{\partial G_b}{\partial\theta_b} > 0$$

and

$$\begin{aligned}\frac{d^2}{d\theta_b^2}G_b[g(\theta_b),\theta_b] &= \left[\frac{\partial^2 G_b}{\partial\theta_a\theta_a}h'(\theta_b) + \frac{\partial^2 G_b}{\partial\theta_a\theta_b}\right]h'(\theta_b) + \frac{\partial G_b}{\partial\theta_a}h''(\theta_b)\\ &+ \frac{\partial^2 G_b}{\partial\theta_b\theta_a}h'(\theta_b) + \frac{\partial^2 G_b}{\partial\theta_b\theta_b}.\end{aligned}$$

Since the following inequalities hold

$$\frac{\partial^2 G_b}{\partial\theta_a\theta_a} < 0, \frac{\partial^2 G_b}{\partial\theta_a\theta_b} < 0, \frac{\partial^2 G_b}{\partial\theta_b\theta_a} < 0, \frac{\partial^2 G_b}{\partial\theta_b\theta_b} < 0, \frac{\partial G_b}{\partial\theta_b} > 0, h'(\theta_b) > 0, h''(\theta_b) < 0,$$

we deduce that

$$\frac{d^2}{d\theta_b^2}G_b[h(\theta_b),\theta_b] < 0.$$

Therefore, in the interval $0 < \theta_b \le 1$, there exists a unique non-zero solution of (9) if and only if $\frac{d}{d\theta_b}G_b[h(0),0] > 1$, from which one can obtain

$$\begin{aligned}&\frac{\lambda_a\lambda_b\langle k_a k_b\rangle^2}{\langle k_a\rangle\langle k_b\rangle}\frac{1}{1-\lambda_a\frac{\langle k_a^2\rangle}{\langle k_a\rangle}} + \lambda_b\frac{\langle k_b^2\rangle}{\langle k_b\rangle} > 1, \text{ which implies}\\ &\frac{\lambda_a\lambda_b\langle k_a k_b\rangle^2}{\langle k_a\rangle\langle k_b\rangle} > \left(1-\lambda_a\frac{\langle k_a^2\rangle}{\langle k_a\rangle}\right)\left(1-\lambda_b\frac{\langle k_b^2\rangle}{\langle k_b\rangle}\right). \qquad (10)\end{aligned}$$

Similarly, if $\lambda_b\frac{\langle k_b^2\rangle}{\langle k_b\rangle} <\neq 1$, we can get the same condition for epidemic outbreak.

At last, we consider the critical case $\lambda_a\frac{\langle k_a^2\rangle}{\langle k_a\rangle} = \lambda_b\frac{\langle k_b^2\rangle}{\langle k_b\rangle} = 1$. It seems very difficult to determine the existence of a positive solution for (6) and (7) in a direct way. So we would like to take an indirect method to solve this issue. Notice that (10) holds for the threshold case. Hence, the critical point $(\lambda_a^c,\lambda_b^c)$ lies outside the curve L defined as

$$\text{curve } L: \quad \frac{\lambda_a\lambda_b\langle k_a k_b\rangle^2}{\langle k_a\rangle\langle k_b\rangle} = \left(1-\lambda_a\frac{\langle k_a^2\rangle}{\langle k_a\rangle}\right)\left(1-\lambda_b\frac{\langle k_b^2\rangle}{\langle k_b\rangle}\right). \qquad (11)$$

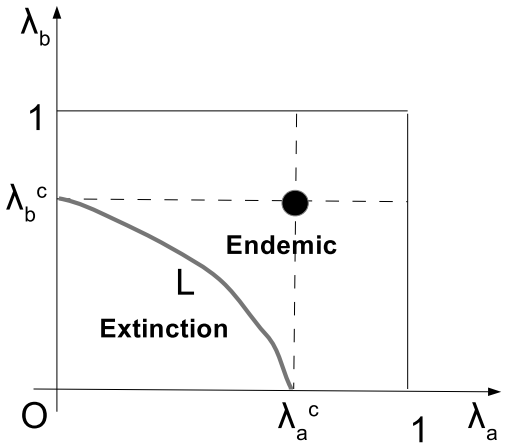

Figure 1: A parametric diagram for λ_a and λ_b, where a threshold curve L (defined in Eq. (11)) divides the parameter space into two parts: the endemic phase and the extinction phase. The curve L is sketched according to its simple properties, such as the monotonic property and the spans of parameter λ_a and λ_b.

In Figure 1, we sketch a parametric diagram for the curve L. By the monotonicity of spectral radius of a nonnegative matrix on parameters, the infectious disease spreads at the critical point.

Summarizing the above arguments, we conclude the condition of an epidemic outbreak as follows:

Case 1: $\lambda_a \frac{\langle k_a^2\rangle}{\langle k_a\rangle} \geq 1$ and $\lambda_b \frac{\langle k_b^2\rangle}{\langle k_b\rangle} \geq 1$. In this case, the epidemic always spreads over the network;

Case 2: $\lambda_a \frac{\langle k_a^2\rangle}{\langle k_a\rangle} < 1$ or $\lambda_b \frac{\langle k_b^2\rangle}{\langle k_b\rangle} < 1$. At this time, an epidemic breaks out when $\frac{\lambda_a\lambda_b\langle k_a k_b\rangle^2}{\langle k_a\rangle\langle k_b\rangle} > \left(1-\lambda_a \frac{\langle k_a^2\rangle}{\langle k_a\rangle}\right)\left(1-\lambda_b \frac{\langle k_b^2\rangle}{\langle k_b\rangle}\right)$.

In particular, when $\lambda_a = 0$ (or $\lambda_b = 0$), the multiplex network is actually a single network and the epidemic threshold λ_c^a (or λ_c^b) can be obtained by the outbreak condition for the case 2. In addition, based on the geometric relation between the extinction and endemic phases as shown in Fig. 1, a unified formulation of outbreak conditions for two cases can be obtained. One formulation can be derived as follows: when $\lambda_a = \lambda_b = \lambda$, if we introduce $c_1 = \frac{\langle k_a k_b\rangle^2}{\langle k_a\rangle\langle k_b\rangle}$, $c_2 = \frac{\langle k_a^2\rangle}{\langle k_a\rangle}$, and $c_3 = \frac{\langle k_b^2\rangle}{\langle k_b\rangle}$, then a simple computation deduces that an epidemic breaks out when

$\lambda > \lambda_c$, where λ_c is defined as

$$\lambda_c = \begin{cases} \frac{c_2+c_3+\sqrt{(c_2-c_3)^2+4c_1}}{2(c_2c_3-c_1)}, & c_2c_3 > c_1, \\ \frac{1}{c_2+c_3}, & c_2c_3 = c_1. \end{cases}$$

In [13], by using the MMA approach, the authors found that the epidemic threshold is inversely proportional to the leading eigenvalue of the summation of each layer's adjacency matrix. Similar to the analysis performed for a single network [29, 30], it is interesting to compare the accuracy between the epidemic thresholds based on the MMA and HMF approaches. However, we are not going to investigate the problem here while leaving it for future work. Instead, we are interested in investigating the sensitivity of the outbreak condition on the correlation of two layers.

