Multiple routes transmitted epidemics on multiplex networks

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Abstract. This letter investigates the multiple routes transmitted epidemic process on multiplex networks. We propose detailed theoretical analysis that allows us to accurately calculate the epidemic threshold and outbreak size. It is found that the epidemic can spread across the multiplex network even if all the network layers are well below their respective epidemic thresholds. Strong positive degree-degree correlation of nodes in multiplex network could lead to a much lower epidemic threshold and a relatively smaller outbreak size. However, the average similarity of neighbors from different layers of nodes has no obvious effect on the epidemic threshold and outbreak size.

Keyword. Multiple transmission routes, Multiplex network, Epidemic threshold, Outbreak size, Percolation theory.

§1 Introduction

In recent years, various types of epidemics have occurred frequently and spread around the world, causing not only great economic losses, but also widespread public alarms. For example, the intense outbreak of SARS caused 8,098 reported cases and 774 deaths. Within weeks, SARS spread from Hong Kong to infect individuals in 37 countries in early 2003 [1]. An outbreak of mobile viruses occurred in China in 2010. The ‘Zombie’ virus attacked more than 1 million smart phones, and created a loss of $300,000 per day [2]. And we have also witnessed how social networks being used for citizens to share information and gain international support in the Arab Spring [3]. In view of these situations, it is thus urgent and essential to have a better understanding of epidemic process, and to design effective and efficient mechanisms for the restraint or acceleration of epidemic spreading.

Valid epidemic spreading models can be used to estimate the scale of an epidemic outbreak before it actually occurs in reality and evaluate new and/or improved countermeasures for the

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restraint or acceleration of epidemic spreading. In the last decade, there have been extensive studies on the modeling of epidemic dynamics [4-10], and various protection strategies have been proposed and evaluated [11-18]. However, these existing researches have been dominantly focusing on the cases that epidemics spread through only single transmission route. While in reality, many epidemics can spread through multiple transmission routes [19] simultaneously. For example, it has been well recognized that AIDS can propagate via three routes simultaneously including sexual activity, blood and breast milk; rumor or information can spread among human through verbal communication and social networks; malwares can move to computers by P2P file share, email, random-scanning and instant messenger [20]; and some mobile malwares can attack smart phones through both short messaging service (SMS) and bluetooth (BT) at the same time [21]. In this letter, the epidemic which spreads via single transmission route and multiple transmission routes are called single route transmitted epidemic and multiple routes transmitted epidemic, respectively. When a multiple routes transmitted epidemic spreading on a network, the network node could be infected via one of the transmission routes even if it cannot be infected via the other routes. And the node can be infected with a higher probability if it can be infected via more than one transmission route of the epidemic. Therefore, the range and the intensity of the multiple routes transmitted epidemic will be greater than those of the traditional single route transmitted epidemic. Meanwhile, different transmission routes are supported by different networks. For instance, the underlying network of the mobile malware which propagates via SMS is a SMS network formed based on the social relationships among mobile users. And the BT network formed according to the geographically positions of mobile devices is the underlying network of the mobile malware which can spread through BT. Therefore, the underlying network of the multiple routes transmitted epidemic is actually a multiplex network [22-25], rather than a single network. Multiplex network can be regarded as a set of coupled layered networks in which each layer could have very particular features different from the rest and support different dynamical processes. Based on the above analyses, the study of multiple routes transmitted epidemic on multiplex network is definitely a very meaningful and necessary topic.

To the best of our knowledge, the theory describing the multiple routes transmitted epidemic process on multiplex network has not been fully developed yet. In this letter, we propose and evaluate a two routes transmitted epidemic spreading on multiplex network with two network layers following the typical Susceptible-Infected-Removed (SIR) model [6,7]. But the proposed research methods can be easily extended to analyze the epidemics which spread via any number of transmission routes. By mapping the SIR model into the bond percolation [7], we develop equations which allow accurate calculations of epidemic threshold [6] of the multiplex network and outbreak size [6] of the epidemic. It is found that the epidemic can spread across the multiplex network even if the two network layers are well below their respective epidemic thresholds. We also introduce two quantities for measuring the level of inter-similarity between these two layers. One is the average similarity of neighbors (ASN) from different layers of nodes. ASN evaluates how many neighbors of nodes in one layer are also their neighbors in another layer. We find that both epidemic threshold and outbreak size are not significantly affected by the
Table 1: Symbols used in this letter and their meanings.

