Epidemics spreading in interconnected complex networks

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Abstract

We study epidemic spreading in two interconnected complex networks. It is found that in our model the epidemic threshold of the interconnected network is always lower than that in any of the two component networks. Detailed theoretical analysis is proposed which allows quick and accurate calculations of epidemic threshold and average outbreak/epidemic size. Theoretical analysis and simulation results show that, generally speaking, the epidemic size is not significantly affected by the inter-network correlation. In interdependent networks which can be viewed as a special case of interconnected networks, however, impacts of inter-network correlation on the epidemic threshold and outbreak size are more significant.

Keywords: Interconnected network, epidemic spreading, epidemic threshold, infection size

1. Introduction

Epidemic dynamics in complex networks has been under extensive studies [1–7], yielding, among many other results, deep insights into the effects of network structure on epidemic threshold and infection size. Such work however has been dominantly focusing on cases with a single network, while many real-life complex systems have to be conceptualized as multiple complex networks jointed together (hereafter termed as *interconnected* networks) [8]. For instance, the smart-grid systems integrate the electrical grid networks and the metering and control networks to save energy and enhance network reliability [9]; the wide deployments of smart phones may bridge between the Internet, cellular networks and Bluetooth networks, and consequently allow information/virus spreading over multiple networks. Other examples include the HIV epidemic in human population where in different genders the virus may propagate differently due to biological and social determinants [10, 11]; and information/rumors diffusing across different networks such as twitters, blogs and emails, etc. In all these examples, the interconnected networks may have different internal structures and different epidemic dynamics.

A special case of the interconnected networks is *interdependent* networks [8, 12], where the two end nodes of each interconnection depend on each other to survive. Death or infection of one end node causes the other one to die or be infected as well. Interdependent networks can be viewed as a special case of interconnected networks where spreading along the inter-network links has no resistance. An example of interdependent networks is smart power grid and its control network [8]. A failure of the power grid may make the control network lose its power supply if the control network is not carefully protected

from such kind of power interruption at the first place, which may in turn cause more nodes in the power grid network to fail. The cascading failures may cause blackout in a very large area. Another example is when each individual appears in two different networks. For example, a user of Facebook and Twitter shall have no inter-network resistance to pass the information from one network to another though whether to spread the information would still be a personal decision.

Research on epidemics in interconnected or interdependent networks only started recently. In [8], it was revealed that two interdependent scale-free (SF) networks, unlike a single SF network which is highly robust against random failure [13], is vulnerable to cascade of random failure. Funk *et al.* showed that cross-immunity is most effective where high-degree nodes in two overlay networks are coupled [14]. Leicht *et al.* showed that percolation in interconnected/interdependent networks may display a lower phase-transition threshold when the inter-network links are randomly distributed [15, 16]. When we nearly finished writing this manuscript, two preprints were posted online, studying on epidemic spreading in interconnected networks [17, 18]. In [18], the authors investigated the epidemic spreading in strongly and weakly interconnected networks; and a mixture phase-transition is identified in the weakly interconnected network model. In [17], epidemic propagation in interconnected networks was studied at mean-field level: it is found that the epidemic threshold of interconnected networks is associated with the correlation of inter/intra links. Both references revealed that the epidemic threshold in interconnected networks is lower than that in any of its two component networks.

In this contribution, we propose and evaluate the epidemic spreading over a rather simple interconnected network model. Specifically, the system is composed of two interconnected networks which may have different topologies. To simplify notation and analysis, we assume that the two networks are of

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the same size, and each node in one network is connected to a single node in the other network. The interconnections can be arbitrarily distributed. We term the interconnected networks as *positively correlated* if high-degree nodes in one network tend to connect to high-degree nodes in the other network; and *negatively correlated* otherwise (Detailed definitions will be provided later in Section 2.). Such definitions can be viewed as extensions of assortative/dissortative connection patterns in a single network [19] to inter-network connections. We assume that epidemic can propagate within and across networks following the typical Susceptible-Infected-Removed (SIR) scheme [20].

In our model, the interconnected network is found to possess an epidemic threshold lower than that in any of the two distinct networks regardless of the inter-network correlations, which agrees to the observations in [17, 18]. We also find that a strong positive correlation between the two networks leads to a clearly lower epidemic threshold if both of the networks are with similar homogeneous or inhomogeneous structures, which has also been observed in [18]. The effects, however, may be insignificant if the two networks have significantly different structures and epidemic thresholds, e.g., when one network is homogeneous and the other is inhomogeneous. Other than these observations, our main contribution can be summarized as follows:

- We derive equations which allow accurate calculations of the *epidemic threshold* [2] and *average outbreak size/epidemic size* [2] in the interconnected networks.

- We prove and demonstrate that the epidemic size is not significantly affected by the inter-network correlation.

- Epidemic spreading in interdependent networks is also covered, which has similar features but a much lower epidemic threshold and thereby, a much larger average outbreak size and epidemic size. Moreover, we prove and demonstrate that the inter-network correlation has stronger impacts on interdependent networks than those on interconnected networks.

Such results provide useful tools and insights which help pave the way for further studies on epidemic spreading in interconnected networks.

2. Models and analysis

The epidemic propagation in population can be described by the stochastic Susceptible-Infected–Removed (SIR) model, in which each individual is in one of the susceptible, infected or removed states [20, 21]. The whole population can be described as one or multiple complex networks in which individuals are nodes (vertexes) and contacts between individuals, along which epidemic can spread, are links (edges). Susceptible nodes may acquire infection from their infected neighbors, while infected nodes can be dead or recovered, in both cases regarded as being removed. The probability that an infected node can pass the epidemic to one of its susceptible neighbors before it recovers is defined as the *transmissibility* of the epidemic [2]. The general SIR model can be perfectly mapped into bond percolation in complex networks where transmissibility corresponds to the probability that a link is occupied in percolation [2]. In this paper, SIR model and bond percolation theory are adopted to investigate the spread of infection in interconnected complex networks.

