Layer-crossing overhead and information spreading in multiplex social networks

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We propose and study a model of information or disease spreading on multiplex social networks, in which agents interact or communicate through multiple channels (layers), say online vs. offline, and there exists a layer-switching overhead for transmission across the interaction layers. The model is characterized by the path-dependent transmissibility over a contact, that is dynamically determined dependent on both incoming and outgoing transmission layers due to the switching overhead. We formulate a generalized theory with a mapping to deal with such a path-dependent transmissibility, and demonstrate that network multiplexity can bring about non-additive and non-monotonic effects in spreading dynamics. Our results suggest that explicit consideration of multiplexity can be crucial in realistic modeling of spreading processes on social networks in an era of ever-diversifying social interaction layers.

Introduction—Networks are penetrating ever more deeply through every facet of individual lives and societal functions [1]. At its center, the explosive rise of social media driven by the information communication technology or ICT revolution has transformed the landscape of human interactions. Human interactions mediated by social media could defy the spatial and temporal limitations of traditional human communication in an unprecedented way, thereby offering not just another means of communication but a qualitatively new layer of the social interaction, which coexist and cooperating to define the multiplex social networks [2]. Different interaction channels or network layers in a multiplex system do not function completely autonomously and independently; while each layer can support some function within its scope, it is the crosstalk and interplay between the layers that can fulfill the complete functionality of a society and give rise to nontrivial and unanticipated outcomes such as the recently uprising civil movements in the Middle East [3]. This poses theoretical challenge as well to extend existing single network framework [4–6] by formulating and disseminating the role of multiplex network layers that do not always play the same roles in network dynamics, the understanding of which is only beginning to emerge [7–14].

Epidemic models on networks are one of the most developed branches in complex network theory [15–20]. Using the epidemic spreading framework we can address not only spreading of infectious diseases but also many other contagious phenomena such as information and rumor spreading on social networks. Recently, a few studies of epidemic spreading extended the single-network framework to overlay networks [19], multitype networks [20], interconnected networks [21–22], interdependent networks [23], and multiplex networks [14], observing for example a peculiar phase [21] and synergistic effects [22]. Here we propose a related but different problem of information spreading on multiplex social networks with multiple social interaction layers across which there exists nonzero layer-switching cost or overhead. For example, when one received new information through an online social medium, say Twitter, she would more likely spread it again through Twitter as it’s most handy, than do it over other online media, such as e-mail, or even offline social networks, as it might require additional effort or necessary spatiotemporal delay in switching the medium (network layer).

In this paper, we will show that this seemingly trivial and commonplace factor of layer-switching overhead can modify information spreading dynamics on multiplex social network in a significant and nontrivial way. Most importantly, it introduces the path-dependent transmissibility over a contact, that is dynamically determined dependent on both incoming and outgoing transmission layers, which requires a new theoretical formalism over the existing ones [16–20]. Based the prototypical susceptible-infected-recovered (SIR) model framework [24], we formulate a generating-function based theory to cope with the path-dependent transmissibility and show that the network multiplexity and layer-switching overhead can alter the information spreading dynamics in non-monotonic fashion and that the multiplex interactions cannot simply be aggregated into a single one generically.

Model—In the SIR model, each node is in one of three states, susceptible, infected, or recovered (or removed) [16–20, 24]. An infected node can spread information (or rumor or disease) to a susceptible neighbor with the infection rate $\beta$, and each infected node is recovered after time $\tau$ from the moment of infection. The probability that an infected agent infects its neighbors before recovery, denoted by $T$, is called the transmissibility and given by $T = 1 - e^{-\beta \tau} = 1 - e^{-\lambda}$, defining the effective infection rate $\lambda \equiv \beta \tau$. In the $t \to \infty$ limit, all nodes are either susceptible or recovered. The average final fraction of recovered nodes, $\rho$, is called the epidemic outbreak size.

To take account of network multiplexity and layer-switching overhead, we consider a network with two distinct types of links, or a duplex network (Fig. 1). Each node has $k_1$ and $k_2$ degrees for type-1 and type-2 links,
FIG. 1. Schematic illustration of the model. The network has two types of links, type-1 (solid) and type-2 (dashed). The filled (open) circles represent finally recovered (susceptible) nodes and red (blue) circles represent nodes infected via the type-1 (2) transmission. Transmissibility $T_{ij}$ are determined by the types of both incoming (color of nodes) and outgoing (type of links) infection channels.

