



How demography-driven evolving networks impact epidemic transmission between communities

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HIGHLIGHTS

- We develop a complex network susceptible-infected-susceptible (SIS) model which captures the transmission by short-time travelers to investigate the impact of demographic factors on disease spreads.
- The disease-free equilibrium exists and is globally asymptotically stable if $R_0 < 1$, while $R_0 > 1$ leads to a globally asymptotically stable endemic equilibrium.
- The population size on networks evolves with time due to the demographic factors, which causes the degree distribution vary with time.
- Our numerical simulations show that demographic factors, such as birth, immigration, and short-time travels, play important roles in epidemic propagation from one community to another.
- Q3 • Mathematically, our analytical method provides new insights into high dimensional dynamics.

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ABSTRACT

In this paper, we develop a complex network susceptible–infected–susceptible (SIS) model to investigate the impact of demographic factors on disease spreads. We carefully capture the transmission by short-time travelers, by assuming the susceptibles randomly travel to another community, stay for a daily time scale, and return. We calculate the basic reproductive number R_0 and analyze the relevant stability of the equilibria (disease-free equilibrium and endemic equilibrium) of the model by applying limiting system theory and comparison principle. The results reveal that the disease-free equilibrium is globally asymptotically stable given $R_0 < 1$, whereas the condition $R_0 > 1$ leads to a globally asymptotically stable endemic equilibrium. Our numerical simulations show that demographic factors, such as birth, immigration, and short-time travels, play important roles in epidemic propagation from one community to another. Moreover, we quantitatively demonstrate how the distribution of individual's network degree would affect the result of disease transmission.

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1. Introduction

To understand the transmission of epidemics in human society, mathematical models have been extensively used as the significant tools. In the past few centuries, a large number of investigations have been performed using compartment models, which were first introduced by Bernoulli (Dietz and Heesterbeek, 2002) in the 18th century. Afterwards, the studies on epidemic spread have experienced a variety of backgrounds, which are essentially based on the compartment models (for example, Bailey et al., 1975; Busenberg and Vanden Driessche, 1990; Anderson et al.,

1992). The infections of diseases are constrained to take place only along the contacts between susceptible individuals and infectious individuals, whereas the aforementioned models cannot well capture the contacts of humans. Therefore, due to the consideration of heterogeneous contacts among the individuals, network-based epidemic models emerged and have been well developed (Moreno et al., 2002; Albert and Barabási, 2002; Colizza and Vespignani, 2008; Cohen and Havlin, 2010; Newman, 2010; Wang and Li, 2014; Wang et al., 2015b,a), attributed to the prosperous studies of network science, including small-world (Watts and Strogatz, 1998) and scale-free (SF) (Barabási and Albert, 1999) properties.

Apart from the spread within the populations, travel from one subpopulation to another becomes a significant path for transmission at the beginning of the emerging diseases. Plenty of papers

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and books existed that have studied this phenomenon on complex networks ranging from the general properties such as community networks (Britton and Lindholm, 2010; Zhang and Jin, 2012) and metapopulation networks (Hanski, 1998; Wang and Zhao, 2004; Wang et al., 2011, 2013b; Poletto et al., 2013) to the specific networks in detail (Wang and Dai, 2008; Newman, 2010; He et al., 2015). However, they do not take account of the demographics and the visit that can be returned per unit of time, which is very common in real world. Studying the effects of demographic factors is one of the greatest challenges in network epidemiology (Ball et al., 2014). There are some network models that consider with demographics. For instance, Liu et al. (2004) introduced an epidemic model with birth and death in networks, however, they also assumed that the size of the network was constant, and each site on the network was occupied by at most one individual and was otherwise empty. Jin et al. (2014) initially proposed an epidemic model on networks with demographics and conducted various dynamic analyzes based on this model.

Throughout this paper, we refer “birth” as the community inflow rate led by immigration and natural birth, and refer “death” as the community outflow rate resulted from emigration and natural death. These are significant factors for infectious diseases such as tuberculosis which have existed as endemic for thousands of years in China. Moreover, nowadays the domestic transportation between cities become very common, hence it facilitates frequent short-time travels even within days. People contact with local people randomly during their short-time travels, however, the infected people prefer to stay at their original community due to illness. Clearly, unlike the diffusion in patchy models, short-time travels mentioned here can better characterize people’s behaviors for commuting or transportation between cities. In order to investigate the impacts of demographics when a disease emerges in one community, we present an SIS model on networks composed of two communities, in which susceptible individuals randomly travel to another community and return in a daily time scale.