Case 1 is trivial as it does not incorporate the connections between layers, we focus on case 2 in the following analysis, highly motivated by [14]. In order to investigate the effect of inter-layer correlation on the outbreak threshold, we employ the Pearson correlation coefficient to quantify how the degree sequences of two layers are correlated

$$r = \frac{\langle (k_a - \langle k_a \rangle)(k_b - \langle k_b \rangle) \rangle}{\sqrt{\langle k_a^2 \rangle - \langle k_a \rangle}\sqrt{\langle k_b^2 \rangle - \langle k_b \rangle}} = \frac{\langle k_a k_b \rangle - \langle k_a \rangle \langle k_b \rangle}{\sqrt{\langle k_a^2 \rangle - \langle k_a \rangle}\sqrt{\langle k_b^2 \rangle - \langle k_b \rangle}}$$

where $r \in [-1, 1]$. The outbreak condition (10) can be expressed in terms of r as

$$\begin{aligned} \Delta &:= \sqrt{\lambda_a \lambda_b} \left(r\sqrt{\langle k_a^2 \rangle - \langle k_a \rangle}\sqrt{\langle k_b^2 \rangle - \langle k_b \rangle} + \langle k_a \rangle \langle k_b \rangle \right) \\ &\quad - \sqrt{\langle k_a \rangle - \lambda_a \langle k_a^2 \rangle}\sqrt{\langle k_b \rangle - \lambda_b \langle k_b^2 \rangle} \\ &> 0. \end{aligned} \tag{12}$$

Hence the sign of Δ determines whether or not an epidemic outbreak happens. In some sense, the value of δ also quantifies the possibility of epidemic outbreak. Based on the expression of Δ in (12), it is easy to see that Δ is positively correlated with the Pearson correlation coefficient r. When $r > 0$, there is a high possibility that hub nodes in layer A are also hub ones in layer B. These hub nodes become the bridges that effectively transmit the pathogen rapidly from one layer to the other one. In the regime $[0, \lambda_a^c] \times [0, \lambda_b^c]$ of the coordinate plane $\lambda_b - \lambda_a$, we examine the effect of r on the threshold curve $\Delta = 0$ in Figure 2. Hence, a larger r can lead to a higher possibility of epidemic outbreak. From the location and pattern of the threshold curve $\Delta = 0$ in Fig. 2, one can also see that the inter-layer correlation has a strong impact on the outbreak threshold.

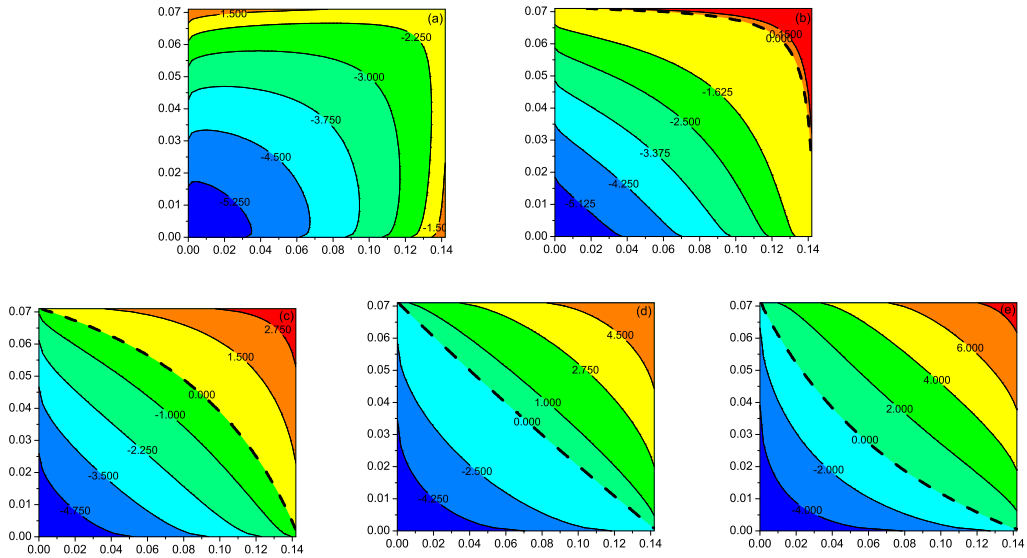

Figure 2: The contour plot of Δ (defined in Equation (12)), where the x coordinate is the infection rate λ_b and the y coordinate is the infection rate λ_a. Five panels correspond to different r values: $r = -1$ (a), -0.5 (b), 0 (c), 0.5 (d) and 1.0 (e), respectively. In a multiplex network, layer A is a Barabási-Albert (BA) scale-free network [27] with degree distribution $p(k) \sim k^{-3}$ and average degree $\langle k \rangle = 6$, while layer B is an Erdös-Rényi (ER) network with connecting probability $p = 0.006$ [28]. The dashed line in each panel represents the curve L ($\Delta = 0$). In panel (a), the line L is very close to the boundary and not easy to observe since the boundary is a little smaller than the epidemic threshold for a single network.

3. The immunization model in multiplex networks

On the basis of the results in the previous section, we further consider immunization schemes in multiplex networks [19, 16]. Before or during the transmission process, an immunized node will be removed and can not get infected from or infect other nodes. Since the infection occurs along the links of the network, the immunization in multiplex network can be classified into two basic schemes:

(i) The multiplex node-based immunization, where each immunized node can not get infected from or pass pathogens to nodes in all layers;

(ii) The layer node-based immunization, where each immunized node can not get infected by or transmit the pathogen to other nodes in a certain layer, and at the meanwhile, immunized nodes can still get infected from or pass pathogen to nodes in other layers.

