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Modeling vaccination in a heterogeneous metapopulation system

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HIGHLIGHTS

- Dynamics of heterogeneous metapopulations that contain vaccinated individuals is proposed.
- Epidemic threshold only dependent on the diffusion coefficient of the infected population.
- With low diffusion coefficient, reproduction number can be calculated.
- Reproduction number dependent on the number of neighbors a city can have.

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ABSTRACT

We present here a multicity SIS epidemic model with vaccination. The model describes the dynamics of heterogeneous metapopulations that contain imperfectly vaccinated individuals. The effect of vaccination on heterogeneous multicity models has not been previously studied. We show that under very generic conditions, the epidemic threshold does not depend on the diffusion coefficient of the vaccinated individuals, but it does depend on the diffusion coefficient of the infected population. We then show, using a novel methodology, that the reproduction number is determined by the homogeneous model parameters and by the maximal number of neighbors a city can have, when the diffusion coefficient of the infected population is low. Finally, we present numerical simulations to support the analytical results.

1. Introduction

The spread of disease among human and animal populations, or viruses among computer networks, has been studied for many decades. Several classical mathematical models have been proposed to describe this behavior [1–4]. When a vaccination is introduced into real-life and model systems, disease progression can be slowed and, in some cases, even completely stopped. This is clearly demonstrated in the many mathematical models that describe the vaccination process [5–7].

The classical epidemic models have been extended in many ways (e.g., to study diseases spreading in populations divided into subgroups that might influence each other [8]). Network theory has provided another source of inspiration in mathematical epidemiology, where nodes represent individuals and links represent their interactions [9–13]. The structure of the underlying network (e.g., the degree distribution) may strongly influence spreading dynamics [13–25]. This radical change in the behavior of the processes suggests that the standard epidemiological frameworks should be carefully revisited.

While the initial network approaches have focused on networks with nodes that represent individuals and links representing the interactions, a new method has recently been developed to describe more complex intra-population relationships that highlights the importance of describing the development of disease as a metapopulation [26,27]. In these models,

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each node is defined as a city that contains two populations of individuals: infected or susceptibles. A main method used in these models is to describe the disease as occurring with density-dependent transmission so that new contacts are made within a population as it increases in size [28]. The structure of the spatial network of cities (nodes) is described by the adjacency matrix. We here summarize the properties of this matrix through the connectivity (degree) distribution $p(k)$, which is defined as the probability that a randomly chosen city has connectivity k. The model is described as an SIS model using the following reactions:

$$\begin{aligned} &I \xrightarrow{\mu} S \\ &I + S \xrightarrow{\beta} 2I, \end{aligned} \tag{1}$$

where I denotes infected individuals, S denotes susceptible individuals, μ represents recovery from infection, and β represents the transmission processes. The infectious disease spreads through a population of initially susceptible individuals. After the infected individuals recover, they immediately become susceptible. The random movement of infected or susceptible individuals from node to node is represented by the diffusion coefficients D_I and D_S, respectively.

In the present paper, we analyze the spread of infectious disease using an SIS modeling framework. We also include vaccination in the system, similar to Ref. [5]. This study explores the impact of vaccination on a heterogeneous system in an attempt to model an epidemic and identify preventative factors, in particular, the effect of diffusion of vaccinated individuals in the network on disease transmission.

The remainder of the paper is organized as follows. In order to explore the SIS model, including the effect of vaccination on heterogeneous metapopulations with diffusion coefficients, a new model is presented in Section 2. The SIS model studied here contains three independent diffusion rates for the susceptible, infected and vaccinated populations. However, only the diffusion rate of the infected population affects the infectivity threshold for the emergence of epidemics; this conclusion is studied in Section 3. In Section 4, we find a new way to calculate the reproductive number, with which the epidemic threshold of the system can be found. In Section 5, some numerical simulations are performed that illustrate the theoretical analysis. Finally, we conclude in Section 6.

2. Model

Our model is based on the model presented in Refs. [29,30] that describes the spread of infectious diseases in metapopulations as a continuous time framework. Each node is defined as a city that contains a mixture of susceptible, infected, and vaccinated groups. For a network with N nodes, the N by N adjacency matrix is denoted by A. $A_{ij} = 1$ when nodes i and j are adjacent, and $A_{ij} = 0$ otherwise. A is symmetric and we set $A_{ii} = 0$ $(1 \leq i \leq N)$.

Each individual is at a node and adopts either a susceptible or infectious state. SIS dynamics with infection rate β and recovery rate μ occur in each metapopulation. The infection event at node i occurs at a rate of $\beta I_i S_i$, where S_i and I_i are the numbers of susceptible and infected individuals at node i, respectively. This assumption implies all-to-all interactions within each metapopulation. At the same time, individuals perform a simple random walk. In infinitesimal time Δt, a susceptible (infected) individual at node i with degree k_i moves to one of its neighboring nodes with equal probability $\approx \frac{D_S \Delta t}{k_i}$ $(\approx \frac{D_I \Delta t}{k_i})$, where D_S (D_I) is the diffusion rate for the susceptible (infected) individual and k_i is the degree of node i.

The main equations for thus system are given in Ref. [30]:

$$\frac{\mathrm{d}}{\mathrm{d}t} S_i(t) = I_i(\mu - \beta S_i) - D_S S_i + D_S \sum_j A_{ji} \frac{1}{k_j} S_j \tag{2}$$

$$\frac{\mathrm{d}}{\mathrm{d}t} I_i(t) = I_i(\beta S_i - \mu) - D_I I_i + D_I \sum_j A_{ji} \frac{1}{k_j} I_j. \tag{3}$$

In Ref. [5], Krisb-Zeleta and Velasco-Hernandez presented an SIS disease model with a vaccinated class in a constant sized and closed population with homogeneous mixing. This model depended on three factors: the percentage of the vaccinated population, the period of effective vaccination, and the strength of the vaccine.

We added these three vaccination factors to a network of heterogeneous metapopulations, represented above in Eqs. (2) and (3), to examine how they affect the epidemic threshold of the system. This new model can be described as a susceptible-individual-vaccinated (SIV) model as follows:

$$\begin{aligned} &V \xrightarrow{\theta} S \\ &S \xrightarrow{\phi} V \\ &I + V \xrightarrow{\sigma\beta} 2I, \end{aligned} \tag{4}$$

where V denotes vaccinated individuals, σ is the reduction in infection rate, ϕ is the rate of vaccination in the susceptible population, and θ is the rate at which the vaccine wears off, i.e., when the vaccinated individual becomes susceptible again. The value of σ ranges from 0 (a completely effective vaccine) to 1 (a completely ineffective vaccine). As is usual in an SIS