In Section 2, we describe the model formulation and different transmission mechanisms in the intra- and inter-community, then we show the models. In Section 3, we perform theoretical analysis by applying limiting system theory and comparison principle. In Section 4, numerical simulations are made to verify the previous results. Our numerical simulations show that demographic factors, such as birth, immigration, and short-time travels, play important roles in epidemic propagation from one community to another. Moreover, we quantitatively demonstrate how the distribution of individual’s network degree would affect the result of disease transmission.

2. Model description

We study the spread of a SIS type of disease in a pair of connected communities, where the dynamic evolution of inter-personal connections depends on the demographic variation. Fig. 1 illustrates the basic modeling structure. The population size of each community ℓ is N_ℓ , $\ell \in (1, 2)$. Nodes represent individuals, and edges (connections) represent their contacts. Since the communities represent people’s residential locations, each node resides in only one community (Wang et al., 2013a). Each person can have multiple connections with individuals from both communities, and thus, each node is permitted to possess two types of edges, i.e., intra- and inter-community edges. We assume that the intra-community edges are more durable than the inter-community edges because intra-community edges typically capture intimate relations, such as in the household and for relatives and colleagues, whereas inter-community edges describe casual contacts or unstable relationships, such as for deliveries or visiting and business relationships. Define degree k as the number of intra-

community edges of a node, representing the contact pattern of the corresponding person. Within each community ℓ , nodes having the same degree k are organized into a unique subpopulation labeled (ℓ, k) according to the degree-block procedure (Vespignani, 2012). The inter-community edges are realized by the mechanism of the effective force of infection (Diekmann et al., 1995) due to their high-level degree of freedom. The evolution of intra-community networking connections driven by demographic factors is specified below.

2.1. Intra-community demographic evolution

The demographic factors affect the evolution of the network structure within each community. Per unit of time, a number of new individuals are introduced into the community ℓ , in which each newly added is allocated to subpopulation (ℓ, k) with probability $\sigma_{\ell,k}$. Assuming that n is the maximum degree, which is identical in both communities, we obtain $\sum_{k=0}^n \sigma_{\ell,k} = 1$. The lower boundary of the degree is 0, because it is possible to generate a small fraction of isolated nodes during the network evolution. To clarify the analysis, newly introduced individuals are assumed to be susceptible to the disease (Anderson et al., 1992). Induced by natural deaths or people leaving the community, each node is annihilated at a rate μ . Infection-induced death is neglected.

The quantity $\Pi_a^\ell(k)$ represents the probability that an edge emanated from a newly introduced node is connected to a surviving node with degree k in the same community ℓ . Multiple edges between a pair of directly connected nodes and self-looped edges are prohibited. Since the maximal node degree is n , we obtain $\Pi_a^\ell(n) = 0$, implying that nodes with the maximal degree cannot be chosen to perform the edge attachment. From a mathematical perspective, diverse functional formalisms are available to define the quantity $\Pi_a^\ell(k)$. However, the associated analysis might be highly complex and is not the focus of this work. Inspired by the theory of neutral drift (Hanski and Hanski, 1999), we consider that the connection probability is uniformly distributed, i.e.,

$$\Pi_a^\ell(k) = \Pi_a^\ell = 1 / \sum_{k=0}^{n-1} N_{\ell,k} = 1 / (N_\ell - N_{\ell,n}), \quad (1)$$

It means that when a person enters a new city and resides, he or she contacts with the existed habitants there randomly, where $N_{\ell,n}$ is the number of nodes with the maximal degree. The sum of $\Pi_a^\ell(k)$ over all nodes of community ℓ is unity (Lindquist et al., 2009), i.e., $\sum_{k=0}^{n-1} \Pi_a^\ell(k) N_{\ell,k} = 1$. Since real-world large networks exhibiting either a skewed or Poisson-shaped degree distribution only have an extremely small number of nodes with the maximal degree, it is reasonable that $N_{\ell,n} \ll N_\ell$. Accordingly, Eq. (1) is approximated by $1/N_\ell$.

The quantity $\Pi_d^\ell(k)$ represents the probability that the removal of an edge is enforced for a surviving node with degree k in community ℓ due to the disappearance of any neighboring node in the same community. With the assumption of uncorrelated networks (Kiss et al., 2009; Moreno et al., 2002), the probability that a surviving node with degree k is connected to an annihilated node in the same community ℓ is equivalent to the ratio between the degree k and total number of edges in community ℓ , i.e.,

$$\Pi_d^\ell(k) = k / \sum_{k=1}^n k N_{\ell,k}. \quad (2)$$

Individuals with more connections are prone to lose one of the connections because each connection in the networks is removed randomly, where the sum starts from $k=1$ because of the exclusion of isolated nodes. The sum of $\Pi_d^\ell(k)$ over all nodes of community ℓ is unity, i.e., $\sum_{k=1}^n \Pi_d^\ell(k) N_{\ell,k} = 1$.

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