



Finding another yourself in multiplex networks



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ABSTRACT

Recently multiplex networks have attracted a great deal of attentions in the science of complex networks, since they provide more natural and reasonable way to describe realistic complex systems. However, one of the biggest challenges for this issue is the lack of real-world multiplex data, which is mainly caused by the difficulty to distinguish who the replicas of nodes in different network layers (namely, finding another yourself (FAY) problem). In this paper, we consider two kinds of epidemic spreading models named SIR-DIAL model and SIR-NIAL model, and propose methods to solve the FAY problem based on the replica similarity during the epidemic process. To acquire high accuracy, our methods need to observe the spreading information of as many epidemics as possible, and record state information of nodes at as many time steps as possible during the epidemic spreading process with SIR-DIAL model; but just the final results after the epidemic spreading process ends in SIR-NIAL model.

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1. Introduction

Complex network theory provides an important tool to describe and analyze complex systems, ranging from biological, physical to technological and social systems [1,2]. Up to the present, the topological characteristics of complex networks and dynamical process (such as evolutionary game [3–7], disease spreading [8–10], random diffusion [11–13], control theory [14] and synchronization [15–17]) upon them have been extensively studied in both theoretical and empirical areas. However, nearly all studies of networks generally focus on the case of single-layer networks where nodes are connected to each other by a single type of links. While in reality, in many real and engineered systems, the nodes are usually connected to others through multiple channels. For example, human can communicate with each other by verbal communication and different kinds of social networks like Facebook, Twitter. Cities in transportation networks are linked by railway, highway and airline simultaneously. Such systems can be well embedded into the framework of multiplex networks with multiple types of links [18–20]. Each link type in the system defines a network layer, which has interplay with other layers to fulfill the system's function (see Fig. 1 for schematic illustration).

Since multiplex networks may provide a more natural way to describe real complex systems, they have attracted a great deal of attentions [21–30]. In particular, uncovering multiplex networks structure from real data is becoming a hot topic, and it is also fundamental to understand and control collective dynamics upon these architectures. However, one of the biggest challenges that we face currently is the lack of related empirical data. Even if getting data, how to extract multiplex framework still face many conundrums [31–33]. Take multiplex social networks coupled by Facebook network and Twitter network as one example. To capture realistic multiplex networks, we not only need to be familiar with respective topologies of Facebook and Twitter,

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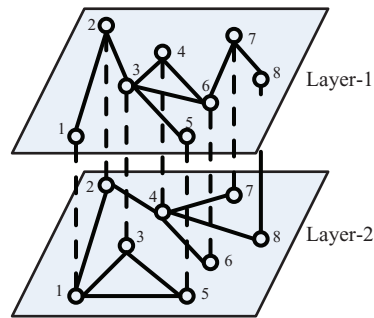


Fig. 1. Schematic illustration of multiplex networks consisting of two network layers, which are interrelated in nontrivial ways. In this architecture, each layer contains the same nodes yet different intra-layer connections (solid lines). Besides, nodes can also have inter-layer connections with their replicas (dash lines).

but also require to distinguish who is also a Facebook user in Twitter communication network and vice versa. For problem of obtaining the respective topologies of each network layer, it may be relatively easy with the help of some techniques like “web crawler”; while the latter one however is very hard to be settled due to the privacy protection of users and the social networks. An interesting question naturally poses itself, which we aim to address in this paper. That is how to distinguish the replicas of given nodes in different layers if we just know the topology of network layers (namely, *FAY* problem).

Since each node has its replicas on every network layer (like the Facebook account and Twitter account of a user), these replicas may exhibit similar features under certain dynamical processes. Based on the shown similarity of replicas, we can get valid information to solve the *FAY* problem. Actually, in the case of single-layer networks, some works have studied the reconstruction of propagation networks based on the node similarity under epidemic dynamics [34,35]. The basic idea of these works is that nodes receiving similar epidemic in spreading are more likely to be connected in the propagation network.

Aiming to resolve *FAY* problem, here we assume the topology of each network layer is known, and then focus on the potential methods based on the replica similarity under epidemic dynamics. Furthermore, since the replicas from different layers may exhibit diverse similarities under different kinds of epidemic models, we consider two kinds of epidemic model on multiplex network. The accuracy of the proposed methods is tested on multiplex scale-free (SF) networks and multiplex Erdős–Rényi (ER) networks.

2. Model

To begin with, we specify multiplex networks model and epidemic spreading model which will be used in what follows.

For simplicity, here we consider the multiplex networks coupled by only two network layers, layer-1 and layer-2 (like Fig. 1). But our proposed methods can be easily extended to multiplex networks consisting of more layers. The multiplex networks contains N nodes, and the average degrees of two layers are defined by z_1 and z_2 . For node i , its replicas in layer-1 and layer-2 are denoted by i_1 and i_2 respectively. The aim of this paper is to distinguish which two nodes from the two layers are the replicas of the same node, namely, finding i_2 in layer-2 for i_1 and vice versa.

With respect to the epidemic spreading model, we consider the susceptible-infected-recovered model (SIR) model, which is one of the best studied models in epidemiology and has widely been applied to mimic the propagation process of disease, information, rumor and virus [28,36]. Under the SIR model, every node of network falls into one of three compartments: susceptible (S), infected (I), and recovered (R). Susceptible nodes are free of epidemics, but can be infected via direct contacts with infected nodes. Infected nodes carry the disease and can pass it to susceptible nodes. Recovered state means that the nodes recover from the disease and cannot pass the disease or be infected again. The model uses discrete time steps for the evolution of disease. In single-layer networks, the infected node can infect its susceptible neighbors with a given transmissibility rate, then becomes recovered with another probability at each time step. However, in multiplex networks, the SIR model can be further divided into two different scenarios: SIR with deterministic infection across layers (SIR-DIAL) and SIR with non-deterministic infection across layers (SIR-NIAL).

In either model, we assume that at each time step the infected nodes of layer-1 (layer-2) can infect their neighbors with transmissibility λ_1 (λ_2), and then become recovered with probability δ (without loss of generality, $\delta = 1$ is fixed since it only affects the definition of the time scale of epidemic spreading). The difference between both models is just crossing-layer infection, namely, whether all the replicas are simultaneously infected or recovered if either replica receives infection or immunity. For SIR-DIAL model, if i_1 (i_2) is infected or recovered, the replica i_2 (i_1) must keep consistent state even if it cannot be infected or recovered at this step. At variance, SIR-NIAL can not guarantee the synchronization of being infected for both replicas. In details, when i_1 (i_2) becomes infected, the replica i_2 (i_1) can become the same state with a inter-layer infection probability λ_{12} (λ_{21}).

According to above definitions, it can be found that the SIR-DIAL model is more appropriate to describe the disease spreading in multiplex human contact networks and virus spreading in multiplex data transmission networks. For example, the spreading networks of HIV can be encapsulated into multiplex framework consisting of maternal-infant transmission network, sexual contact network and blood transfusions network. When an individual gets HIV in any type of contact, he/she will become an

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