The case (ii) can approximate the real situation when the immunization means a removed state due to the vaccination or isolation. Taking a social network coupled with the friend and colleague relationship network as an example, when an individual does not go to work, he/she loses all connections with his/her colleagues, but still potentially keeps connected links with his/her friends.

Epidemic spreading process starts with infecting some randomly chosen susceptible nodes and suppose the spreading process follows the SIS dynamics in both layers. Recent work [31] proposed an improved HMF approach to analyze the immunization of an SIS epidemic model in a single network which is shown to be better than previous work [15, 20] through stochastic simulations. In this section, we will extend this approach to analyze the spreading dynamics in multiplex networks with various immunization schemes. We firstly consider the multiplex node-based immunization.

3.1. The multiplex node-based immunization

3.1.1. A general model

Unlike the previous mean-field model with immunization presented in [15], the degree class in each layer consists of not only the old degree before immunization but also the new degree after immunization [31]. To characterise degree variation, we use notation (k_a, l_a) to denote a class of nodes with the old degree k_a and the new degree l_a ($0 \leq l_a \leq k_a$) in layer A. Similar notations are introduced for nodes in layer B. Let $\rho_{k_a,l_a,k_b,l_b}(t)$ represent the densities of infected nodes at time t in class with degree (k_a, l_a, k_b, l_b), which follows the joint probability distribution $p(k_a, l_a, k_b, l_b)$. Then, the respective marginal probability distributions of the old degree and the new degree read as

$$p(k_a) = \sum_{l_a=0}^{k_a} \sum_{k_b=1}^{M_b} \sum_{l_b=0}^{k_b} p(k_a, l_a, k_b, l_b) \text{ and } p(l_a) = \sum_{k_a=l_a}^{M_a} \sum_{k_b=1}^{M_b} \sum_{l_b=0}^{k_b} p(k_a, l_a, k_b, l_b).$$

It is clear that $p(k_a)$ and $p(k_b)$ are degree distributions of layer A and B, respectively. Moreover, the n order moments of the joint probability $p(k_a, l_a, k_b, l_b)$ can be written as

$$\langle k_a^n \rangle = \sum_{k_a=1}^{M_a} \sum_{l_a=1}^{k_a} \sum_{k_b=1}^{M_b} \sum_{l_b=1}^{k_b} k_a^n p(k_a, l_a, k_b, l_b) = \sum_{k_a=1}^{M_a} k_a^n p(k_a),$$

and

$$\begin{aligned}\langle l_a^n \rangle &= \sum_{k_a=1}^{M_a}\sum_{l_a=0}^{k_a}\sum_{k_b=1}^{M_b}\sum_{l_b=0}^{k_b} l_a^n p(k_a,l_a,k_b,l_b) \\ &= \sum_{l_a=0}^{M_a}\sum_{k_a=l_a}^{M_a}\sum_{k_b=1}^{M_b}\sum_{l_b=1}^{k_b} l_a^n p(k_a,l_a,k_b,l_b) = \sum_{l_a=0}^{M} l_a^n p(l_a).\end{aligned}$$

Here, we use

$$\sum_{k,l} u(k,l) = \sum_{l=0}^{M}\sum_{k=l}^{M} u(k,l) = \sum_{k=1}^{M}\sum_{l=0}^{k} u(k,l).$$

Also, one can write its mixed moments as

$$\begin{aligned}\langle l_a l_b \rangle &= \sum_{k_a=1}^{M_a}\sum_{l_a=0}^{k_a}\sum_{k_b=1}^{M_b}\sum_{l_b=0}^{k_b} l_a l_b p(k_a,l_a,k_b,l_b) \\ &= \sum_{l_a=0}^{M_a}\sum_{l_b=0}^{M_b}\sum_{k_a=l_a}^{M_a}\sum_{k_b=l_b}^{M_b} l_a l_b p(k_a,l_a,k_b,l_b) = \sum_{l_a=0}^{M_a}\sum_{l_b=0}^{M_b} l_a l_b p(l_a,l_b).\end{aligned}$$

Other mixed forms $\langle k_a l_a \rangle, \langle k_a k_b \rangle, \langle k_a l_b \rangle, \langle k_b l_b \rangle, \langle l_a k_b \rangle$ can be given in a similar way. Therefore, a general HMF model with immunization can be described by

$$\frac{d\rho_{k_a,l_a,k_b,l_b}}{dt} = -\rho_{k_a,l_a,k_b,l_b} + (1-\rho_{k_a,l_a,k_b,l_b})(\lambda_a l_a \theta_a + \lambda_b l_b \theta_b). \tag{13}$$

When the network is degree-correlated [32], both θ_a and θ_b are defined by

$$\theta_a = \sum_{k'_a,l'_a,k'_b,l'_b} p_a((k'_a,l'_a,k'_b,l'_b)|(k_a,l_a,k_b,l_b))\rho_{k'_a,l'_a,k'_b,l'_b}(t),$$

and

$$\theta_b = \sum_{k'_a,l'_a,k'_b,l'_b} p_b((k'_a,l'_a,k'_b,l'_b)|(k_a,l_a,k_b,l_b))\rho_{k'_a,l'_a,k'_b,l'_b}(t),$$

where the conditional probability $p_a((k'_a,l'_a,k'_b,l'_b)|(k_a,l_a,k_b,l_b))$ means that a randomly chosen link of layer A emanating from a node of degree (k_a,l_a,k_b,l_b) leads

to a node of degree (k'_a, l'_a, k'_b, l'_b). When the connectivity of nodes in the network is uncorrelated (**assumption A1**), we have

$$p_a((k'_a, l'_a, k'_b, l'_b)|(k_a, l_a, k_b, l_b)) = \frac{l'_a p(k'_a, l'_a, k'_b, l'_b)}{\langle l_a \rangle}.$$

Similarly,

$$p_b((k'_a, l'_a, k'_b, l'_b)|(k_a, l_a, k_b, l_b)) = \frac{l'_b p(k'_a, l'_a, k'_b, l'_b)}{\langle l_b \rangle}.$$

Similar to the analysis in Section 2, the condition of epidemic outbreak can be represented as

$$\frac{\lambda_a \lambda_b \langle l_a l_b \rangle^2}{\langle l_a \rangle \langle l_b \rangle} > \left(1 - \lambda_a \frac{\langle l_a^2 \rangle}{\langle l_a \rangle}\right)\left(1 - \lambda_b \frac{\langle l_b^2 \rangle}{\langle l_b \rangle}\right).$$

Hence, the epidemic threshold after immunization is completely determined by the distribution of new degrees. Since the information of new degree distribution is not directly provided, we need to derive the specific expression of the epidemic threshold by using its relation to the degree distribution $p(k_a, k_b)$ before an immunization program is performed.

