



How the distance between regional and human mobility behavior affect the epidemic spreading

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HIGHLIGHTS

- The distance between regions and human mobility behavior are considered in the epidemic spreading.
- The epidemic threshold is theoretically calculated.
- The results show that wherever the virus originates from, the final infection size is similar.

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ABSTRACT

The distance between different regions has a lot of impact on the individuals' mobility behavior. Meanwhile, the individuals' mobility could greatly affect the epidemic propagation way. By researching the individuals' mobility behavior, we establish the coupled dynamic model for individual mobility and transmission of infectious disease. The basic reproduction number is theoretically obtained according to the next-generation matrix method. Through this study, we may get that the stability state of the epidemic system will be prolonged under a higher commuting level. The infection density is almost the same in different regions over a sufficiently long time. The results show that, due to the individual movement, the origin of virus can only speed up or delay the outbreak of infectious diseases, however, it have little impact on the final infection size.

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1. Introduction

Human behavior is the driving force behind many complex social phenomena. The understanding of human behavior has always been the focus of sociology, psychology and economics. Quantitative analysis of human behavior is an important research topic of modern science [1–4]. Studying the human behavior could not only improve the human's understanding of their own behaviors, but improve the human's understanding for the social system.

Human society has always been in the long struggle with infectious diseases. Many of infectious diseases including Ebola virus, pestilence, influenza, plague, AIDS, cholera, SARS and avian flu spread over many areas of the world, and kill tens of thousands of people [5–7]. Therefore, researchers try their best to cover the epidemic spreading mechanism and find the best way to control the epidemic. The wanton transmission of infectious diseases will not only endanger the health of mankind itself, but bring great disaster to the people's livelihood [8–10]. Large-scale outbreak of each infectious disease in the history of mankind has brought physical and psychological suffering to people, while having a great hindrance on the development of human society [11]. In addition, the deterioration of the natural environment and the rapid development

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of social factors do not only provide opportunities for the transmission of existing and new infectious diseases, but lead to the emergence of the virus or bacteria variations, which will seriously endanger human life [12]. With the in-depth exploration of human behavior, some studies that involve the relationship between human behavior and transmission of infectious disease have been proposed in succession [13–15]. However, the ability to fully understand human behavior and study its impact on transmission of infectious disease remains an important project. By this study, to some extent, we could strengthen the human's recognition for behavioral evolution and formulate some significant strategies to curb the epidemic spread. Scholars have adopted a variety of theoretical methods to study the epidemic spreading, such as the percolation theory, mean field theory, game theory, stochastic processes, cellular automaton, etc. [16–20]. As the small-world network and the scale-free network are discovered, scholars have proposed a number of epidemic spread models that perform on those complex networks. The most classic models include: (1) the mean field theory proposed by Pastor-Satorras and Vespignani [21]; (2) the percolation model proposed by Newman [22]; (3) the discrete probability model proposed by Wang et al. [23]. Kihong investigate the generalized epidemic process on modular networks, the results show that the system exhibits a bond-percolation type continuous phase transition for weak social reinforcement [24]. Samue explore the effect of a prudent adaptive behavior on disease transmission. Their results indicate the effects of the prudent could accelerate spread [25]. Han research the epidemic process on activity-driven modular networks, their obtain that the final infected density in the original-infected-community shows different trends with the change of the response strength of vaccination and the spreading rate [26].

Based on the above analysis, this paper studies the influence of individual mobility on epidemic spreading. Firstly, a coupled dynamic model between individual mobility behavior and transmission of infectious diseases is established. Then, the next-generation matrix method is used to calculate the basic reproduction number. Finally, we perform the epidemic spreading on network to study the outbreak time and final epidemic size. The structure of this paper is as follows: in the second section, the new epidemic model is presented, and the basic reproduction number is theoretically calculated. The commuting level, infection rate and recovery rate are numerical studied in the third section. Finally, Section 4 gives the conclusion.

2. Epidemic spreading model

In this section, we examine the effect of regional distance and human mobility behavior on epidemic spreading. According to the actual connectivity between regions, each region is regarded as a node in the network, and the people in this region are evenly mixed. That is to say, an individual in the same place has the same probability to communicate with any other individuals. The individuals in different places can access to any place of the connected networks. However, according to the actual situation, the probability for each individual to stay in different places is different. Here, the commuting form of an individual between place i and place j is set as $p_{ij} = \frac{1}{(1+d_{ij})^\alpha}$, which means that the probability for individuals in place i to stay in (access) the place j is p_{ij} . d_{ij} refers to the shortest distance between the place i and j ; $\alpha \geq 0$ is a parameter, indicating the commuting level. To some extent, the commuting level indicates the degree that an individual would like to stay in the original region. In general, people would stay in the original region all the time while $\alpha = +\infty$. Without loss of generality, p_{ij} is normalized as follows:

$$\bar{p}_{ij} = p_{ij} \left(\sum_j p_{ij} \right)^{-1} = (1 + d_{ij})^{-\alpha} \left(\sum_j (1 + d_{ij})^{-\alpha} \right)^{-1} \quad (1)$$

It can be easily obtained from the formula (1) that $\sum_j \bar{p}_{ij} = 1$, $i = 1, 2, \dots$. And we may get that there is almost no possibility for the individuals in the i place to stay in the j place, when $d_{ij} \rightarrow \infty$.

Due to the fact that individuals may be repeatedly infected with some flu viruses, we here consider the SIRS epidemiological transmission model, where S represents susceptible persons, I represents infected persons, and R represents recovery. Based on individual's movement behavior, the coupled epidemic spreading dynamic model is established as follows:

$$\begin{cases} \frac{dS_i}{dt} = - \sum_{j=1}^n [S_i \text{ infected in community } j] + \gamma_i R_i \\ \frac{dI_i}{dt} = -\mu_i I_i + \sum_{j=1}^n [S_i \text{ infected in community } j] \\ \frac{dR_i}{dt} = \mu_i I_i - \gamma_i R_i \end{cases} \quad (2)$$

Where, S_i , I_i and R_i refer to the susceptible person, infected person and recovery person in the i place, respectively. $[S_i \text{ infected in place } j]$ indicate the infection density of susceptible persons who comes from i and are infected in the place j ; μ_i refers to the recovery rate in the place i ; γ_i refers to the recovery rate in the place i , namely the probability that recovery person becomes susceptible person again due to loss of immunity to infectious disease.

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