We consider a simple interconnected network model consisting of two networks (hereafter termed as *sub-networks*, *subnets* or *SNs*) with the same size. Name the two sub-networks as SN-1 and SN-2 respectively, where each node in one subnet is connected to a single node in the other subnet through an inter-network link. The two sub-networks may have very different internal structures, and the inter-network links can be arbitrarily distributed.

A summary of frequently used symbols in this paper and their meanings is given in Table 1.

Assume that SN-1 and SN-2 have nodal degree distributions $p_1(k)$ and $p_2(k)$ respectively. We allow correlated connections in and between sub-networks, where the intra-/inter-network correlation can be defined by the joint degree distribution of the two end nodes of a randomly selected link. For the intra-network correlation, it can be defined by the probability $e(i, j)$ that a randomly selected link in a sub-network is connected to two nodes with degrees $i + 1$ and $j + 1$, respectively [19]. Following Callaway *et al.* [22], we have that for undirected SN-1, $e_1(i, j) = e_1(j, i)$; and in SN-1 with no degree correlation, $e_1(i, j) = (i+1)(j+1)p_i(i+1)p_{j+1}(j+1)/(\sum_k kp_1(k) \sum_k kp_2(k))$. Similar conclusions apply to $e_2(i, j)$ for SN-2.

The two sub-networks are connected by a set of inter-network links. Analogously to the degree correlation in a single network, correlation of the two sub-networks can also be defined. Specifically, let $e_{1,2}(i, j)$ denote the probability that a randomly chosen inter-network link is connected between a node in SN-1 with a remaining degree i and a node in SN-2 with a remaining degree j. In our model,

$$\sum_{ij} e_{1,2}(i, j) = 1, \sum_j e_{1,2}(i, j) = p_1(i), \sum_j e_{1,2}(j, i) = p_2(i). \quad (1)$$

Generally, $e_{1,2}(i, j) \neq e_{1,2}(j, i)$. The interconnected network can consist two degree correlated sub-networks arbitrarily interconnected by a set of links.

To measure the degree correlation in a single network, network assortativity r has been introduced and defined as [19, 22]

$$r = \frac{\sum_i \sum_j \left[ij \left(e(i, j) - \left(\sum_i e(i, j) \right) \left(\sum_j e(i, j) \right) \right) \right]}{\sum_j j^2 \sum_i e(i, j) - \left(\sum_j j \sum_i e(i, j) \right)^2}. \quad (2)$$

A network is said to be disassortative if $r < 0$, assortative if $r > 0$, and uncorrelated if $r = 0$. Analogously, we can extend the definition of r to measure the inter-network correlation (denoted by r as well) by letting $e(i, j) = (e_{1,2}(i, j) + e_{1,2}(j, i))/2$. Hereafter we term r as the *inter-network correlation coefficient*. The two subnets are termed as positively correlated if $r > 0$, negatively correlated if $r < 0$, and uncorrected if $r = 0$.

We now analyze the epidemic spreading in the defined interconnected networks. Assume that both intra- and inter-network links have the same capability of transmitting (Later we will study a different scenario where inter-network and intra-network links have different resistances to infection spreading.). Denote the epidemic threshold of the interconnected network as T_c. For the case where the epidemic transmissibility T is lower than T_c, by mapping the epidemic spreading into bond percolation [2], we have that each link is occupied at the probability of T where nodes connected by occupied links cannot form into a giant component. Term the size of the cluster formed by infected nodes under such case as *outbreak size* [2]. In SN-1, following a random link connected to a node with a remaining degree i (excluding the inter-network link), the distribution of outbreak size we can reach at the other end of the link can be represented by the PGF h_1 as follows:

$$h_1(i; x; T) = 1 - T + Tx$$
$$\times \frac{\left(\sum_{k \geq 0} e_1(i,k) h_1^k(k; x; T) h_{1 \to 2}(k+1; x; T) \right)}{\sum_k e_1(i,k)} \quad (3)$$

where $h_{1 \to 2}$ represents the distribution of outbreak size in SN-2 reached by following a randomly selected inter-network link from a node in SN-1 with a remaining degree j.

Meanwhile in SN-2, we have

$$h_2(i; x; T) = 1 - T + Tx$$
$$\times \frac{\left(\sum_{k \geq 0} e_2(i,k) h_2^k(k; x; T) h_{2 \to 1}(k+1; x; T) \right)}{\sum_k e_2(i,k)} \quad (4)$$

where h_2 and $h_{2 \to 1}$ are PGFs for outbreak sizes that can be reached by following a random link connected to a node with a remaining degree i in SN-2, and following a randomly chosen inter-network link from a node with a remaining degree j in SN-1, respectively. $h_{1 \to 2}$ and $h_{2 \to 1}$ can be expressed in terms of h_1 and h_2 as

$$h_{1 \to 2}(i; x; T) = 1 - T + Tx \frac{\sum_{k \geq 0} e_{1,2}(i,k) h_2^k(k-1; x; T)}{\sum_k e_{1,2}(i,k)}, \quad (5)$$

$$h_{2 \to 1}(i; x; T) = 1 - T + Tx \frac{\sum_{k \geq 0} e_{1,2}(k,i) h_1^k(k-1; x; T)}{\sum_k e_{1,2}(k,i)}. \quad (6)$$