In order to show the main idea, we use a simplified case by assuming that both degrees of layer A and B are also uncorrelated (**assumption A2**). Then we have

$$p(k_a, l_a, k_b, l_b) = p(k_a, l_a)p(k_b, l_b).$$

So $\langle l_a l_b \rangle = \langle l_a \rangle \langle l_b \rangle$. Hence the threshold condition becomes

$$\lambda_a \lambda_b \langle l_a \rangle \langle l_b \rangle > \left(1 - \lambda_a \frac{\langle l_a^2 \rangle}{\langle l_a \rangle}\right)\left(1 - \lambda_b \frac{\langle l_b^2 \rangle}{\langle l_b \rangle}\right). \tag{14}$$

In what follows, we focus on two specific immunization strategies: the random immunisation (subsection 3.1.2) and the targeted immunisation (subsection 3.1.3). The comparison of two strategies are presented through numerical simulations in subsection 3.1.4.

3.1.2. The random immunization

In the case of random immunization, a fraction g of nodes are removed. In layer $X = A, B$, a typical node, with old degree $k_x (x = a, b)$, gets vaccinated with probability g uniformly. So

$$p(l_x|k_x) = \binom{k_x}{l_x} g^{k_x - l_x}(1-g)^{l_x},\ x = a, b.$$

Moreover, $\langle l_x\rangle = (1-g)\langle k_x\rangle$ and $\langle l_x^2\rangle = (1-g)g\langle k_x\rangle + (1-g)^2\langle k_x^2\rangle$. According to Eq. (14), the outbreak condition for the random immunization becomes

$$\begin{aligned} & \lambda_a\lambda_b(1-g)^2\langle k_a\rangle\langle k_b\rangle \\ > \ & \left(1-\lambda_a g-\lambda_a(1-g)\frac{\langle k_a^2\rangle}{\langle k_a\rangle}\right)\left(1-\lambda_b g-\lambda_b(1-g)\frac{\langle k_b^2\rangle}{\langle k_b\rangle}\right). \end{aligned} \quad (15)$$

It is interesting to consider a trivial case for a single network, that is $\lambda_a = 0$ or $\lambda_b = 0$. For example, when $\lambda_b = 0$, model (17) reduces to

$$\frac{d\rho_{k_a,l_a}}{dt} = -\rho_{k_a,l_a} + (1-\rho_{k_a,l_a})\lambda_a l_a\theta_a$$

with the corresponding outbreak condition

$$0 > 1-\lambda_a g-\lambda_a(1-g)\frac{\langle {k_a}^2\rangle}{\langle k_a\rangle}, \text{ that is } \lambda_a > \frac{\langle k_a\rangle}{(1-g)\langle k_a^2\rangle + g\langle k_a\rangle}.$$

This is consistent with the epidemic threshold for an SIS network model with random immunization [31].

3.1.3. The targeted immunization

In the targeted immunization, those nodes with large degrees are removed. Since the degree of each node has two kinds in layers A and B, we classify five forms of targeted immunization in terms of constant indexes κ_a, κ_b and κ:

(i) All nodes with degree $k_a > \kappa_a$ are removed;
(ii) All nodes with degree $k_b > \kappa_b$ are removed;
(iii) All nodes with degree $k_a > \kappa_a$ or $k_b > \kappa_b$ are removed;
(iv) All nodes with degree $k_a > \kappa_a$ and $k_b > \kappa_b$ are removed;
(v) All nodes with the so-called spreading degree [19] $\lambda_a k_a + \lambda_b k_b > \kappa$ are removed.

We introduce two probabilities first: p_A (p_B) represents the probability that any link in layer A (B resp.) will lead to an immunized node. Now we investigate each immunisation form.

Form (i): All nodes with degree $k_a > \kappa_a$ are removed. In this case, based on [15], we have the following expression

$$p_A = \frac{\sum_{k_a>\kappa_a} k_a p(k_a)}{\sum_{k_a} k_a p(k_a)}.$$

For notational simplicity, we denote $\langle k_a\rangle_t$ and $\langle k_a^2\rangle_t$ as the average quantities $\sum_{k_a=1}^{\kappa_a} k_a p(k_a)$ and $\sum_{k_a=1}^{\kappa_a} k_a^2 p(k_a)$, respectively. Then

$$p_A = \frac{\langle k_a\rangle - \langle k_a\rangle_t}{\langle k_a\rangle}.$$

Therefore, if $k_a \leq \kappa_a$, the conditional probability $p(l_a|k_a) = \binom{k_a}{l_a} p_A^{k_a-l_a}(1-p_A)^{l_a}$; if $k_a > \kappa_a$, then $p(l_a|k_a) = \delta_{l_a 0}$. From this, one can obtain that

$$\langle l_a\rangle = (1-p_A)\langle k_a\rangle_t \text{ and } \langle l_a^2\rangle = (1-p_A)p_A\langle k_a\rangle_t + (1-p_A)^2\langle k_a^2\rangle_t.$$

Similarly, the probability p_B can be computed by

$$p_B = \frac{\sum_{k'_a>\kappa_a,k'_b} k'_b p(k'_a,k'_b|k_b)}{\sum_{k'_a,k'_b} k'_b p(k'_a,k'_b|k_b)} = \frac{\sum_{k'_a>\kappa_a,k'_b} k'_b p(k'_a,k'_b)}{\sum_{k'_a,k'_b} k'_b p(k'_a,k'_b)} = \sum_{k'_a>\kappa_a} p(k'_a).$$

Here we use $p(k'_a,k'_b|k_b) = p(k'_a,k'_b) = p(k'_a)p(k'_b)$. Hence, although there is no direct immunization strategy performed in layer B, the overlapped nodes immunized in layer A also get immunized in layer B but at a random proportion [16]. Therefore, $p(l_b|k_b) = \binom{k_b}{l_b} p_B^{k_b-l_b}(1-p_B)^{l_b}$. Moreover, we have

$$\langle l_b\rangle = (1-p_B)\langle k_b\rangle \text{ and } \langle l_b^2\rangle = (1-p_B)p_B\langle k_b\rangle + (1-p_B)^2\langle k_b^2\rangle.$$

