



Dynamic modeling and analysis of sexually transmitted diseases on heterogeneous networks

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HIGHLIGHTS

- Correlation coefficients about degrees are defined.
- We proposed an SIS mean-field dynamical model of STDs.
- We analyzed the basic reproduction number of the model.
- Influences of homosexual and heterosexual transmissions on STDs are studied.

ARTICLE INFO

Article history:

Received 11 December 2014

Received in revised form 13 January 2015

Available online 9 February 2015

Keywords:

Mean-field model

Correlation coefficient

Basic reproduction number

ABSTRACT

Considering homosexual contacts and heterosexual contacts in the course of sexual contacts, double degrees which describe the numbers of homosexual contacts and heterosexual contacts are introduced, correlation coefficients about degrees based on the joint probability distribution are given, and an SIS mean-field model about sexually transmitted diseases is presented when degrees are uncorrelated. The basic reproduction number of diseases is studied by the method of next generation matrix. Results show that, when homosexual contacts and heterosexual contacts all exist, once the disease is epidemic in the interior of male (female) population which is caused by male (female) homosexual transmissions, or the disease is epidemic between the two species which is caused by heterosexual transmissions, the disease must be epidemic in the whole population. Numerical simulations confirm the theoretical results.

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1. Introduction

The transmission and prevention of diseases have been a major public health problem and attracting more attention of many scholars [1–3]. The spread of diseases on complex networks recently becomes the subject of intense research. Epidemiologists and mathematician devoted themselves to develop mathematical models on complex networks, there are mainly mean-field model based nodes [4,5], Miller model based on edges [6–10], moment closed model based on the method of pair approximation [11–14], percolation theory based on the method of the probability generation function [15–19]. These researches are beneficial to guide to understand how an epidemic spreads and to make immunization and vaccination strategies [20,21].

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Infectiousness of sexually transmitted diseases (STDs) is very strong, and the disease is relatively easy to relapse, therefore, STDs have been attracted comprehensive attentions of biologists and mathematicians. Some mathematical models on STDs have been established [22–27]. It is hoped some effective prevention measures of diseases are obtained by studying the development trend of the diseases. In the process of modeling of STDs, the characterization of the sexual contacts patterns is most important. About the method of modeling, so far, there are mainly two ways, one is classic compartment models [22–24], the other is complex models in which network topology is abstractly described [25–27]. Since classical compartment models are assumed that populations are homogeneously mixed, that is, the probabilities that each individual contacts with other individuals are same, however, it is different from those contacts patterns in real lives. In fact, the probabilities that an individual contacts other individuals residing in different space locations are completely different. Therefore, researches of STDs based on complex networks naturally become hot issues, there are some research works as follows.

A dynamical SIS model of STDs on bipartite graphs representing heterosexual contact networks is built in Ref. [25]. Authors analytically derived the expression for the epidemic threshold. Newman considered the network with sex structure in which the population is divided into men and women [26], and discussed an SIR model by the percolation theory and gave analytic expressions for the sizes of both epidemic and nonepidemic outbreaks and for the position of the epidemic threshold. However, some data indicated that homosexual contacts also play an important role in STDs on the scale-free networks [28–31]. According to CDC's recent data, gay and bisexual men continue to be the risk group who are severely infected by HIV [29]. Some sub-populations of MSM, such as student MSM and ethnic minority MSM, who were previously believed to be low risk group of HIV, have also become high-risk groups [30]. To be more realistic, Zhang et al. [27] incorporated homosexual contacts into a model of STDs, they obtained the basic reproduction number and proved the global stability of the endemic equilibrium. However, every individual has only a degree representing the total number of male sex partners and female sex partners in Ref. [27], it cannot still specifically characterize homosexual contacts and heterosexual contacts for some given individual. So, in this paper, we assume that the disease is transmitted not only among contacts between men and women, but also among homosexual contacts (namely between men and men, and, between women and women). Considering different infection rates (from an infected male to a susceptible female, from an infected female to a susceptible male, from an infected male to a susceptible male, and from an infected female to a susceptible female), we assume every individual has two types of degrees (male degree and female degree) which describe the numbers of its male sex partners and female sex partners, this is different from Ref. [27]. Our aim is to study the influence of homosexual transmission and heterosexual transmission on STDs through the establishment of the dynamic model.

2. Dynamic modeling

We assume that there are male nodes and female nodes in the network, the total numbers of male nodes and female nodes are respectively N^m and N^f , $q = \frac{N^f}{N^m}$ is the sex fraction in the network. For any two nodes in the network, they are network neighbors to each other if there exists an edge between them, it represents that they are sexual partners to each other in real lives. For some given male (female) node, i ($i = 0, 1, 2, \dots, n_1$) is the number of male (female) neighbors, namely, i is the number of sexual partners of the same sex with a given node. j ($j = 0, 1, 2, \dots, n_2$) is the number of female (male) neighbors, namely, j represents the number of sexual partners of the opposite sex with a given node. $N_{i,j}^m$ ($N_{i,j}^f$) is the number of male (female) nodes with i male (female) neighbors and j female (male) neighbors. The total number of nodes N in the network satisfies $N = \sum_{i,j} N_{i,j} = \sum_{i,j} (N_{i,j}^m + N_{i,j}^f) = \sum_{i,j} (S_{i,j}^m + I_{i,j}^m + S_{i,j}^f + I_{i,j}^f)$.

To study the influence of network topology on the diseases, we need to know the degree distribution of the network, we assume two degree distributions of men and women nodes are respectively $p_{i,j}^m = \frac{N_{i,j}^m}{N^m}$ and $p_{i,j}^f = \frac{N_{i,j}^f}{N^f}$. We assume that every individual has at least a sexual partner, namely, i and j cannot be simultaneously equal to 0. In the transmission process of STDs, homosexual (intra-species) transmission and heterosexual (inter-species) transmission are both considered. Thus, for intra-species transmission, there are two contacts networks: male sexual contacts network and female sexual contacts network. For inter-species transmission, there is a heterosexual contacts network between male and female. Because of bisexual contacts in the whole population, there is an interplay between intraspecies transmission and interspecies transmission, the above three networks can be merged into a single network. In other words, we consider a sexual contacts network which can be decomposed into three subnetworks. Specifically, subnetwork 1 describes male homosexual contacts, the degree distribution is

$$p_{i,\cdot}^m = \begin{cases} \sum_{j=1} p_{0,j}^m, & i = 0, \\ p_{i,0}^m + \sum_{j=1} p_{i,j}^m, & i = 1, 2, \dots, n_1, \end{cases} \quad (1)$$

subnetwork 2 describes female homosexual sexual contacts, its degree distribution

$$p_{i,\cdot}^f = \begin{cases} \sum_{j=1} p_{0,j}^f, & i = 0, \\ p_{i,0}^f + \sum_{j=1} p_{i,j}^f, & i = 1, 2, \dots, n_1, \end{cases} \quad (2)$$

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