| Symbols | Meanings |
|---------|----------|
| ASN     | Average similarity of neighbors from different layers of nodes. |
| DDC     | Correlation of nodes’ degrees in one layer and that in another layer. |
| $\lambda_A$ | The probability that a susceptible node is infected only via route-A. |
| $\lambda_B$ | The probability that a susceptible node is infected only via route-B. |
| $\lambda_C$ | The probability that a susceptible node is infected via route-A and route-B simultaneously. |
| $(\lambda_A, \lambda_B)$ | The spreading rate of a two routes transmitted epidemic, where $\lambda_A$ and $\lambda_B$ are the spreading rates of this epidemic when spreading on layer-A and layer-B, respectively. |
| $k_A$ | Degree of node in layer-A. |
| $k_B$ | Degree of node in layer-B. |
| $k_C$ | The number of same neighbors of node in layer-A and layer-B. |
| $k_M$ | Vector degree of node on multiplex network. |
| $\{\lambda_A, \lambda_B\}_c$ | Epidemic threshold of multiplex network with two layers. |
| $s$ | Outbreak size of epidemic. |

ASN. The second quantity is the degree-degree correlation (DDC) of nodes which describes the correlation of nodes’ degrees in one layer and that in another layer. Positive DDC indicates that high degree nodes in one layer are also high degree ones in another layer, and vice versa. It is found that strong positive DDC could lead to a clearly lower epidemic threshold and a relatively smaller outbreak size.

Some symbols used throughout this letter and their meanings are summarized in Table 1.

\section{2 Models and analysis}

\subsection{2.1 Multiple routes transmitted epidemic spreading model}

The epidemic spreading model adopted here is the Susceptible-Infected-Removed (SIR) model which is the most basic and well-studied epidemic spreading model \cite{6,7}. In the SIR model, the nodes of the network can be divided into three compartments, including susceptibles (S, those who are prone to be infected), infectious (I, those who have been infected), and recovered (R, those who have recovered from the disease). At each time step, a susceptible node becomes infected with probability $\lambda$ if it is directly connected to a infected node. The parameter $\lambda$ is called the spreading rate. Meanwhile, an infected node becomes a recovered node with probability $\delta$.

In this letter, what we study is a simple case that a two routes transmitted epidemic spreads among network individuals. Therefore, we need to specify the corresponding epidemic spreading processes separately. It is assumed that these two transmission routes of the epidemic are route-A and route-B, respectively. Then we assume that a susceptible node becomes infected with probability $\lambda_A$ or $\lambda_B$ if it can be infected only through route-A or route-B. Besides, if a susceptible node can be infected via route-A and route-B simultaneously, the probability that this susceptible node becomes infected is assumed to be $\lambda_C$. Obviously, $\lambda_C = 1 - (1 - \lambda_A)(1 - \lambda_B)$. 

Meanwhile, an infected node becomes a recovered node with probability $\delta$. Without loss of generality, we let $\delta = 1$.

### 2.2 Multiplex networks model

Since different transmission routes are supported by different networks, the underlying network of a two routes transmitted epidemic should be a multiplex network with two network layers. In this section, as shown in Fig.1(a), we propose a multiplex network model which contains two network layers, i.e., layer-$A$ and layer-$B$. Nodes are the same in both layers, and layer-$A$ and layer-$B$ are the underlying networks of the epidemic spreading via route-$A$ and route-$B$, respectively. Fig.1(b) shows this multiplex network in the form of the superposition of layer-$A$ and layer-$B$. In the rest of this paper, the multiplex network, unless otherwise noted, is assumed to be the network in the form of the superposition of layer-$A$ and layer-$B$.

![Figure 1: (Color online) (a) A multiplex network with two network layers, i.e., layer-$A$ and layer-$B$. (b) The multiplex network in the form of the superposition of layer-$A$ and layer-$B$.](image)

Each node in the proposed multiplex network has up to three types of edges where edge-$A$ belongs only to layer-$A$, edge-$B$ belongs only to layer-$B$, and edge-$C$ belongs to both layer-$A$ and layer-$B$. The vector degree $k_M \equiv (k_A - k_C, k_B - k_C, k_C)$ is used to characterize the node of multiplex network, where $k_A - k_C$, $k_B - k_C$ and $k_C$ represent the numbers of edge-$A$, edge-$B$ and edge-$C$ of the node, respectively. The numerical value of vector degree of the node is defined by $|k_M| = k_A + k_B - k_C$. For instance, the vector degree of node 3 in Fig.1 is $k_M \equiv (4 - 1, 2 - 1, 1)$ and its numerical value is 5.