...drawn from the joint degree distribution $p(k_1, k_2)$. We define the type-$i$ transmission to be the infection event in which the infection occurs through a type-$i$ link. In presence of multiplexity, the infection rates can become dependent on the types of both incoming and outgoing infection channels. To be specific, when a node is infected via a type-$i$ transmission, then the effective infection rate through the same type-$i$ link is $\lambda_{ii}$ while that for type-$j$ link is $\lambda_{ij}$, where these infection rates are different in general. Consequently, we have different transmissibilities $T_{ij}$ dependent on the types of both incoming and outgoing infection channels (Fig. 1).

**THEORY**

Outbreak probability—We first generalize the well-known theory for the SIR model on locally-treelike networks [15, 16] to our model. Let $G_0(x, y)$ be the generating function of the joint degree distribution $p(k_1, k_2)$, $G_0(x, y) = \sum_{k_1 = 0, k_2 = 0} p(k_1, k_2) x^{k_1} y^{k_2}$. The generating function $G_0(x, y; p, q)$ of the joint distribution of the numbers of occupied edges when the edges are independently occupied with the probability $p$ in layer 1 and $q$ in layer 2 can be written as $G_0(x, y; p, q) = G_0 (1 + (x-1)p, 1 + (y-1)q)$. Let $x_i$ be the probability that a node infected by type-$i$ transmission does not belong to the epidemic outbreak. $x_i$’s satisfy the coupled self-consistency equations

$$x_i = \frac{1}{z_i T_{ii}} \frac{\partial}{\partial x_i} G_0(x_1, x_2; T_{1i}, T_{2i}),$$

with $i = 1, 2$, where $z_i$ is the mean degree of the layer $i$. The probability that a type-$i$ seed infection gives rise to an epidemic outbreak, denoted by $P_i$, is given by

$$P_i = 1 - G_0(x_1, x_2; T_{1i}, T_{2i}).$$

Outbreak size—Another important quantity of the epidemic spreading is the average epidemic size once the epidemic outbreak occurs, denoted $S$ and called the outbreak size, equivalent to the final fraction of recovered nodes. The outbreak size can be in general different with the outbreak probability due to the effective directionality of the transmissibility in our model [17, 18]. In order to obtain the outbreak size, one should deduce the incoming transmissibility of each type of links, which however is not given *a priori*.

Here we propose to estimate the required incoming transmissibility in the following effective way. First we define the average probability, $\pi_{ij}$, that a node reached by following a type-$i$ link is infected by the type-$j$ transmission. On locally-treelike networks, $\pi_{ij}$’s satisfy the coupled self-consistency equations given by

$$\pi_{ii} = \frac{K_i}{\pi_i} (T_{ii} \pi_{ii} + T_{1i} \pi_{ij}),$$

$$\pi_{ij} = \frac{K_i}{\pi_i} (T_{ji} \pi_{ji} + T_{jj} \pi_{jj}),$$

with $i, j = 1, 2$ and $K_i = \langle k_i^2 \rangle - z_i$, $K_i = \langle k_i k_j \rangle / z_i$, and $\pi_i$ is the normalization factor imposed by $\pi_{ii} + \pi_{ij} = 1$ for distinct $i, j \in \{1, 2\}$. Solving these equations, one can obtain the effective average incoming transmissibility through the type-$i$ link, denoted $\bar{T}_i$, as $\bar{T}_i = T_{ii} \pi_{ii} + T_{ij} \pi_{ij}$. Then, the probability that an incoming node reached by following a type-$i$ link does not belong to the epidemic outbreak, $y_i$, is given similarly to Eq. (1) as

$$y_i = \frac{1}{z_i \bar{T}_i} \frac{\partial}{\partial y_i} G_0(y_1, y_2; \bar{T}_1, \bar{T}_2)$$

with distinct $i, j \in \{1, 2\}$. Finally, the outbreak size $S$ can be obtained as

$$S = 1 - G_0(y_1, y_2; \bar{T}_1, \bar{T}_2).$$

Epidemic threshold—The epidemic threshold can be obtained by the linear stability criterion of the trivial fixed point $(x_1, x_2) = (1, 1)$ of Eq. (1). The condition of the epidemic outbreak requires the largest eigenvalue $\Lambda$ of the Jacobian matrix $\mathbf{J}$ of Eq. (1) at $(1, 1)$ to be larger than unity, $\Lambda > 1$, which is the condition of the fixed point being unstable. The Jacobian matrix $\mathbf{J}$ at $(1, 1)$ can be simply expressed as

$$\mathbf{J} = \begin{pmatrix} T_{11} K_1 & T_{21} K_1 \\ T_{12} K_2 & T_{22} K_2 \end{pmatrix}.$$  