According to Eq. (14), the outbreak condition for this case is

$$\begin{aligned} & \lambda_a\lambda_b(1-p_A)(1-p_B)\langle k_a\rangle_t\langle k_b\rangle \\ > \; & \left(1-\lambda_a p_A - \lambda_a(1-p_A)\frac{\langle k_a^2\rangle_t}{\langle k_a\rangle_t}\right)\left(1-\lambda_b p_B - \lambda_b(1-p_B)\frac{\langle k_b^2\rangle}{\langle k_b\rangle}\right). \end{aligned}$$

We are interested in a special case when a single network is involved, that is, $\lambda_a = 0$ or $\lambda_b = 0$. For example, when $\lambda_b = 0$, the outbreak condition of model (16) is given by

$$0 > 1-\lambda_a p_A - \lambda_a(1-p_A)\frac{\langle k_a^2\rangle_t}{\langle k_a\rangle_t}, \text{ that is } \lambda_a > \frac{\langle k_a\rangle}{\langle k_a^2\rangle_t + \langle k_a\rangle - \langle k_a\rangle_t}.$$

This result agrees with those obtained in [15, 31].

Form (ii): All nodes with degree $k_b > \kappa_b$ are removed. Letting $\langle k_b^n \rangle_t = \sum_{k_b=1}^{\kappa_b} k_b^n p(k_b)$, we have

$$p_A = \sum_{k_b > \kappa_b} p(k_b) \text{ and } p_B = \frac{\langle k_b \rangle - \langle k_b \rangle_t}{\langle k_b \rangle}.$$

Using a similar argument to the previous analysis, the outbreak condition is given by

$$\begin{aligned} & \lambda_a \lambda_b (1-p_A)(1-p_B)\langle k_a \rangle \langle k_b \rangle_t \\ > \quad & \left(1 - \lambda_a p_A - \lambda_a (1-p_A)\frac{\langle k_a^2 \rangle}{\langle k_a \rangle}\right)\left(1 - \lambda_b p_B - \lambda_b (1-p_B)\frac{\langle k_b^2 \rangle_t}{\langle k_b \rangle_t}\right). \end{aligned}$$

Form (iii): All nodes with degree $k_a > \kappa_a$ or $k_b > \kappa_b$ are removed. In this case, we have

$$p_A = 1 - \left(1 - \frac{\langle k_a \rangle - \langle k_a \rangle_t}{\langle k_a \rangle}\right)\left(1 - \sum_{k_b > \kappa_b} p(k_b)\right)$$

and

$$p_B = 1 - \left(1 - \frac{\langle k_b \rangle - \langle k_b \rangle_t}{\langle k_b \rangle}\right)\left(1 - \sum_{k_a > \kappa_a} p(k_a)\right).$$

Notice that $l_a \leq \kappa_a$ for layer A and $l_b \leq \kappa_b$ for layer B after immunization, so we have

$$\langle l_a \rangle = (1-p_A)\langle k_a \rangle_t \text{ and } \langle l_a^2 \rangle = (1-p_A)p_A \langle k_a \rangle_t + (1-p_A)^2 \langle k_a^2 \rangle_t.$$

Similarly, for nodes in layer B, we have

$$\langle l_b \rangle = (1-p_B)\langle k_b \rangle_t \text{ and } \langle l_b^2 \rangle = (1-p_B)p_B \langle k_b \rangle_t + (1-p_B)^2 \langle k_b^2 \rangle_t.$$

Here $\langle k_a \rangle_t$, $\langle k_a^2 \rangle_t$, $\langle k_b \rangle_t$, $\langle k_b^2 \rangle_t$ are defined as in Form (i). Substituting these into Eq. (14), we obtain the condition of an epidemic outbreak as follows

$$\begin{aligned} & \lambda_a \lambda_b (1-p_A)(1-p_B)\langle k_a \rangle_t \langle k_b \rangle_t \\ > \quad & \left(1 - \lambda_a p_A - \lambda_a (1-p_A)\frac{\langle k_a^2 \rangle_t}{\langle k_a \rangle_t}\right)\left(1 - \lambda_b p_B - \lambda_b (1-p_B)\frac{\langle k_b^2 \rangle_t}{\langle k_b \rangle_t}\right). \end{aligned}$$

Form (iv): All nodes with degree $k_a > \kappa_a$ and $k_b > \kappa_b$ are removed. In this case,

$$p_A = \frac{\langle k_a \rangle - \langle k_a \rangle_t}{\langle k_a \rangle} \sum_{k_b > \kappa_b} p(k_b) \text{ and } p_B = \frac{\langle k_b \rangle - \langle k_b \rangle_t}{\langle k_b \rangle} \sum_{k_a > \kappa_a} p(k_a).$$

Considering the fact that nodes with large degrees may exist in each layer after immunization, an infectious disease can prevail under the following condition

$$\begin{aligned} & \lambda_a\lambda_b(1-p_A)(1-p_B)\langle k_a\rangle\langle k_b\rangle \\ > \quad & \left(1-\lambda_a p_A-\lambda_a(1-p_A)\frac{\langle k_a^2\rangle}{\langle k_a\rangle}\right)\left(1-\lambda_b p_B-\lambda_b(1-p_B)\frac{\langle k_b^2\rangle}{\langle k_b\rangle}\right) \end{aligned}$$

where $\langle k_a\rangle_t$, $\langle k_a^2\rangle_t$, $\langle k_b\rangle_t$, $\langle k_b^2\rangle_t$ are defined as above.