Actually, for the vector degree of node in multiplex network, $k_C$ evaluates how many neighbors of the nodes in layer-$A$ are also their neighbors in layer-$B$ which can affect the topology of the multiplex network. Here, we develop a measure, $\alpha$, to assess the average similarity of the neighbors (ASN) from different layers of nodes in the multiplex network and it is defined as

$$\alpha = \frac{\sum_i k_C(i)}{\sum_i |k_M(i)|};$$

(1)
where \( k_C(i) \) and \( |k_M(i)| \) are the values of \( k_C \) and \( |k_M| \) of node \( i \) of the multiplex network, respectively. For increasing values of \( \alpha \), more of the neighbors of nodes in one layer are also their neighbors in another layer and these two layers become more similar. For \( \alpha = 1 \), these two layers must be identical.

For the node of the multiplex network, it may be a high degree node in layer-\( A \) and a low degree one in layer-\( B \), or a high degree node in layer-\( A \) and also a high degree one in layer-\( B \). The influence of the correlation of nodes' degrees in one layer and that in another layer for the multiple routes transmitted epidemic dynamics is one of our main research problems. Analogously to the degree correlation in the single network [26,27] and the network assortativity in interconnected networks [10], we define the degree-degree correlation (DDC) of the nodes in multiplex network as follows

\[
\beta = \frac{\sum_{k_A} \sum_{k_B} (k_A k_B p(k_A, k_B) - (\sum_{k_A} p(k_A, k_B))(\sum_{k_B} p(k_A, k_B)))}{\sum_{k_B} k_B^2 \sum_{k_A} p(k_A, k_B) - (\sum_{k_B} \sum_{k_A} p(k_A, k_B))^2},
\]

(2)

where \( p(k_A, k_B) \) denotes the probability that a randomly chosen node of multiplex network has degree \( k_A \) in layer-\( A \) and \( k_B \) in layer-\( B \). The two layers are said to be negative correlation if \( \beta < 0 \), positive correlation if \( \beta > 0 \), and uncorrelation if \( \beta = 0 \).

### 2.3 Calculations of epidemic threshold

The traditional epidemic threshold [6] of the single network is a value, \( \lambda_c \), above which the epidemic will spread to the whole network, i.e., the infected nodes will form into a giant component. Otherwise, the epidemic outbreak will not affect a finite portion of the nodes and will die out in a finite time. However, unlike the epidemic threshold of the single network, the epidemic threshold of the multiplex network with \( M \) layers should be a set of \( M \)-dimensional points, \( \{ (\lambda_1, \lambda_2, ..., \lambda_M)_c \} \). The multiplex network with two layers is taken as an example. As shown in Fig.2, the epidemic threshold of the two-layers network is a set of 2-dimensional points, \( \{ (\lambda_A, \lambda_B)_c \} \). For a two routes transmitted epidemic with spreading rate \( (\lambda_A, \lambda_B) \), where \( \lambda_A \) and \( \lambda_B \) are the spreading rates of this epidemic when spreading on layer-\( A \) and layer-\( B \) respectively, if \( (\lambda_A, \lambda_B) \) is a point in the grey shaded area of Fig.2, this two routes transmitted epidemic can spread across the multiplex network. Otherwise, it will not affect a finite portion of the nodes and will die out in a finite time.

In this section, by using the SIR model and the bond percolation theory [7], we propose detailed theoretical analysis that allows us to accurately calculate the epidemic threshold of multiplex network. Traditionally the percolation process is parametrized by a probability \( \varphi \), which is the probability that a node is functioning in the network. In technical terms of percolation theory, one says that the functional nodes are occupied and \( \varphi \) is called the occupation probability. Through only slight modifications, the general SIR model can be perfectly mapped into the bond percolation in complex networks where the spreading rate corresponds to the probability that a link is occupied in percolation [7,10]. Therefore, for the multiplex network with two layers, we can assume that the three types of edges, edge-\( A \), edge-\( B \) and edge-\( C \) are
Figure 2: (Color online) The solid line connected with circles indicates the epidemic threshold of a two layers networks whose two layers are an ER network comprised of 2000 nodes with average degree 2.858 and an ER network comprised of 2000 nodes with average degree 1.891, respectively. If the spreading rate \((\lambda_A, \lambda_B)\) of a two routes transmitted epidemic is a point belonging to the grey shaded area, this epidemic can spread across the multiplex network. Otherwise, it will not affect a finite portion of the nodes and will die out in a finite time.

occupied at the probabilities of \(\lambda_A, \lambda_B\) and \(\lambda_C\) respectively.

