



Coupled effects of local movement and global interaction on contagion

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HIGHLIGHTS

- Segregated spatial domain and individual-based linkage are incorporated into SIS model.
- Activating a small number of individual-based linkage between different spatial domains can prompt the outbreak of epidemic globally.
- Narrowing segregated spatial domain and reducing mobility are conducive to suppression of infectious disease.

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ABSTRACT

By incorporating segregated spatial domain and individual-based linkage into the SIS (susceptible–infected–susceptible) model, we propose a generalized epidemic model which can change from the territorial epidemic model to the networked epidemic model. The role of the individual-based linkage between different spatial domains is investigated. As we adjust the timescale parameter τ from 0 to unity, which represents the degree of activation of the individual-based linkage, three regions are found. Within the region of $0 < \tau < 0.02$, the epidemic is determined by local movement and is sensitive to the timescale τ . Within the region of $0.02 < \tau < 0.5$, the epidemic is insensitive to the timescale τ . Within the region of $0.5 < \tau < 1$, the outbreak of the epidemic is determined by the structure of the individual-based linkage. As we keep an eye on the first region, the role of activating the individual-based linkage in the present model is similar to the role of the shortcuts in the two-dimensional small world network. Only activating a small number of the individual-based linkage can prompt the outbreak of the epidemic globally. The role of narrowing segregated spatial domain and reducing mobility in epidemic control is checked. These two measures are found to be conducive to curbing the spread of infectious disease only when the global interaction is suppressed. A log–log relation between the change in the number of infected individuals and the timescale τ is found. By calculating the epidemic threshold

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and the mean first encounter time, we heuristically analyze the microscopic characteristics of the propagation of the epidemic in the present model.

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1. Introduction

Over the past two decades, the world has witnessed the threat of infectious disease with long-range transmission, such as the severe acute respiratory syndrome (SARS), the pandemic Influenza A (H1N1) and the 2014 Ebola epidemic. An outbreak of the epidemic in human society is closely related to the spatial scale and the interaction structure. G. Chowell et al. have investigated the growth patterns of the 2014 Ebola epidemic at different spatial scales [1]. They have found that the global and the local growth rates exhibit different scaling laws. Depending upon the Cuban contact-tracing detection system, S. Clemençon et al. have studied the HIV/AIDS epidemics in Cuba [2]. They have found that the contact network exhibits a pattern with high intra-connectivity and low inter-connectivity. Understanding the reaction–diffusion processes in complex systems and finding an effective way to prevent and control the outbreak of infectious disease have become an urgent but difficult challenge [3].

In modeling the propagation of infectious disease, the susceptible–infected–susceptible (SIS) model and the susceptible–infected–recovered (SIR) model represent two distinctive disease transmission processes [4–6]. In the SIS model, each individual is initially in one of the two states: S (susceptible) and I (infected). A susceptible individual may become infected as he encounters an infected individual, and an infected individual may become susceptible again after some time. In the SIR model, each individual is initially in one of the three states: S, I and R (recovered). The only difference between the SIS model and the SIR model is that, in the SIR model, an infected individual firstly becomes healthy (recovered), when he is immune to the disease. After some time, the recovered individual may become susceptible to the disease again.

The spread of infectious disease is closely related to mobility patterns and interaction patterns of the population [7–10]. An individual may move about aimlessly like a floating boat in the ocean or travel along a certain path like a move on the chessboard. Two individuals may interact with each other day after day because they are in the same firm or only have a chance encounter because neither of them likes establishing a fixed relationship with any other people. The mobility patterns and the interaction patterns have been extensively studied in the coevolutionary dynamics. M. Perc et al. have studied the coevolution of individual strategies and interaction structures, the coevolutionary rules are quite important in the occurrence of a variety of dynamical effects [11]. A. Szolnoki et al. have studied the effects of mobility patterns on the emergence of cyclic dominance, the mutual relations of pattern formation, the impact of mobility and the emergence of cyclic dominance are found [12]. The original research related to the promising field can be found in Refs. [13–15]. In order to understand the role of underlying structure in the evolution of collective behaviors, different network models are usually borrowed to simulate the mobility patterns and the interaction patterns [16–22]. The existing network models can be classified into two families: the network with a single layer, including regular network, random network and scale-free network [23–27], and the network with multiple-layers [28–32], which consists of two or more sub-networks. S.V. Buldyrev et al. have studied the properties of two interdependent networks [33], a broader degree distribution is found to increase the vulnerability of the interdependent networks. J.X. Gao et al. have studied the percolation properties of interacting networks [34], an analytical framework has been developed.

In relation to the role of network structures in the outbreak of the epidemic, Z.H. Liu et al. have investigated the role of community structure in epidemic propagation [35–37]. They have found that the existence of community structure leads to a smaller threshold of epidemic outbreak. Z.M. Yang et al. have studied the effect of connection patterns on the outbreak of epidemic. They have found that a heterogeneous network structure accelerates the spread of infectious disease [38–41]. K.P. Chan et al. have investigated the effect of aging and links removal on epidemic spread in scale-free networks. The local and global spreads are found to be related to the number of links removed [42]. M. Dickison et al. have studied the epidemic spreading on interconnected networks. A global endemic state is found to be related to the strongly-coupled or weakly-coupled network systems [43]. X.F. Fu et al. have studied the effect of mobility patterns on the outbreak of epidemic. They have found that the change of encounter probability, which may result from the change of population density or the change of moving probability, plays an important role in the change of infected individuals [44,45]. V. Colizza et al. have investigated the invasion dynamics in metapopulation systems. They have found that the heterogeneous connectivity and the mixed mobility pattern play an important role in the outbreak of epidemic [46]. C. Granell et al. have studied the interrelation between the spread of an epidemic and the risk awareness [47]. They have found that there exists a critical point for the onset of the epidemics. M. Boguna et al. have studied the conditions for the absence of an epidemic threshold in heterogeneous networks [5]. A delicate balance between the number of nodes with a high degree and the topological distance is found to be quite important for the occurrence of the threshold.

Until today, in relation to the role of mobility patterns and connection patterns in the outbreak of epidemic, most of the studies consider the two factors respectively. However, in the real world, the evolutionary dynamics in reaction–diffusion systems is usually determined by the coupling of mobility and connectivity, especially the group dynamics in social and economic systems [48–52]. For example, a susceptible individual may be infected by an unknown individual in a random

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