Eqs. (3)-(6) give the detailed distribution of outbreak size that can be reached by following a randomly selected link in an interconnected network. Since epidemic always starts from a network node, we proceed to analyze outbreak size distribution for epidemic sourced from a randomly selected node. For epidemic sourced from a randomly selected node in SN-1, the PGF of the outbreak size is

$$H_1(x; T) = x \sum_k p_1(k) h_1^k(k-1; x; T) h_{1 \to 2}(k; x; T). \quad (7)$$

Similarly for epidemic starting from a randomly selected node in SN-2, we have

$$H_2(x; T) = x \sum_k p_2(k) h_2^k(k-1; x; T) h_{2 \to 1}(k; x; T). \quad (8)$$

H_1 and H_2 encapsulate the outbreak size distributions. From PGF, the average outbreak sizes for epidemic starting from SN-1 (SN-2) can be derived by taking derivates of Eq. (7) (Eq. (8)) at $x = 1$. Specifically,

$$\langle s_1 \rangle = \left. \frac{dH_1(x; T)}{dx} \right|_{x=1} = H_1'(1; T) = 1$$
$$+ \sum_k k p_1(k) h_1'(k-1; 1; T) + \sum_k p_1(k) h_{1 \to 2}'(k; 1; T) \quad (9)$$

and

$$\langle s_2 \rangle = \left. \frac{dH_2(x; T)}{dx} \right|_{x=1} = H_2'(1; T) = 1$$
$$+ \sum_k k p_2(k) h_2'(k-1; 1; T) + \sum_k p_2(k) h_{2 \to 1}'(k; 1; T). \quad (10)$$

Hence, the average outbreak size of epidemic in the interconnected network is $\langle s \rangle = (\langle s_1 \rangle + \langle s_2 \rangle)/2$. In Eqs. (9) and (10), functions $h_1'(k-1; 1; T)$, $h_2'(k-1; 1; T)$, $h_{1 \to 2}'(k; 1; T)$ and $h_{2 \to 1}'(k; 1; T)$ can be derived from Eqs. (3)-(6). Taking derivatives on both sides of Eqs. (3)-(6) at $x = 1$, we have

$$\begin{aligned}
h_1' &= TI_V + TD_1^{-1}M_A h_1' + TD_1^{-1}M_B h_{1 \to 2}' \\
h_2' &= TI_V + TD_2^{-1}N_A h_2' + TD_2^{-1}N_B h_{2 \to 1}' \\
h_{1 \to 2}' &= TI_V + TD_3^{-1}R h_2' \\
h_{2 \to 1}' &= TI_V + TD_4^{-1}Q h_1'
\end{aligned} \quad (11)$$

where $I_V = [1, 1, 1...1]^T$ is a unit vector, and D_1, D_2, D_3, D_4 are diagonal matrixes with diagonal entries

$$D_1(i) = diag\left(\sum_k e_1(i,k) \right), D_2(i) = diag\left(\sum_k e_2(i,k) \right),$$
$$D_3(i) = diag\left(\sum_k e_{1,2}(i,k) \right), D_4(i) = diag\left(\sum_k e_{1,2}(k,i) \right), \quad (12)$$

respectively. M_A, M_B, N_A, N_B, R and Q are connectivity matrixes encapsulating the topological information of the interconnected network. Specifically,

$$\begin{aligned}
M_A(i,j) &= je_1(i,j), M_B(i,j) = e_1(i,j), \\
N_A(i,j) &= je_2(i,j), N_B(i,j) = e_2(i,j), \\
R(i,j) &= je_{1,2}(i,j), Q(i,j) = je_{1,2}(j,i).
\end{aligned} \quad (13)$$

From Eq. (11), we have that

$$\left(D_1 - TM_A - T^4 M_B D_3^{-1} R (D_2 - TN_A)^{-1} N_B D_4^{-1} Q \right) h_1' = TD_1 I_V$$
$$+ T^2 M_B \left(I_V + TD_3^{-1} R (D_2 - TN_A)^{-1} (D_2 I_V + TN_B I_V) \right) \quad (14)$$

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$$\left(D_2 - TN_A - T^4 N_B D_4^{-1} S (D_1 - TM_A)^{-1} M_B D_3^{-1} R\right) h_2' = TD_2 I_V$$
$$+ T^2 N_B \left(I_V + TD_4^{-1} Q (D_1 - TM_A)^{-1} (D_1 I_V + TM_B I_V)\right). \tag{15}$$

h_1' in Eq. (14) diverges at the point where

$$\det\left(D_2 - TN_A\right) = 0 \tag{16}$$

or

$$\det\left(D_1 - TM_A - T^4 M_B D_3^{-1} R (D_2 - TN_A)^{-1} N_B D_4^{-1} Q\right) = 0. \tag{17}$$

Similarly, h_2' in Eq. (15) diverges when

$$\det\left(D_1 - TM_A\right) = 0 \tag{18}$$

or

$$\det\left(D_2 - TN_A - T^4 N_B D_4^{-1} Q (D_1 - TM_A)^{-1} M_B D_3^{-1} R\right) = 0. \tag{19}$$

Eqs. (16)-(19) yield four different critical transmissibility values named as $T_{1,c}$, $T_{2,c}$, $T_{3,c}$ and $T_{4,c}$ respectively, above any of which $\langle s \rangle$ will diverge, i.e., infection will spread to the whole network. From Eqs. (16) and (17), we see that for any value T which makes Eq. (16) diverges, Eq. (17) also diverges. Therefore $T_{2,c} \leq T_{1,c}$ always holds. Similarly, $T_{4,c} \leq T_{3,c}$ is always true. Defining the threshold T_c as the one above which $\langle s \rangle$ diverges, hence

$$T_c = T_{1,c} \wedge T_{2,c} \wedge T_{3,c} \wedge T_{4,c} = T_{2,c} \wedge T_{4,c}. \tag{20}$$

Note that $T_{1,c}$ and $T_{3,c}$ correspond to the critical transmissibility values where epidemic outbreak happens in each of the sub-networks with no inter-network links [4, 19, 23]. Therefore we conclude that the epidemic threshold of the interconnected network is always lower than that in any of the sub-networks regardless of the interconnection pattern between them. Hence, if a random homogeneous network is connected to an inhomogeneous scale-free network, epidemic spreading within the two networks will be greatly amplified. Details of the effects of correlations between sub-networks on epidemic thresholds and epidemic outbreak sizes will be demonstrated in the next section.