Let \(h_A(x)\) \((h_B(x), h_C(x))\) be the generating function [27,28] for the distribution of the sizes of components which are reached by an edge with type of edge-\(A\) (edge-\(B\), edge-\(C\)) and following it to one of its ends. Then we have

\[
h_A(x) = 1 - \lambda_A + x\lambda_A \sum_{k_M, k_A \geq 1} \frac{|k_M| p_{k_M} h_A^{k_A - k_C}(x) h_B^{k_B - k_C}(x) h_C^{k_C}(x)}{\sum_{k_M} |k_M| p_{k_M}},
\]

\[
h_B(x) = 1 - \lambda_B + x\lambda_B \sum_{k_M, k_B \geq 1} \frac{|k_M| p_{k_M} h_A^{k_A}(x) h_B^{k_B - k_C - 1}(x) h_C^{k_C}(x)}{\sum_{k_M} |k_M| p_{k_M}},
\]

\[
h_C(x) = 1 - \lambda_C + x\lambda_C \sum_{k_M, k_C \geq 1} \frac{|k_M| p_{k_M} h_A^{k_A}(x) h_B^{k_B}(x) h_C^{k_C - 1}(x)}{\sum_{k_M} |k_M| p_{k_M}},
\]

where \(p_{k_M}\) denotes the probability that a randomly chosen node of the multiplex network has the vector degree \(k_M\). Later the size of the component formed by infected nodes will be called the outbreak size.

Generally, an epidemic always starts from a network node, not an edge, therefore we proceed to analyze the outbreak size distribution for epidemic sourced from a randomly selected node. If we start at a randomly chosen node in multiplex network, then we have one such outbreak size at the end of each edge leaving that node, and hence the generating function for the outbreak
size caused by a network node is
\[ H(x) = x \times \sum_{k_M} p_{k_M} h_A^{k_A-k} (x) h_B^{k_B-k} (x) h_C^{k_C} (x). \]  

(6)

Although it is usually impossible to find a closed-form expression for the complete distribution of outbreak size in a network, we can find closed-form expressions for the average outbreak size of an epidemic in multiplex network from Eqs.(6). This average outbreak size can be derived by taking derivatives of Eqs.(6) at \( x = 1 \), and then we have
\[ < s > = H'(1) = 1 + \sum_{k_M} p_{k_M} (k_A - k_C) h_A'(1) + \sum_{k_M} p_{k_M} k_C h_C'(1). \]

(7)

In Eq.(7), the functions \( h_A'(1) \), \( h_B'(1) \) and \( h_C'(1) \) can be derived from Eqs.(3)-(5). Taking derivatives on both sides of Eqs.(3)-(5) at \( x = 1 \), we have
\[ h_A'(1) = \lambda_A + \lambda_A < k_M > -1 (m_{11} h_A'(1) + m_{12} h_B'(1) + m_{13} h_C'(1)), \]
\[ h_B'(1) = \lambda_B + \lambda_B < k_M > -1 (m_{21} h_A'(1) + m_{22} h_B'(1) + m_{23} h_C'(1)), \]
\[ h_C'(1) = \lambda_C + \lambda_C < k_M > -1 (m_{31} h_A'(1) + m_{32} h_B'(1) + m_{33} h_C'(1)), \]