Form (v): All nodes with the so-called spreading degree [19] $\lambda_a k_a+\lambda_b k_b>\kappa$ are removed. In order to compute two relevant quantities p_A and p_B, we first define two probabilities: (i) the probability that any link in layer A will lead to a node with degree (k_a,k_b), denoted by $q_A(k_a,k_b)$; (ii) the probability that any link in layer B will lead to a node with degree (k_a,k_b), denoted by $q_B(k_a,k_b)$. Under both two assumptions (assumptions **A1** and **A2**), we have

$$q_A(k_a,k_b)=\frac{k_a p(k_a,k_b)}{\sum_{\vec{k}} k_a p(k_a,k_b)}=\frac{k_a p(k_a)p(k_b)}{\langle k_a\rangle},\ \text{and}$$

$$q_B(k_a,k_b)=\frac{k_b p(k_a,k_b)}{\sum_{\vec{k}} k_b p(k_a,k_b)}=\frac{k_b p(k_a)p(k_b)}{\langle k_b\rangle}.$$

So we can obtain

$$p_A=\sum_{\lambda_a k_a+\lambda_b k_b>\kappa} q_A(k_a,k_b)=\sum_{\lambda_a k_a+\lambda_b k_b>\kappa}\frac{k_a p(k_a)p(k_b)}{\langle k_a\rangle},$$

and

$$p_B=\sum_{\lambda_a k_a+\lambda_b k_b>\kappa} q_B(k_a,k_b)=\sum_{\lambda_a k_a+\lambda_b k_b>\kappa}\frac{k_b p(k_a)p(k_b)}{\langle k_b\rangle}.$$

In order to determine the expression of $p(l_x|k_x), x=a,b$, we need to know what degree classes are all removed after immunization. Apparently, those with large original degrees are likely removed. However, we should try to find the exact threshold value $\vec{z}$ about the original degree (k_a,k_b), above which the nodes with $\vec{k}>\vec{z}$ (this means the inequality holds for each component) are all removed. To this end, we define two integers (if both exist)

$$z_a^{\max}=\max\left\{z_a:\lambda_a z_a+\lambda_b\le\kappa \text{ and } 1\le z_a\le M_a\right\} \text{ and}$$

$$z_b^{\max}=\max\left\{z_b:\lambda_a+\lambda_b z_b\le\kappa \text{ and } 1\le z_b\le M_b\right\}.$$

According to the domain of (k_a, k_b) determined by the constraint $\lambda_a k_a + \lambda_b k_b > \kappa$, we can obtain $\vec{z} = (z_a^{\max}, z_b^{\max})$. Then the outbreak condition can be written as

$$\begin{aligned} & \lambda_a\lambda_b(1-p_A)(1-p_B)\langle k_a\rangle_t\langle k_b\rangle_t \\ > \quad & \left(1-\lambda_a p_A-\lambda_a(1-p_A)\frac{\langle k_a^2\rangle_t}{\langle k_a\rangle_t}\right)\left(1-\lambda_b p_B-\lambda_b(1-p_B)\frac{\langle k_b^2\rangle_t}{\langle k_b\rangle_t}\right) \end{aligned}$$

where

$$\langle k_x^n\rangle_t = \sum_{k_x=1}^{z_x^{\max}} k_x^n p(k_x),\ n=1,2,\ x=a,b.$$

3.1.4. Simulation observations and comparisons

Although outbreak conditions are obtained in six immunization schemes, it is not easy to compare the effectiveness of these immunization strategies qualitatively. However, finding the most effective and optimal immunization strategy is an interesting and important problem. Herein, we will perform simulations to give a visual comparison. Similar to the previous simulation in Figure 2, we take a multiplex network coupled with a BA scale network (layer A) and an ER random network (layer B) as an example.

In order to investigate the effacacy of immunization strategies, Pastor-Satorras and Vespignani [15] analyzed the critical immunization thresholds g_c, above which the epidemic dies out. By using the HMF approach, they obtained the respective immunization thresholds for random/proportional/targeted immunization strategies. In contrast to a single network, the extinction conditions as stated above hold under a certain condition, which are similar to case 2 in Sec. 2.2.

Let us take the random immunization as an example. In this case, when $\lambda_a g + \lambda_a(1-g)\frac{\langle k_a^2\rangle}{\langle k_a\rangle} < 1$ and $\lambda_b g + \lambda_b(1-g)\frac{\langle k_b^2\rangle}{\langle k_b\rangle} < 1$, the epidemic dies out under the condition (15). For simplicity, we introduce three notations:

$$\begin{aligned} (i)\ \Delta_1 &= \lambda_a g + \lambda_a(1-g)\frac{\langle k_a^2\rangle}{\langle k_a\rangle} - 1; \\ (ii)\ \Delta_2 &= \lambda_b g + \lambda_b(1-g)\frac{\langle k_b^2\rangle}{\langle k_b\rangle} - 1;\ \text{and} \\ (iii)\ \Delta_3 &= -\left(1-\lambda_a g-\lambda_a(1-g)\frac{\langle k_a^2\rangle}{\langle k_a\rangle}\right)\left(1-\lambda_b g-\lambda_b(1-g)\frac{\langle k_b^2\rangle}{\langle k_b\rangle}\right)+ \\ &\quad \lambda_a\lambda_b(1-g)^2\langle k_a\rangle\langle k_b\rangle. \end{aligned} \tag{16}$$

Hence, the epidemic dies out if and only if $\Delta_x < 0$ hold for all $x = 1, 2, 3$. Notice that $\Delta_x, x = 1, 2$ decrease with g, then from $\Delta_x = 0$ for $x = 1, 2$, one

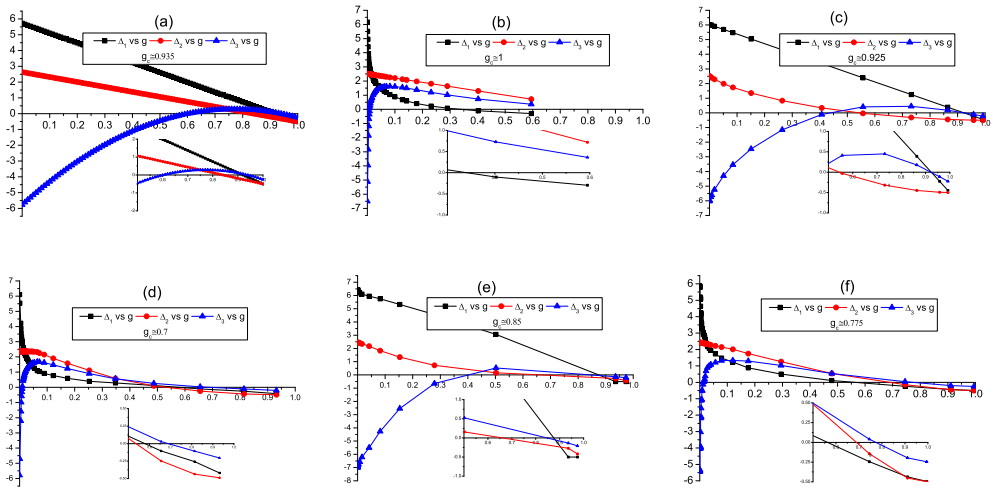

Figure 3: Plots of Δ_x ($x = 1, 2, 3$ as defined in Eq. (16)) as functions of the immunization fraction g. Six Panels correspond to different immunization schemes: The random immunization (a), the targeted immunization form (i) (b), (ii) (c), (iii) (d), (iv) (e) and (v) (f). In a multiplex network, layer A is a Barabási-Albert (BA) scale-free network [27] with degree distribution $p(k) \sim k^{-3}$ and average degree $\langle k \rangle = 6$, while layer B is an Erdös-Rényi (ER) network with connecting probability $p = 0.006$ [28]. In each panel, the inset shows the zoom in results for a small range and all simulations assume $\lambda_a = \lambda_b = 0.5$. In addition, it is assumed that $\kappa_a = \kappa_b$ for the targeted immunization (iii) and (iv).