For the case where $T > T_c$, the infection will spread to the whole network, i.e., the infected nodes will form into a giant component. In such a case, we define $u_1(i)$ as the probability that a link connected to a node with a remaining degree i in SN-1 is connected to another node that does *not* belong to the infected giant component in the same sub-network. $u_2(i)$ is defined similarly in SN-2. Let $u_{1\to2}(i)$ represent the probability that a link from a degree-i node in SN-1 is connected to another node in SN-2 which does not belong to the infected giant component. $u_{2\to1}(i)$ is defined similarly. We have

$$u_1(i) = \frac{\sum_k e_1(i,k)(1 - T + Tu_1(k))^k (1 - T + Tu_{1\to2}(k))}{\sum_k e_1(i,k)}, \tag{21a}$$

$$u_2(i) = \frac{\sum_k e_2(i,k)(1 - T + Tu_2(k))^k (1 - T + Tu_{2\to1}(k))}{\sum_k e_2(i,k)}, \tag{21b}$$

$$u_{1\to2}(i) = \frac{\sum_k e_{1,2}(i,k)(1 - T + Tu_2(k))^k}{\sum_k e_{1,2}(i,k)}, \tag{21c}$$

$$u_{2\to1}(i) = \frac{\sum_k e_{1,2}(k,i)(1 - T + Tu_1(k))^k}{\sum_k e_{1,2}(k,i)}. \tag{21d}$$

Hence the epidemic size can be expressed as

$$S = 1 - \frac{\sum_k p_1(k) u_1^k (k-1) u_{1\to2}(k)}{2} - \frac{\sum_k p_2(k) u_2^k (k-1) u_{2\to1}(k)}{2}. \tag{22}$$

Eq. (21) can be solved numerically to get the values of $u_1(i)$, $u_2(i)$, $u_{1\to2}(i)$ and $u_{2\to1}(i)$ respectively, bringing which to Eq. (22) we can calculate the epidemic size for $T > T_c$. The degree correlations within and between sub-networks are taken in account.

Note that in Eq. (21c), the term $(1 - T + Tu_2(k))^k$ is approximated as $1 - T$: the value of j is no less than 2. From the definition of $u_2(k)$ we see that it gets smaller under larger transmissibility T. The higher order terms of T and $u_2^k(k)$ are therefore ignored in Eq. (21c). Similar approximation applies to Eq. (21d). After approximations, we see that in Eqs. (21c) and (21d), the values of $u_{1\to2}(i)$ and $u_{2\to1}(i)$ are not affected by inter-network correlations. And $u_1(k)$ and $u_k(j)$ in Eqs. (21a) and (21b) are also independent of inter-network correlation. Therefore, we have the conclusion that the epidemic size of the interconnected network in Eq. (22) is not significantly affected by inter-network correlation, which will be further verified in Section 3 by numerical simulations.

Interdependent networks, as far as epidemic spreading is concerned, may be viewed as a special case of interconnected networks. Specifically, epidemic spreading in interdependent networks can be analyzed by adopting the analytical framework presented above by letting the transmissibility of inter-network links be equal to 1. Therefore, Eqs. (5) and (6) can be modified as

$$h_{1\to2}(i; x; T) = x \frac{\sum_{k\geq0} e_{1,2}(i,k) h_2^k(k-1; x; T)}{\sum_k e_{1,2}(i,k)}, \tag{23}$$

$$h_{2\to1}(i; x; T) = x \frac{\sum_{k\geq0} e_{1,2}(k,i) h_1^k(k-1; x; T)}{\sum_k e_{1,2}(k,i)}. \tag{24}$$

Consider the scenario where the interdependent and interconnected networks have the same topology and the epidemic has the same transmissibility in both networks. The value of $h_{1\rightarrow2}$ in Eq. (23) for interdependent networks is larger than that for interconnected networks as shown in Eq. (5). From Eq. (23), we know that a larger $h_{1\rightarrow2}$ leads to a larger value of h_1. Similarly, we have $h_{2\rightarrow1}$ and h_2 also become larger in interdependent networks. Therefore, the average outbreak size in the interdependent networks is always higher than that in the corresponding interconnected networks with the same network topologies, inter-network correlation and epidemic transmissibility. Following the same procedure as presented above, we have $T_c = T_{2c} \wedge T_{4c}$, where T_{2c} and T_{4c} are defined by

$$\det\left(D_1 - TM_A - T^2 M_B D_3^{-1} R(D_2 - TN_A)^{-1} N_B D_4^{-1} Q\right) = 0, \quad (25)$$

$$\det\left(D_2 - TN_A - T^2 N_B D_4^{-1} Q(D_1 - TM_A)^{-1} M_B D_3^{-1} R\right) = 0, \quad (26)$$

respectively. The infection size in interdependent networks can be expressed by Eqs. (25) and (22), with Eqs. (21a) and (21b) respectively being modified to be

$$u_1(i) = \frac{\sum\limits_k e_1(i,k)(1 - T + Tu_1(k))^k u_{1\rightarrow2}(k)}{\sum\limits_k e_1(i,k)}, \quad (27a)$$

$$u_2(i) = \frac{\sum\limits_k e_2(i,k)(1 - T + Tu_2(k))^k u_{2\rightarrow1}(k)}{\sum\limits_k e_2(i,k)}. \quad (27b)$$

Comparing Eq. (25) and Eq. (19), we see that the only difference is that the term T^4 in Eq. (19) is replaced by T^2 in Eq. (25). Since $0 < T < 1$ and all the matrices are non-negative, the solution of Eq. (25) is smaller than that of Eq. (19) with the same network structures. Hence we have that the epidemic threshold of an interdependent network is lower than that of the corresponding interconnected network with the same topology.