(8)
(9)
(10)

where
\[ < k_M > = \sum_{k_M} |k_M| p_{k_M}, \]
\[ m_{11} = \sum_{k_M,k_A-k_C \geq 1} |k_M| p_{k_M} (k_A - k_C - 1), \]
\[ m_{12} = \sum_{k_M,k_A-k_C \geq 1} |k_M| p_{k_M} (k_B - k_C), \]
\[ m_{13} = \sum_{k_M,k_A-k_C \geq 1} |k_M| p_{k_M} k_C, \]
\[ m_{21} = \sum_{k_M,k_B-k_C \geq 1} |k_M| p_{k_M} (k_A - k_C), \]
\[ m_{22} = \sum_{k_M,k_B-k_C \geq 1} |k_M| p_{k_M} (k_B - k_C - 1), \]
\[ m_{23} = \sum_{k_M,k_B-k_C \geq 1} |k_M| p_{k_M} k_C, \]
\[ m_{31} = \sum_{k_M,k_C \geq 1} |k_M| p_{k_M} (k_A - k_C), \]
\[ m_{32} = \sum_{k_M,k_C \geq 1} |k_M| p_{k_M} (k_B - k_C), \]
\[ m_{33} = \sum_{k_M,k_C \geq 1} |k_M| p_{k_M} (k_C - 1). \]

From Eqs.(8)-(10), we have
\[ M h = - < k_M > e, \]

(11)

where
\[ M = \begin{pmatrix} -\lambda_A^{-1} < k_M > + m_{11} & m_{12} & m_{13} \\ m_{21} & -\lambda_B^{-1} < k_M > + m_{22} & m_{23} \\ m_{31} & m_{32} & -\lambda_C^{-1} < k_M > + m_{33} \end{pmatrix}. \]
\[ h = (h'_A(1) \ h'_B(1) \ h'_C(1))^T, \] and \[ e = (1 \ 1 \ 1)^T. \] Therefore, \( h'_A(1), h'_B(1), h'_C(1) \) diverge at the point where

\[ \det M = 0. \quad (12) \]

The solution of Eq.\((12)\) yields a set of different critical 2-dimensional points as \( \{(\lambda_A, \lambda_B)\} \), above any of which (like the points belonging to the grey shaded area of Fig.2) \( \langle s \rangle \) will diverge, i.e., the epidemic can spread to the whole network.

Therefore, through above analysis we can see that the epidemic threshold of the multiplex network with two layers is a set of 2-dimensional points as \( \{(\lambda_A, \lambda_B)\} \), where \( (\lambda_A, \lambda_B) \) satisfies Eq.\((12)\).

### 2.4 Calculations of outbreak size

If a two routes transmitted epidemic with spreading rates \( (\lambda_A, \lambda_B) \) can spread across a multiplex network, the infected nodes will form into a giant component. Let \( u_A, u_B \) and \( u_C \) be the average probabilities that a node is not connected to the giant component via edge-\( A \), edge-\( B \) and edge-\( C \), respectively. According to percolation theory, there are two ways that may occur: either the edge in question can be unoccupied, or it is occupied but the node at the other end of the edge is itself not a member of the giant component. The latter happens only if that node is not connected to the giant component via any of its other edges. Thus, we have

\[ u_A = 1 - \lambda_A + \lambda_A \times \sum_{k_M, k_A - k_C \geq 1} |k_M| |p_{k_M} u_A^{k_A - k_C - 1} u_B^{k_B - k_C} u_C^{k_C} |, \quad (13) \]

\[ u_B = 1 - \lambda_B + \lambda_B \times \sum_{k_M, k_B - k_C \geq 1} |k_M| |p_{k_M} u_A^{k_A} u_B^{k_B - k_C - 1} u_C^{k_C} |, \quad (14) \]

\[ u_C = 1 - \lambda_C + \lambda_C \times \sum_{k_M, k_C \geq 1} |k_M| |p_{k_M} u_A^{k_A - k_C} u_B^{k_B - k_C} u_C^{k_C} |. \quad (15) \]

Therefore, the outbreak size of the two routes transmitted epidemic over the multiplex network can be calculated by

\[ s = 1 - \sum_{k_M} p_{k_M} u_A^{k_A - k_C} u_B^{k_B - k_C} u_C^{k_C}. \quad (16) \]

It is worth to notice that the traditional single route transmitted epidemic process on single network can be regarded as a special case of multiplex routes transmitted epidemic process on multiplex network. When layer-\( A \) is regarded as a single network, the epidemic threshold \( \lambda_{Ac} = \langle k_A \rangle / (\langle k_A^2 \rangle - \langle k_A \rangle) \) \([7]\) and the outbreak size \( s = 1 - \sum_{k_A} p_{k_A} u_A^{k_A} \) \([7]\) can be obtained from Eq.\((12)\) and Eq.\((16)\) when we let \( k_B = 0 \). That is to say, the results of this letter are accurate and applicable in a more general situation.
§3 Simulation results and discussions