The largest eigenvalue $\Lambda$ can be explicitly calculated as

$$\Lambda = \frac{1}{2} \left[ T_{11} K_1 + T_{22} K_2 + \sqrt{(T_{11} K_1 - T_{22} K_2)^2 + 4 T_{12} T_{21} K_1 K_2} \right],$$

depending also on the degree correlations between network layers. Note that $\Lambda \geq \max(T_{11} K_1, T_{22} K_2)$, meaning that the epidemic threshold of the multiplex network cannot be larger than the epidemic thresholds of individual layers.
Duplex ER networks—We proceed to explicit calculations for the randomly-coupled multiplex networks with two Erdős-Rényi (ER) layers [9]. For simplicity, we set $\lambda_{11} = \lambda_{22} \equiv \lambda_1$ and $\lambda_{12} = \lambda_{21} \equiv \lambda_2$. We further assume $\lambda_1 \geq \lambda_2$, meaning that information (or disease) spreading along the same-type links is easier than those across different link types. The coupled equations of $x_i$’s for the duplex ER graphs simply can be written as

$$\begin{align*}
x_1 &= e^{z_1 T_1(x_1-1) + z_2 T_2(x_2-1)}, \\
x_2 &= e^{z_1 T_2(x_1-1) + z_2 T_1(x_2-1)}.
\end{align*}$$

For a more systematic analysis, we use the following parametrization for the mean degrees as $z_{1,2} = (1 \pm \delta z)z_0/2$. Similarly, the effective infection rates are parameterized as $\lambda_{1,2} = (1 \pm \delta \lambda)\bar{\lambda}$, where $\bar{\lambda}$ is the average value of $\lambda_{1,2}$. In this parametrization, we keep the total link density and the average infection rate constant, and investigate the effects of the difference of mean degrees $\delta z$ and that of infection rates $\delta \lambda$.

First, we investigate the epidemic threshold dependent on $\delta z$ and $\delta \lambda$. For the duplex ER graphs, the largest eigenvalue is $\Lambda = \frac{z_0}{2} \left[ T_1 + \sqrt{\delta z^2(T_1^2 - T_2^2) + T_2^2} \right]$. The epidemic threshold, $\lambda_c$, as a function of $\delta z$ and $\delta \lambda$ for $z_0 = 2.5$ is shown in Fig. 2. When ER layers with equal mean degrees are multiplexed ($\delta z = 0$), we have $\Lambda = z_0 (T_1 + T_2)/2$, which monotonically decreases with $\delta \lambda$, so the epidemic threshold increases. Next, with increasing $\delta z$, the type-1 network (layer 1) gets denser so more and more same-type transmission channels become available, facilitating the spreading. Therefore, for given $\delta \lambda$, epidemic threshold decreases with $\delta z$. For larger $\delta z$, above the dashed line ($\partial \Lambda / \partial \delta \lambda > 0$ for all $\delta \lambda$) in Fig. 2, the epidemic threshold monotonically decreases with $\delta \lambda$. And for intermediate $\delta z$, we have non-monotonic dependence of epidemic threshold on $\delta \lambda$ as a consequence of non-additive effect of network multiplexity. This result offers optimal strategy to produce global impact of spreading whether concentration on the dominant channel or evenly dividing regardless of types of links.

Results

Duplex ER networks—We proceed to explicit calculations for the randomly-coupled multiplex networks with two Erdős-Rényi (ER) layers [9]. For simplicity, we set $\lambda_{11} = \lambda_{22} \equiv \lambda_1$ and $\lambda_{12} = \lambda_{21} \equiv \lambda_2$. We further assume $\lambda_1 \geq \lambda_2$, meaning that information (or disease) spreading along the same-type links is easier than those across different link types. The coupled equations of $x_i$’s for the duplex ER graphs simply can be written as

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Numerical simulations—We perform numerical simulation on the randomly-coupled ER graphs to check our analytic calculation. Initially, all nodes are susceptible except for one randomly-chosen seed which is assumed to be infected by a type-i transmission. Infected nodes transmit the disease to its neighbors with an infection rate dependent on incoming and outgoing channels and each infected node recover after a fixed recovery period, $\tau$. Until all infected nodes recover, the spreading process proceeds. Then, the epidemic outbreak size is the product of the probability of epidemic outbreak and its average size, $\rho_i = P_i S$. Numerical results for $P_i$, $S$, and $\Delta$.
\[ ρ \text{ on duplex scale-free networks with the degree exponent } \gamma = 4.5, \text{ the mean degree of the whole network } z_0 = 4 \text{ and } δz = 1/2, \text{ for } δλ = 0 (○), 1/4 (∇), 1/2 (△), 3/4 (▽), \text{ and } 1 ( ◦). \text{ Theoretical curves (lines) and numerical results obtained with } N = 10^4 \text{ nodes (points) are shown together.} \]

\[ ≥ 1, \text{ the transmission via the cross channels is confined in one layer for large } δλ, \text{ decreasing with } δλ \text{ decreases with } δλ \text{ completely blocked, leading to effective isolation of the two layers. Therefore, a curve of epidemic size for larger } δλ \text{ crosses with that for smaller one.} \]