can determine two critical values $g_{c,x}$, $x = 1, 2$ for the immunization rate g when infection rates λ_a and λ_b are given. Furthermore, when $g \geq \max\{g_{c,1}, g_{c,2}\}$, the immunization threshold g_c can be derived by solving $\Delta_3 = 0$. Similar notations and analysis can be made for the targeted immunization.

In Fig. 3, the immunization thresholds g_c for different immunization strategies are shown when $\lambda_a = \lambda_b = 0.5$. One can read that the random immunization is not effective since the immunization threshold $g_c \simeq 1$. We also find that the targeted immunization based on hub nodes in one layer is not very effective, regardless of the heterogeneity of the network layer. In contrast, other targeted immunization schemes shown in the second row of Fig. 3 are much more effective. Moreover, the most effective immunization strategy is the targeted immunization (iii), i.e, all the nodes with degree $k_a > \kappa_a$ or $k_b > \kappa_b$ are removed. This indicates that hub nodes to be immunized should include all layers rather than one layer.

3.2. The layer node-based immunization

In the layer node-based immunization, each immunized node can not get infected from or transmit pathogen to nodes in a certain layer while in the meantime still can be infected by or infect nodes in other layers [19, 16, 17]. In other words, the immunization strategy is only implemented in one layer. This kind of immunization is different from the asymmetrical interaction on two-layer networks [33, 34] but similar to the immunization in a single network [15, 35]. Hence, the layer node-based immunization is more simpler than the multiplex node-based immunization.

Without loss of generality, we assume that the immunization is implemented in layer A. Then, the epidemic dynamics are described by

$$\frac{d\rho_{k_a,l_a,k_b,l_b}}{dt} = -\rho_{k_a,l_a,k_b,l_b} + (1-\rho_{k_a,l_a,k_b,l_b})(\lambda_a l_a \theta_a + \lambda_b k_b \theta_b).$$

Similar analysis to that in the above section gives the condition of epidemic outbreak

$$\frac{\lambda_a\lambda_b\langle l_a k_b\rangle^2}{\langle l_a\rangle\langle k_b\rangle} > \left(1-\lambda_a\frac{\langle {l_a}^2\rangle}{\langle l_a\rangle}\right)\left(1-\lambda_b\frac{\langle {k_b}^2\rangle}{\langle k_b\rangle}\right). \tag{17}$$

By using **assumption A2**, we can simplify Eq. (17) into the following form

$$\lambda_a\lambda_b\langle l_a\rangle\langle k_b\rangle > \left(1-\lambda_a\frac{\langle {l_a}^2\rangle}{\langle l_a\rangle}\right)\left(1-\lambda_b\frac{\langle {k_b}^2\rangle}{\langle k_b\rangle}\right). \tag{18}$$

Next, we consider a specific immunization strategy by taking the random immunization as an example. In the case of random immunization, a fraction g of nodes are removed, that is, in layer A, for the node with old degree k_a, its neighbors are immunized with rate g uniformly. Then

$$p(l_a|k_a) = \binom{k_a}{l_a} g^{k_a-l_a}(1-g)^{l_a}.$$

Hence $\langle l_a\rangle = (1-g)\langle k_a\rangle$ and $\langle l_a^2\rangle = (1-g)g\langle k_a\rangle + (1-g)^2\langle k_a^2\rangle$. Plugging these into (18), we obtain the epidemic threshold for the layer node-based random immunization

$$\lambda_a\lambda_b(1-g)\langle k_a\rangle\langle k_b\rangle > \left(1-\lambda_a g-\lambda_a(1-g)\frac{\langle {k_a}^2\rangle}{\langle k_a\rangle}\right)\left(1-\lambda_b\frac{\langle {k_b}^2\rangle}{\langle k_b\rangle}\right).$$

4. Discussions

In this paper, we investigate two problems: (i) the epidemic spreading of an SIS model on multiplex networks; and (ii) the immunization of an SIS model on multiplex networks. These two issues are basic and important for the spreading dynamics and disease control on networks. Motivated by previous work [6, 24], we utilize the HMF theory with multiple degree to solve these issues.

We analytically derive the explicit condition of epidemic outbreak through analyzing the self-consistency equation together with the monotonicity of spectral radius of nonnegative matrices. Furthermore, we propose a general framework that allows us to investigate the immunization strategy of SIS models on multiplex networks. This framework includes not only the old degree information before immunization, but also the new degree information after immunization, therefore it allows us to study some general immunization problems.

As we know, the immunization of SIR models on multiplex networks has been studied by the percolation theory [16, 19, 17]. However, the immunization of SIS models on multiplex networks has not been explored in previous studies but deserves detailed investigations as some diseases, such as the common cold, are more appropriately described by an SIS compartmental model. Hence the present research fills this gap. Although our work only focuses on the multiplex network with two layers, the proposed approach can be used for general cases with many layers. We also expect our approach to be extended to the immunization of the partially overlapped multiplex networks [11] and the interconnected networks [6, 36].

Acknowledgments

Q.W. would like to thank National Natural Science Foundation of China for its support under No. 61203153. Y.L. is supported in part by NSFC (11301442) and RGC (PolyU 253004/14P). We thank the referees for their supportive comments which highly improve the whole manuscript.

References

[1] M. Salehi, P. Siyari, M. Magnani, et al., Multidimensional epidemic thresholds in diffusion processes over interdependent networks, Chaos, Solitons & Fractals 72 (2015) 59-67.