In this section, we show the theoretical calculation methods of the epidemic threshold and the outbreak size proposed in Section 2 is accurate and reasonable by the comparison between the theoretical values and the experimental results. Three different types of multiplex network with two layers are constructed where (i) both of these two layers are scale-free (SF) networks, denoted by SF-SF; (ii) one layer is Erdős-Rényi (ER) random network and the other one is SF network, denoted by ER-SF; and (iii) both of these two layers are ER random networks, denoted by ER-ER. We use ‘X(\(a, b\))’ to describe a network layer, where ‘X’ refers to the network type, ‘\(a\)’ is the network size and ‘\(b\)’ is the average degree. For example, SF(2000,3) denotes a SF network comprised of 2000 nodes with average degree 3. Each given simulation result is averaged over 500 realizations.

3.1 Epidemic threshold and outbreak size

In Fig.3(a, b and c), the numerically simulated outbreak sizes of the two routes transmitted epidemic with spreading rate (\(\lambda_A, \lambda_B\)) are color coded, and the solid black lines indicate the theoretical epidemic threshold of the multiplex network calculated according to Eq.(12). We can see that the outbreak size is a relatively large value, that is, the infected nodes form into a giant component, when the spreading rate (\(\lambda_A, \lambda_B\)) of the epidemic is a point above the solid black line. Instead, the outbreak size is a very small value when the spreading rate (\(\lambda_A, \lambda_B\)) is below the solid black line which means that the theoretical epidemic threshold of the multiplex network calculated according to Eq.(12) is accurate in judging the epidemic state. In order to better describe the accurate degree of the theoretical epidemic threshold, panel d, e and f of Fig.3 show four longitudinal sections of panel a, b and c, respectively, where \(\lambda_{Bc}\) can be regarded as the epidemic threshold of the multiplex network when \(\lambda_A\) are set to some fixed values. It can also be found that the epidemic could spread across the multiplex network even if these two layers are well below their respective epidemic thresholds. The multiplex network ER(2000,5.922)-ER(2000,5.965) shown in Fig.3(c), is taken as an example. Since the epidemic threshold of ER network is \(1/\langle k\rangle\) [6] when following the SIR model, where \(\langle k\rangle\) is the average degree of the network, we can calculate that the epidemic thresholds of the layers ER(2000,5.922) and ER(2000,5.965) are \(1/5.922 \approx 0.169\) and \(1/5.965 \approx 0.168\) respectively when they are regarded as single networks. However, from Fig.3(c) we can see that the outbreak size of the epidemic is 0.3 if the spreading rate is \((0.12 < 0.169, 0.12 < 0.168)\), and 0.45 if the spreading rate is \((0.14 < 0.169, 0.15 < 0.168)\), and etc. These illustrate that the epidemic can infect a large number of nodes of the multiplex network even if these two layers are well below their respective epidemic thresholds.

Fig.4 shows the numerically simulated and the theoretical outbreak sizes of the epidemic as a function of \(\lambda_B\) when \(\lambda_A\) are set to some fixed values. The theoretical results are calculated according to Eq.(16). From Fig.4 we can see that theoretical results are in good agreement with the experimental results.
Figure 3: (Color online) Panel a, b and c show theoretical epidemic threshold of the multiplex network calculated according to Eq.(12) (solid black line) and the numerically simulated outbreak sizes of the epidemic with spreading rate \((\lambda_A, \lambda_B)\) (color coded). Panel d, e and f show four longitudinal sections of panel a, b and c, respectively. Three multiplex networks are (a,d) SF(2000,3.997)-SF(2000,3.998), (b,e) ER(2000,5.883)-SF(2000,3.997) and (c,f) ER(2000,5.922)-ER(2000,5.965), respectively.

Figure 4: (Color online) Numerically simulated and theoretical outbreak sizes of the epidemic as a function of \(\lambda_B\) when \(\lambda_A\) are set to some fixed values. Three multiplex networks are (a) SF(2000,3.997)-SF(2000,3.998), (b) ER(2000,5.883)-SF(2000,3.997) and (c) ER(2000,5.922)-ER(2000,5.965), respectively.