Next, we examine effects of the gap of infection rates between the same-type and across-type transmissions, δλ. We take the initial infection to be a type-1 transmission. When two ER layers with equal mean degrees are coupled (δz = 0), the epidemic outbreak size is monotonically suppressed, with δλ. In this case, the concavity of \( T \) with respect to λ leads to decrease of the cross-type transmissibility always exceeding the increase in the same-type transmissibility, and thereby the overall suppression of epidemic spreading. More complicated features can emerge when the layers with different mean degrees are multiplexed (δz ≠ 0). Specific example for δz = 1/2 with z0 = 2.5 is shown in Fig. 3(b). When δz is large (such that \( δλ/∂δλ > 0 \) for all δλ), the epidemic threshold decreases monotonically with δλ. Therefore the epidemic outbreak size in the vicinity of the threshold becomes larger with δλ, that is, the epidemic spreading gets facilitated. But eventually, for large λ, ρ again decreases with δλ because transmission is effectively confined in one layer for large δλ. In the extreme case of δλ = 1, the transmission via the cross channels is completely blocked, leading to effective isolation of the two layers. Therefore, a curve of epidemic size for larger δλ crosses with that for smaller one.

**Duplex scale-free networks**—We also study the spreading dynamics on duplex static scale-free networks. For the scale-free networks with uncorrelated coupling, \( \kappa_i \) is in general much larger than \( \kappa_i \) due to heterogeneity in degree distributions. The same-type transmissibility \( T_1 \) is the major factor governing the spreading dynamics on multiplex scale-free networks. Therefore, the epidemic outbreak size increases with δλ which is in proportion to \( T_1 \). Numerical result for \( γ = 4.5 \) and \( δz = 1/2 \) with \( z_0 = 4 \) are well agreement with our prediction (Fig. 4). The epidemic threshold decreases and the epidemic outbreak size monotonically increases, with as δλ increases.

**Correlated multiplex networks**—So far, we consider the epidemic spreading on randomly-coupled multiplex networks. For many real-world networks, however, layers of a network combine not randomly but with a correlation between degrees in a node at different layers. Such interlayer degree correlations could affect the epidemic threshold as can be seen from Eq. (7). To take account the correlated multiplexity, we simply consider duplex networks with three representative patterns of interlayer degree correlation: \[ \] the maximally-positive correlated case that a node’s degree in different layers are maximally correlated in their degree order, the maximally-negative correlated case that a node’s degree in different layers are maximally anti-correlated in their degree order, and the uncorrelated case by random coupling case.

As a simplest example, we consider the correlated duplex ER networks with the equal link density \( δz = 0 \), so that \( \kappa_i = \kappa \) and \( \kappa_i = \kappa \). The largest eigenvalue of the Jacobian matrix can be simply expressed as \( \Lambda = T_1(κ) + T_2(κ) \). Thus, the epidemic threshold decreases with the interlayer degree correlation, \( ⟨k_i k_j⟩ \), as shown in numerical results for \( z_0 = 2.5 \) (Fig. 5). For large enough \( λ \), by contrast, the epidemic size is largest for the negatively coupled case. Therefore, the interlayer degree facilitates epidemics for low transmissibilities but hinders large-scale epidemic for high transmissibilities, reminiscent of the effect of degree assortative mixing in single network.

**Summary**—To conclude, we proposed information spreading model on multiplex social networks with the layer-switching cost, leading to path-dependent transmis-
sibilities. We have formulated generalized theory to deal with the path-dependent transmissibility and illustrated how the epidemic threshold and the epidemic outbreak size depend on the multiplexity factors such as the densities of network layers and the infection rates, as well as the type of seed infections and degree correlation between network layers.

Our formalism and results show that the seemingly trivial switching factor can alter the macroscopic dynamic outcome in a nontrivial way and the multiplex interactions cannot simply be aggregated into a simplex one. Therefore, the network multiplexity should be taken into account in order to understand and predict spreading dynamics accurately on multiplex social networks. It also offers insight to optimal strategy for spreading of new information through population with multiple different relations. For example, when population is mostly interacting with a particular type of interaction (large $\delta z$), it would be more effective to spread mostly through the dominant channel (large $\delta \lambda$). On the other hand, if different interaction channels are equally active (small $\delta z$), layer-indiscriminate transmission rates (small $\delta \lambda$) could bring out the most impact.

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