3. Simulation results and discussions

To evaluate the effects of inter-network connections, we consider a few typical cases where (i) both of the two sub-networks are SF networks with the same size and dgree distribution [24, 25]; (ii) both of them are Erdős–Rényi (ER) random networks with the same size; and (iii) they are different scale-free networks with the same size. To facilitate discussions, we term the three cases as SF-SF, ER-ER and SF-SF$'$ interconnected network models, respectively. Assume that each sub-network has 10,000 nodes. For the SF network in SF-SF and SF-SF$'$ models, let $p(k) = ck^{-3}$, and the minimum and maximum degrees be 2 and 100 respectively [26, 28]; for the SF$'$ in SF-SF$'$ model, we let $p(k) = ck^{-2.5}$, and the minimum and maximum degrees be 2 and 100 respectively; for the ER network, the probability that there exists a link between each pair of nodes is set

as $p_r = 3.14 \times 10^{-4}$. Both SF and ER networks have an average nodal degree 3.14, while SF$'$ has an average nodal degree 4.14. Unless otherwise specified, we assume that both of the two sub-networks are uncorrelated random networks.

A targeted value of inter-network correlation coefficient generally speaking can be achieved as follows: let the two sub-networks be randomly interconnected, only subject to the constraint that each node is connected to a single inter-network link. Randomly select two inter-network links, rewire them by exchanging their end nodes in one of the two sub-networks if and only if such an operation makes the inter-network correlation coefficient change towards the desired value. Repeat the rewiring operations unless the desired correlation level is achieved or until the coefficient cannot be further changed towards the desired value.

Obviously not all the desired values can be achieved by the proposed rewiring operations. The strongest positive correlation happens when all highest-degree nodes in one sub-network try their best to connect to highest-degree nodes in the other sub-network, while the strongest negative correlation is obtained when all highest-degree nodes in one sub-network try to connect to lowest-degree nodes in the other sub-network. In the SF-SF model, the coefficient value r roughly lies in the interval of $[-0.12, 1]$, while for the ER-ER and SF-SF$'$ models, the corresponding intervals are $[-0.88, 1]$ and $[-0.12, 0.45]$ respectively. In our simulations, we always make the targeted coefficient value achievable by using the proposed rewiring method. In our simulation, each type of interconnected networks, for instance SF-SF networks, has 100 randomly generated networks with the parameters as we described. Rewiring the inter-network connections, we can get different desired inter-network correlations. Each given simulation result is averaged over 10 realizations on each of these 100 networks.

3.1. Epidemic threshold and average outbreak size

As analyzed, an interconnected network has an epidemic threshold lower than that in any of its two sub-networks regardless of the inter-network correlation level. The specific epidemic threshold value, however, is affected not only by the structures of the sub-networks, but also the inter-network correlation level.

When both of the sub-networks have similar structures, e.g., both of them are inhomogeneous SF networks or homogeneous ER networks, the epidemic threshold of the interconnected network is much lower than that of any of the sub-networks. Under such case, the epidemic threshold may significantly change with the inter-network correlation level. Specifically, the calculated epidemic thresholds of a standalone SF, a standalone SF$'$ and a standalone ER networks are $T_c = 0.1788, 0.087$ and 0.333, respectively. As shown in Fig. 1(a), the epidemic threshold of the SF-SF network is lowered to $T_c = 0.166, 0.164$ and 0.152 for different cases with inter-network correlation coefficients $r = -0.12, 0$ and 1, respectively (Note that $r = -0.12$ and $r = 1$ correspond to cases with the lowest and the highest inter-network correlation coefficients that can be achieved by using the proposed rewiring method and $r = 0$ is for the case with
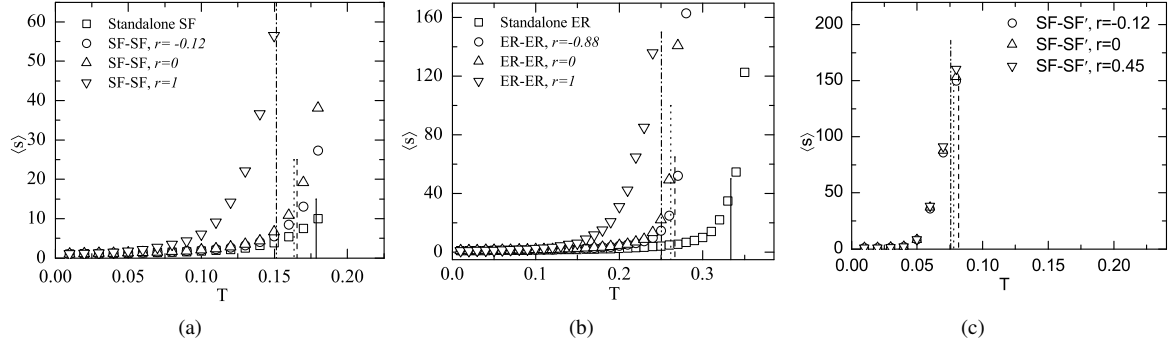
Figure 1: Average outbreak size for epidemic spreading in (a) SF-SF; (b) ER-ER; and (c) SF-SF′ network models. Vertical lines indicate the theoretical epidemic thresholds. Square boxes, circles, upper-triangles and down-triangles represent the average outbreak sizes.

random, uncorrelated interconnections. Hereafter, unless otherwise specified, we will show simulation results for cases with lowest, highest and zero inter-network correlation coefficients respectively.). Similarly, in Fig. 1(b), the epidemic threshold of the ER-ER network is reduced to $T_c = 0.267$, 0.261 and 0.250 for cases where $r = -0.88$, 0 and 1, respectively.