[2] Y. Min, J. Hu, W. Wang, et al., Diversity of multilayer networks and its impact on collaborating epidemics, Phys. Rev. E 90(6) (2014) 062803.

[3] A. Vespignani, Complex networks: The fragility of interdependency, Nature 464(7291) (2010) 984-985.

[4] S. Boccaletti, G. Bianconi, R. Criado, et al., The structure and dynamics of multilayer networks, Phys. Rep. 544(1) (2014) 1-122.

[5] M. Dickison, S. Havlin and H. E. Stanley, Epidemics on interconnected networks, Phys. Rev. E 85 (2012) 066109.

[6] A. Saumell-Mendiola, M. Serrano and M. Boguna, Epidemic spreading on interconnected networks, Phys. Rev. E 86 (2012) 026106.

[7] R. Pastor-Satorras and A. Vespignani, Epidemic spreading in scale-free networks, Phys. Rev. Lett. 86 (2001) 3200.

[8] G. H. Zhu, X. C. Fu, Q. Tang, et al., Mean-field modeling approach for understanding epidemic dynamics in interconnected networks, Chaos, Solitons & Fractals 80 (2015) 117-124.

[9] P. van den Driessche and J. Watmough, Reproduction numbers and subthreshold endemic equilibria for compartmental models of disease transmission, Math. Biosci. 180 (2002) 29-48.

[10] K. M. Lee, B. Min and K. I. Goh, Towards real-world complexity: An introduction to multiplex networks, Eur. Phys. J. B 88(2) (2015) 1-20.

[11] C. Buono, L. G. Alvarez-Zuzek, P. A. Macri, et al., Epidemics in partially overlapped multiplex networks, PloS one 9(3) (2014) 5.

[12] S. Gómez, A. Arenas, J. Borge-Holthoefer, S. Meloni and Y. Moreno, Discrete-time Markov chain approach to contact-based disease spreading in complex networks, Europhys. Lett. 89 (2010) 38009.

[13] Q. C. Wu, H. F. Zhang, M. Small and X. C. Fu, Threshold analysis of the susceptible-infected-susceptible model on overlay networks, Commun. Nonlinear Sci. Numer. Simul. 19(7) (2014) 2435-2443.

[14] F. D. Sahneh and C. Scoglio, Competitive epidemic spreading over arbitrary multilayer networks, Phys. Rev. E 89(6) (2014) 062817.

[15] R. Pastor-Satorras and A. Vespignani, Immunization of complex networks, Phys. Rev. E 65 (2002) 036104.

[16] C. Buono and L. A. Braunstein, Immunization strategy for epidemic spreading on multilayer networks, Europhys. Lett. 109(2) (2015) 26001.

[17] L. G. A. Zuzek, C. Buono and L. A. Braunstein, Epidemic spreading and immunization strategy in multiplex networks, arXiv preprint:1507.01837, 2015.

[18] D. W. Zhao, L. X. Li, H. P. Peng, Q. Luo and Y. X. Yang, Multiple routes transmitted epidemics on multiplex networks, Phys. Lett. A 378(10) (2014) 770-776.

[19] D. W. Zhao, L. H. Wang, S. D. Li, Z. Wang, L. Wang and B. Gao, Immunization of epidemics in multiplex networks, PloS one 9(11) (2014) e112018.

[20] X. C. Fu, M. Small, D. M. Walker and H. F. Zhang, Epidemic dynamics on scale-free networks with piecewise linear infectivity and immunization, Phys. Rev. E 77 (2008) 036113.

[21] I. Z. Kiss, D. M. Green and R. R. Kao, The effect of contact heterogeneity and multiple routes of transmission on final epidemic size, Math. Biosci. 203(1) (2006) 124-136.

[22] S. Funk and V. A. A. Jansen, Interacting epidemics on overlay networks, Phys. Rev. E 81 (2010) 036118.

[23] R. Pastor-Satorras and A. Vespignani, Epidemic dynamics in finite size scale-free networks, Phys. Rev. E 65 (2002) 035108(R).

[24] J. Sanz, C. Y. Xia, S. Meloni, et al., Dynamics of interacting diseases, Phys. Rev. X 4(4) (2014) 041005.

[25] J. Z. Wang and Z. R. Liu, Mean-field level analysis of epidemics in directed networks, J. Phys. A: Math. Theor. 42 (2009) 355001.

[26] X. G. Zhang, G. Q. Sun, J. L. Ma and Z. Jin, Epidemic dynamics on on semi-directed complex networks, Math. Biosci. 246(2) (2013) 242-251.

[27] A. L. Barabási and R. Albert, Emergence of scaling in random networks, Science 286(5439) (1999) 509-512.

[28] P. Erdös and A. Rényi, On the evolution of random graphs, Publ. Math. Inst. Hung. Acad. Sci 5 (1960) 17-61.

[29] C. Li, R. van de Bovenkamp and P. van Mieghem, Susceptible-infected-susceptible model: A comparison of N-intertwined and heterogeneous mean-field approximations, Phys. Rev. E 86(2) (2012) 026116.

[30] S. C. Ferreira, C. Castellano and R. Pastor-Satorras, Epidemic thresholds of the susceptible-infected-susceptible model on networks: A comparison of numerical and theoretical results, Phys. Rev. E 86(4) (2012) 041125.

[31] Q. C. Wu and X. C. Fu, Immunization and epidemic threshold of an SIS model in complex networks, Physica A 444(15) (2016) 576-581.

[32] M. Boguna, R. Pastor-Satorras and A. Vespignani, Absence of epidemic threshold in scale-free networks with degree correlations, Phys. Rev. Lett. 90 (2003) 028701.

[33] H. H. Jo, H. T. Moon and S. K. Baek, Immunization dynamics on a 2-layer network model, Physica A 361(2) (2006) 534-542.

[34] W. Wang, M. Tang, H. Yang, Y. Do, Y. C. Lai and G. Lee, Asymmetrically interacting spreading dynamics on complex layered networks, Sci. Rep. 4 (2014) 5097.

[35] N. Madar, T. Kalisky, R. Cohen, D. ben-Avraham and S. Havlin, Immunization and epidemic dynamics in complex networks, Eur. Phys. J. B 38(2) (2004) 269-276.

[36] F. D. Sahneh, C. Scoglio and F. N. Chowdhury, Effect of coupling on the epidemic threshold in interconnected complex networks: A spectral analysis, American Control Conference (ACC), IEEE (2013) 2307-2312.