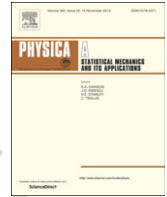




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Q1 Epidemic spreading on dual-structure networks with mobile agents

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HIGHLIGHTS

- We propose a dual structure network model on SIRS dynamics.
- We explain two thresholds of SIRS model both on numeral simulations and theoretical analyses.
- A disease, dies out in both isolated areas who have different population densities, may have a sustainable spreading once two areas are connected.
- The connections between dual structure network could aggravate the prevalence of an epidemic.
- Our findings provide a new angle to explain the persistent spreading of an infectious disease.

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ABSTRACT

The rapid development of modern society continually transforms the social structure which leads to an increasingly distinct dual structure of higher population density in urban areas and lower density in rural areas. Such structure may induce distinctive spreading behavior of epidemics which does not happen in a single type structure. In this paper, we study the epidemic spreading of mobile agents on dual structure networks based on SIRS model. First, beyond the well known epidemic threshold for generic epidemic model that when the infection rate is below the threshold a pertinent infectious disease will die out, we find the other epidemic threshold which appears when the infection rate of a disease is relatively high. This feature of two thresholds for the SIRS model may lead to the elimination of infectious disease when social network has either high population density or low population density. Interestingly, however, we find that when a high density area is connected to a low density may cause persistent spreading of the infectious disease, even though the same disease will die out when it spreads in each single area. This phenomenon indicates the critical role of the connection between the two areas which could radically change the behavior of spreading dynamics. Our findings, therefore, provide new understanding of epidemiology pertinent to the characteristic modern social structure and have potential to develop controlling strategies accordingly.

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1. Introduction

The study of epidemic spreading has lasted for centuries and we have witnessed a prosperous age with the development of networked theory in the last decades. By the integration of large scale data sets and the explicit simulation from entire populations to the scale of single individuals, the real-world accuracy of the study in epidemiology has been considerably improved [1–7]. Many mathematical models and methods have evolved into microsimulation that can be computationally implemented by keeping track of billions of individuals. By providing quantitative analyses, these work have gained importance in the public-health domain, especially in infectious disease epidemiology. Many researchers are advocating the use of these models as real-time, predictive tools [8–10]. Furthermore, these work offers a number of interesting and unexpected phenomenon, whose theoretical understanding represents a new challenge, and have stimulated an intense research activity. In particular, epidemic modeling approaches have expanded into schemes that include explicitly individual heterogeneity, spatial structures and the multiple time scales during the evolution of an epidemic [11].

The core of all data-driven epidemic modeling approaches lies the structure of human interactions, mobility, and contact patterns. And it is found that its best representation is in the form of networks [12–16]. The complex topological properties shown by many real-world networks have profound effects on the behavior of several phenomena characterizing the dynamics and stability of these systems. By representing human society with complex networks, where agents are represented by nodes and connections are the links between the nodes, substantial advances have been achieved in understanding the dynamics of the epidemic spreading [17–20], which includes infectious thresholds [20–24], the influence of system structure [25–29], immunization strategy [30], the epidemic predictability [31–35], et al. Although networks have been acknowledged long as a key ingredient of epidemic modeling, the recent abundance of data is changing our understanding of a wide range of phenomena and calls for a detailed theoretical understanding of the interplay between epidemic processes and networks. A large number of work has shown that most real-world networks exhibit dynamic self-organization and are statistically heterogeneous, which are typical hallmarks of complex systems [16–18,36–42]. Epidemic spreading in real-world networks is different from which is in regular lattices. Networks are hierarchically organized with a few nodes that may act as hubs and where the vast majority of nodes have few interactions. Both social and infrastructure networks are organized in communities of tightly interconnected nodes. Although the connection process of nodes is always randomly, organizing principles and correlations in the connectivity patterns define network structures that are deeply affecting the evolution and behavior of epidemic and contagion processes. Furthermore, networks complex features often find their signature in statistical distributions which are generally heavy tailed, skewed, and varying over several orders of magnitude.

Here we notice, in modern society, in order to adapt the worldwide competition and to squeeze the efficiency of manpower, people continually gather to big cities so that they could collaborate more closely and utilize social resources more efficiently. This process makes the population densities in cities become higher and correspondingly in rural areas lower. Thus, as a consequence, it leads to a typical type of structure that in one part of the society, i.e. cities, the population density is very high, while in the other part of the society, i.e. rural areas, the population density is very low, here referred as *dual structure*. The feature of dual structure of modern society is being more distinct which may cause social dynamics that are unexpected in traditional social networks. Therefore, studies about this typical structure are increasingly demanding and important.

In this paper, we study epidemic spreading on networks with dual structure. We use Susceptible–Infected–Recovered–Susceptible (SIRS) epidemic model to describe the infectious disease. First, we find that there are two infectious thresholds in this model: β_1 and β_2 . When the infection rate of a disease β is either $\beta < \beta_1$ or $\beta > \beta_2$, the spreading of the disease cannot persist in the network. More interestingly, we find that for two networks where an infectious disease cannot persistently spread on neither of them, if they are connected the same disease may have a consistent spreading on both of them. We will show that this phenomenon actually comes from the two thresholds feature of SIRS model.

Our findings offer a new understanding for the epidemic spreading in modern society. As we mentioned above, with the modern urbanization process, massive people continually gather to big cities, which leads to a urban–rural dual structure and this structure becomes increasingly distinct. On one hand, the population density in urban area could be unprecedented high leading to a low threshold. On the other hand the population density in rural area continually decreases leading to a high threshold. Our study shows the possibility that infectious disease may vanish in the two areas when they are isolated, but persists when they are connected.

This paper is organized as follows. In Section 2, we introduce the networked model of dual structure. In Section 3, we study the two thresholds of the SIRS model. In Section 4, we present the results of epidemic spreading in the dual structure. Finally, we conclude this work in Section 5.

2. The model

We propose a simple model to represent dual structure of a modern society (see Fig. 1). In this model, two squared areas, denoted as A and B , with periodic boundary condition are used to describe the high density city and low density rural area where the lengths of which are L_A and L_B , respectively. We consider a total number of N agents which could move freely in either of the two areas. When an agent i stays in an area, it could move with velocity \mathbf{v}_i , and the position of agent i is updated under the rule as follows

$$\mathbf{x}_i^Z(t + \Delta t) = \mathbf{x}_i^Z(t) + \mathbf{v}_i(t) \Delta t, \quad (1)$$

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