When the two sub-networks are of different structures, even if both of them are inhomogeneous networks as that in SF-SF′ model, on the other hand, the one with the lower epidemic threshold (e.g., the SF′ sub-network in the SF-SF′ network) tends to dominate the epidemic threshold of the interconnected network. As shown in Fig. 1(c), for different cases with inter-network correlation coefficient $r = -0.12$, 0 and 0.45, the epidemic thresholds of the interconnected network remain largely unchanged at $T_c = 0.081$, 0.072 and 0.065, respectively, which are quite close to that of a standalone SF′ sub-network at $T_c = 0.087$. This can be understood since it is much easier for epidemic to prevail in the sub-network with a significantly lower epidemic threshold. Whether there is an outbreak in the interconnected network is therefore largely decided by whether there is an epidemic outbreak in this sub-network. Such phenomenon will become more obvious (though not shown here due to space limit) when an inhomogeneous networks with a very low epidemic threshold is connected to a homogeneous network with a much higher epidemic threshold, e.g. in an SF-ER model.

As shown in Fig. 1, having a higher correlation coefficient value generally leads to a lower epidemic threshold and a larger average outbreak size. This is not a surprise since under low transmissibility, higher-degree nodes tend to have a higher chance to be infected. If such infection manages to reach the other network, reaching higher degree nodes in the other network helps increase the infection size there. From a percolation point of view, higher-degree nodes in each sub-network tend to be involved in larger size clusters. Existence of more high-to-high inter-network links, which leads to a higher inter-network correlation coefficient value and a lower epidemic threshold, tends to joint those larger size clusters together, and thereby leading to a larger average outbreak size.

3.2. Epidemic size

Unlike that in a single network where epidemic size (a.k.a the giant component size [2, 19]) of a strong infection becomes smaller in networks with higher assortativity values [19, 28], the epidemic size in interconnected networks is barely affected by the inter-network correlation, as illustrated in Fig. 2. A proof on this has been shown in Eqs. (21)-(22). And the reasons can be further explained as follows: for epidemics with high transmissibility, there is a large-size giant component in each sub-network formed by infected nodes. Since each node has an inter-network connection, every node in a giant component of a sub-network has a non-zero probability of connecting to the giant component in the other sub-network. When the two networks are large enough, the two giant components are almost surely connected to each other regardless of the network correlation level. The two connected giant components play the most significant role in deciding the infection size in the interconnected network model. Besides the giant components, there is a certain number of small-size clusters linked to the giant components by occupied inter-network links. The total size of these small clusters is not trivial, and interestingly, it is not significantly affected by the inter-network correlation level. This observation can be understood: between two positively correlated networks, there are more occupied links between their giant components since they have more links between their higher-degree nodes, and higher-degree nodes have higher chances to be involved in the giant component. As a result, the number of the occupied inter-network links between giant components and small-size clusters is lower. However, since those small-size clusters connected to the giant components tend to involve some relatively higher degree nodes, the average size of them is bigger. To summarize, the effect is that in positively correlated interconnected networks, there are fewer small-size clusters connected to the giant components yet the average size of these small-size clusters is larger; in negatively correlated interconnected networks, more small-size clusters are connected to giant components through occupied inter-network links, yet the average size of these small-size clusters is smaller. The overall sizes of all the small-size clusters connected to giant components in the two different cases therefore are not very different from each other.
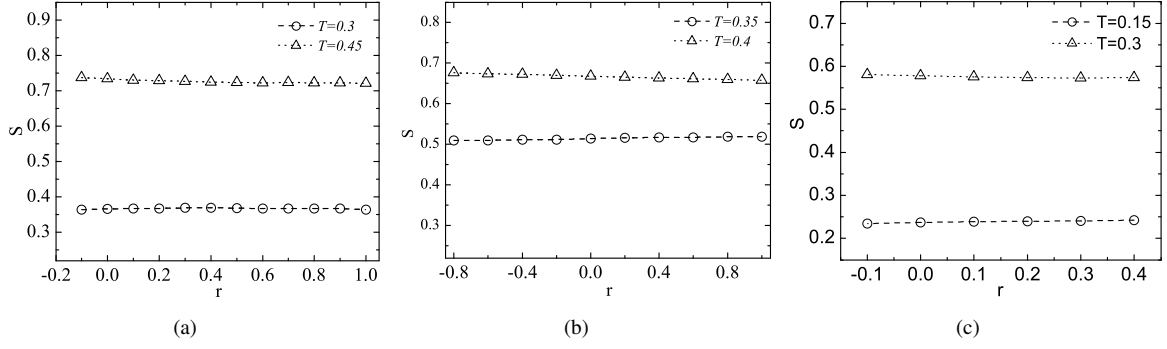
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Figure 2: Epidemic size in (a) SF-SF, (b) ER-ER and (c) SF-SF′ interconnected network models. Square boxes, circles and upper triangles represent the epidemic sizes in the interconnected networks with different transmissibilities.

We present an example case in some details. Let $T = 0.3$ in the SF-SF model. In each sub-network, there is a giant component formed by 1975 nodes. When $r = 0$, there are 118 occupied links between the two giant components; meanwhile there are 1331 small-size clusters, with a total size of 3258 nodes connected to the two giant components via 1402 occupied inter-network links. The average size of each small-size cluster is only 2.45. When $r = 1$, there are 155 occupied links between the two giant components, and 1255 small-size clusters connected to the giant components via 1341 occupied inter-network links. The overall size of all the small clusters is 3309 with an average size of 2.65 for each cluster. Fig. 3 shows how the number of clusters (including the giant component itself) and their accumulated size increase with the hop distance from the giant component. Here we define the hop distance between a small-size cluster and the giant cluster as the minimal number of occupied inter-network links we have to go through to reach the small-size cluster from the giant component. Having a hop distance "0" means that the cluster is the giant component itself. We see that the number of clusters increases more slowly when $r = 1$ compared to that when $r = 0$; yet the accumulated infection size increases at nearly the same speed. Similar observations have been made in the ER-ER and SF-SF′ models as well.