3.2 ASN and DDC

In the real world, the nodes of the multiplex network may have some same neighbors in the two layers. In Section 2, we used a measure ASN to assess the average similarity of the neighbors
from different layers of nodes in the multiplex network. Another quantity DDC is also developed to describe the correlation of nodes’ degrees in one layer and that in another layer. While the topologies of the two layers remain unchanged, the topology of the multiplex network could be affected to some extent by the ASN and DDC, and may ultimately impact the processes of the epidemic over it.

It is easy to achieve any targeted value of ASN for SF-SF and ER-ER. These two ER(SF) network layers can be obtained by randomly(preferentially) adding edges to a same ER(SF) network which has been constructed, respectively. The value of ASN is determined by the number of the edges added and the edges of the initial network. It is hard, however, to achieve a large range of ASN for ER-SF. Assume that the nodes have same tabs in each layer, then we can get some different values of ASN of ER-SF by randomly exchanging the tabs of nodes for one layer. In the ER-SF model shown in Figs.5(b,e), the value of ASN roughly lies in the interval [0.02 0.14], while for the SF-SF and ER-ER models, the corresponding intervals are all [0, 1].

In the following experiments, we assume the epidemic has the same spreading rates when propagates on the two layers, i.e., $\lambda_A = \lambda_B$. As shown in Fig.5, the epidemic threshold and the outbreak size are seldom affected by the ASN no matter what type of the multiplex network. This can be understood that when the topologies of the two layers remain unchanged, high ASN means nodes can affect much of their neighbors with the large spreading rate $\lambda_C$, but the average number of their neighbors is relatively small. Instead, although low ASN implies the nodes have more neighbors, most of the spreading rates between them and their neighbors are the relatively small $\lambda_A$ and $\lambda_B$. In such cases, the average number of new infected nodes at a time step may be equivalent no matter what the values of ASN.

Fig.6 shows the influences of DDC on the epidemic threshold and the outbreak size. Different values of DDC can be achieved by randomly exchanging the tabs of nodes of one layer. As shown in Fig.6, a higher DDC can lead to a much lower epidemic threshold and a relatively smaller outbreak size no matter what type of the multiplex network. The reasons can be explained as follows: high DDC means that high degree nodes in one layer are also high nodes in another layer and low degree nodes in one layer also low degree nodes in another layer, which leads to increasing differences between the degrees of nodes in the multiplex network. Instead, low DDC leads to decreased differences between the degrees of nodes in the multiplex network. That is, high DDC makes the SF-SF and ER-SF be the strengthened inhomogeneous networks and ER-ER a proximate inhomogeneous network, low DDC however makes the three types of multiplex network be the proximate homogeneous networks. It is known that [29], the epidemic in the inhomogeneous network has a faster spread since the existence of high degree nodes and smaller outbreak size since the low degree nodes are not prone to be infected, than in the homogeneous network when these two networks have the same average degrees. This theory perfectly explains the results of the experiments.
Figure 5: Epidemic threshold and outbreak size for epidemic spreading on (a,d) SF-SF; (b,e) ER-SF; and (c,f) ER-ER.

§4 Conclusions

In this letter, we demonstrated the dynamics of two routes transmitted epidemic spreading on multiplex network with two network layers following the SIR model. Our main contributions can be summarized as follows: (1) We presented the multiple routes transmitted system of epidemics and derived equations to accurately calculate the epidemic threshold and the outbreak size in the multiplex network. (2) We found that the epidemics could spread across the multiplex network even if the two layers are well below their respective epidemic thresholds. (3) We proposed two quantities for measuring the level of inter-similarity between two layers. ASN evaluates how many neighbors of nodes in one layer are also their neighbors in another layer which is found barely affect the epidemic threshold and the outbreak size. DDC describes the correlation of node’s degree in one layer and that in another layer. It is found that higher DDC could lead to much lower epidemic threshold and relatively smaller outbreak size.

Although we only consider the two routes transmitted epidemic process on multiplex network with two network layers, the proposed research methods are easily extended to analyze the epidemics which spread via any number of transmission routes. Our research provides useful tools and novel insights for further studies of dynamics of multiple routes transmitted epidemic spreading on the multiplex networks.
Figure 6: Epidemic threshold and outbreak size for epidemic spreading on (a,d) SF(2000,3.997)-SF(2000,3.995); (b,e) ER(2000,4.005)-SF(2000,3.997); and (c,f) ER(2000,5.950)-ER(2000,5.956).

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