It is worth noting that when the transmissibility is very high, e.g., $T = 0.45$ and $T = 0.4$ in Fig. 2, the overall infection size slightly decreases when the inter-network correlation coefficient value changes from negative to positive. This can be easily explained: under very strong infection, the high-degree nodes are easily infected and form into a giant component in each sub-network. Having more inter-network links between high-degree nodes only enhance the connections between the two giant components. Having more inter-network links between high-degree and low-degree nodes helps the infection reach more low-degree nodes and hence increases the epidemic size.

3.3. Interdependent networks

The interdependent networks are defined similarly as the interconnected networks. We obtain an interdependent network model by letting the transmissibility along the inter-network
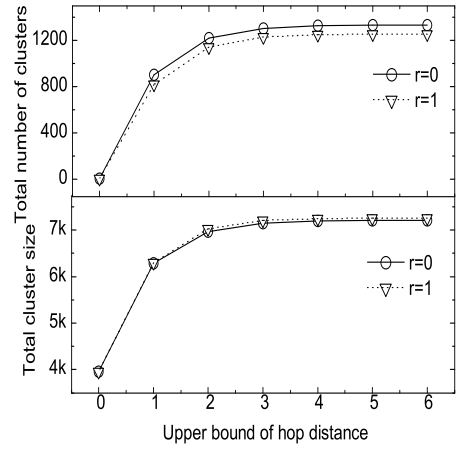

Figure 3: Number of infected clusters and their accumulated size vs. upper bound of hop distance in SF-SF model. $T = 0.3$.

links be equal to 1. We still carry out numerical simulations on SF-SF, ER-ER and SF-SF′ models.

It can be safely expected that compared to the interconnected network models where the inter-network links have some resistance to infection spreading, interdependent networks have a lower threshold, a larger average outbreak size and a large epidemic size. Indeed, it can be calculated that the epidemic thresholds are $T_c = 0.121$, 0.115 and 0.083 for the most negatively correlated, uncorrelated, and the most positively correlated SF-SF interdependent networks respectively. In the ER-ER interdependent network model, the corresponding values are $T_c = 0.172$, 0.163 to 0.143, and in the SF-SF′ model, $T_c = 0.064$, 0.06 and 0.051, respectively. In all the cases, the threshold values are much lower than those in standalone networks. As can be observed in Fig. 4, a smaller epidemic threshold leads to a larger average out break size.

The simulation results confirm our earlier analysis that inter-network correlation in interdependent networks has greater impacts on epidemic threshold and average outbreak size than those on interconnected networks. For example, when the inter-network correlation changes from 0 to 1, in SF-SF interdepen-
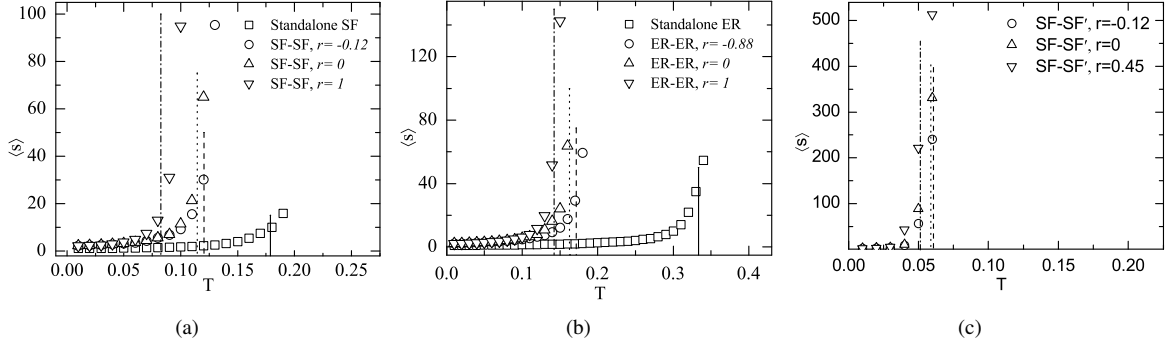
Figure 4: Average outbreak size for epidemic spreading in (a) SF-SF, (b) ER-ER and (c) SF-SF′ interdependent network models. Vertical lines indicate the theoretical epidemic thresholds. Square boxes, circles, upper-triangles and down-triangles represent the average outbreak sizes.
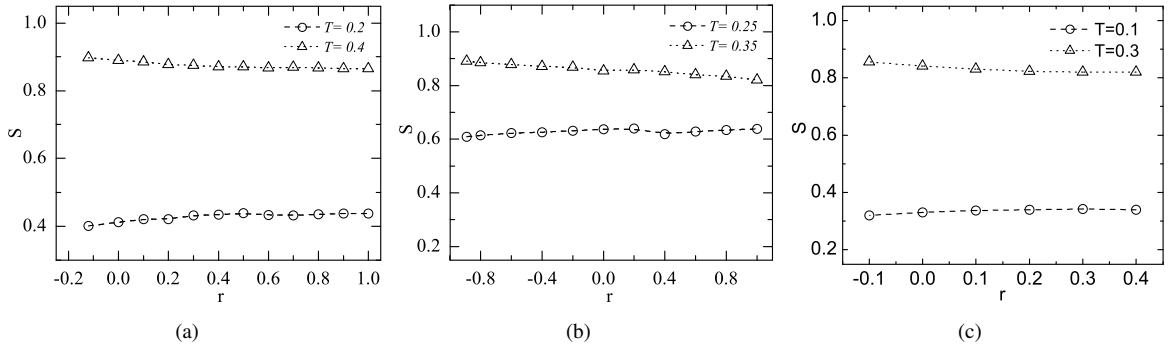

Figure 5: Epidemic size in (a) SF-SF, (b) ER-ER and (c) SF-SF′ interdependent network models. Circles and upper triangles represent the epidemic sizes.

dent network, the epidemic threshold changes from T_c =0.115 to 0.083, while in SF-SF interconnected network, the epidemic threshold changes from T_c = 0.164 to 0.152. When T = 0.08, the average outbreak sizes for r = 0 and 1 are $\langle s \rangle$ = 1.63 and 3.45 respectively in SF-SF interconnected networks, and $\langle s \rangle$ =5.58 and 13.0 respectively in SF-SF interdependent networks. Similarly to that in the interconnected networks, the epidemic size is not significantly affected by inter-network correlation, as can be seen in Fig. 4. And once again, under high transmissibility, a higher correlation coefficient value leads to a slightly smaller infection size, due to the same reasons as explained earlier.

4. Conclusion

In this paper, we demonstrated the dynamics of epidemic spreading in interconnected networks. Equations were derived for quickly and accurately calculating the epidemic threshold and average outbreak size/epidemic size in the interconnected networks. We also proved and demonstrated that epidemic size is not significantly affected by the inter-network correlation. Moverover, it was revealed that inter-network correlation has stronger impacts on interdependent networks than those on interconnected networks.

It would be interesting to extend our work to cases with more general interconnection models, e.g., where each node

may be connected to none or multiple nodes in the other network. This is of our future research interest. Another interesting topic would be to develop protection strategies for interconnected/independent networks.

Acknowledgment

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Figure captions

Fig. 1. Average outbreak size for epidemic spreading in (a) SF-SF; (b) ER-ER; and (c) SF-SF$'$ network models. Vertical lines indicate the theoretical epidemic thresholds. Square boxes circles, upper-triangles and down-triangles represent the average outbreak sizes.

Fig. 2. Epidemic size in (a) SF-SF, (b) ER-ER and (c) SF-SF$'$ interconnected network models. Square boxes, circles and upper triangles represent the epidemic sizes in the interconnected networks with different transmissibilities.

Fig. 3. Accumulated number of infected nodes and total number of clusters in SF-SF model when $T = 0.3$.

Fig. 4. Average outbreak size for epidemic spreading in (a) SF-SF, (b) ER-ER and (c) SF-SF$'$ interdependent network models. Vertical lines indicate the theoretical epidemic thresholds. Square boxes, circles, upper-triangles and down-triangles represent the average outbreak sizes.

Fig. 5. Epidemic size in (a) SF-SF, (b) ER-ER and (c) SF-SF$'$ interdependent network models. Circles and upper triangles represent the epidemic sizes.

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Tables

Table 1: Summary of symbols adopted and their meanings.

Symbols	Meanings
$p_1(k)$	Degree distribution of SN-1.
$p_2(k)$	Degree distribution of SN-2.
$e(i, j)$	The probability that a randomly selected link in SN-1 or SN-2 is connected to two nodes with degrees $i + 1$ and $j + 1$.
$e_1(i, j)$	The probability that a randomly selected link in SN-1 is connected to two nodes with degrees $i + 1$ and $j + 1$.
$e_2(i, j)$	The probability that a randomly selected link in SN-2 is connected to two nodes with degrees $i + 1$ and $j + 1$.
$e_{1,2}(i, j)$	The probability that a randomly chosen inter-network link is connected between a node in SN-1 with a remaining degree i and a node in SN-2 with a remaining degree j.
r	Inter-network correlation coefficient.
T	Transmissibility of epidemics.
x	The indeterminate in probability generating function.
$h_1(i; x; T)$	PGF for the distribution of outbreak size that we can reach following a randomly chosen link, whose other end is connected to a node with a remaining degree i (excluding the inter-network link) in SN-1.
$h_2(i; x; T)$	PGF for the distribution of outbreak size that we can reach following a randomly chosen link, whose other end is connected to a node with a remaining degree i (excluding the inter-network link) in SN-2.
$h_{1 \to 2}(i; x; T)$	PGF for the distribution of outbreak size in SN-2 reached by following a randomly selected inter-network link from a node in SN-1 with a remaining degree i
$h_{2 \to 1}(i; x; T)$	PGF for the distribution of outbreak size in SN-1 reached by following a randomly selected inter-network link from a node in SN-2 with a remaining degree i
$H_1(x; T)$	PGF of the epidemic outbreak size that is sourced from a randomly selected node in SN-1.
$H_2(x; T)$	PGF of the epidemic outbreak size that is sourced from a randomly selected node in SN-2.
$\langle s_1 \rangle$	Average outbreak size for epidemic that is sourced from a randomly selected node in SN-1.
$\langle s_2 \rangle$	Average outbreak size for epidemic that is sourced from a randomly selected node in SN-2.
$\langle s \rangle$	Average outbreak size of epidemic.
D_1, D_2, D_3, D_4	Diagonal matrices.
M_A, M_B, N_A, N_B, R, Q	Connectivity matrixes.
T_c	Epidemic threshold of the interconnected network.
$u_1(i)$	The probability that a link connected to a node with a remaining degree i in SN-1 is connected to another node that does *not* belong to the infected giant component in the same sub-network.
$u_2(i)$	The probability that a link connected to a node with a remaining degree i in SN-2 is connected to another node that does *not* belong to the infected giant component in the same sub-network.
$u_{1 \to 2}(i)$	The probability that a link from a degree-i node in SN-1 is connected to another node in SN-2 which does not belong to the infected giant component.
$u_{2 \to 1}(i)$	The probability that a link from a degree-i node in SN-2 is connected to another node in SN-1 which does not belong to the infected giant component.
S	Epidemic size.