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# Stochastic spatial structured model for vertically and horizontally transmitted infection

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## HIGHLIGHTS

- An epidemic process with horizontal and vertical transmission is analyzed.
- The epidemic stochastic lattice model is studied by Monte Carlo simulations.
- The epidemic stochastic lattice model is studied also by a pair mean-field approach.
- The phase diagram may display a healthy and infected coexisting state.

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## ABSTRACT

We study a space structured stochastic model for vertical and horizontal transmitted infection. By means of simple and pair mean-field approximation as well as Monte Carlo simulations, we construct the phase diagram, which displays four states: healthy (H), infected (I), extinct (E), and coexistent (C). In state H only healthy hosts are present, whereas in state I only infected hosts are present. The state E is characterized by the extinction of the hosts whereas in state C there is a coexistence of infected and healthy hosts. In addition to the usual scenario with continuous transition between the I, C and H phases, we found a different scenario with the suppression of the C phase and a discontinuous phase transition between I and H phases.

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## 1. Introduction

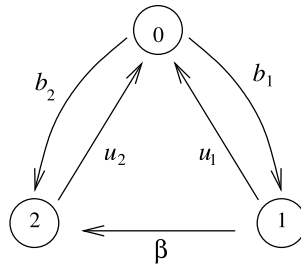
The transmission of disease between hosts of the same species occurs either vertically, when the pathogen is transmitted directly from the parents to the child, or horizontally, when the hosts are not in a parent-child relationship. Several diseases are transmitted in both horizontal and vertical ways [1–11]. A question that arises in the study of horizontally and vertically transmitted diseases is the determination of the amount of horizontal transmission needed to maintain a vertical transmission. This problem was analyzed by Lipsitch et al. [7] who proposed that in the stationary state, the prevalence of infection can be higher when there are both types of transmissions as compared to the case when only one type is present. This result implies that for the case of virulent pathogens, the high number of infected cases coming from vertical transmission is a consequence of a high rate of horizontal transmission.

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**Fig. 1.** Illustration of the reactions of the stochastic lattice model. The states 0, 1 and 2 represent, respectively, an empty site, a site occupied by a healthy host and by an infected host. The quantities  $u_1, b_1, u_2, b_2$ , and  $\beta$  are the transition rates.

One approach in the study of population biology of infectious diseases consists in setting up differential equations for the densities of the various types of population [12], similar to equations used in chemical kinetics in which the law of mass action is employed. The model of Lipsitch et al. [7] is of this type and consists of two differential equations for the densities of infected and uninfected populations. It is possible, on the other hand, to set up stochastic population models with space structure to describe the spreading of diseases and, more generally, population dynamics [13–21]. In fact, a space structured stochastic model with the same reactions as the model used by Lipsitch et al. has been introduced by Schinazi [17]. For a particular case, he showed that if the vertical transmission is sufficiently high then infected hosts can be eliminated even if the horizontal transmission is high. Here, we analyze a space structured stochastic model which is a slight modification of the Schinazi’s model. The model is investigated by means of two mean-field approaches, the simple mean-field approximation and the pair mean-field approximation, and by numerical simulations on a square lattice. The evolution equations at the level of simple mean-field approximation are found to be equivalent to the differential equations used by Lipsitch et al. [7].

The analysis of the mean-field equations and the numerical simulations on a square lattice reveal that the model may display four states: an extinction (E) state, where the hosts have disappeared, a healthy (H) state, with healthy hosts and the absence of infected hosts, an infected (I) state, with infected hosts and the absence of healthy hosts, and a coexistence (C) state, where both infected and healthy hosts are present. For some set of values of the parameters, the H and I states are not contiguous and are separated by the C state. The transition lines HC and IC of the phase diagram correspond to continuous phase transitions. However, for other sets of values of the parameters, it is possible that the H and I states be contiguous. In this case the transition line HI corresponds to a discontinuous phase transition. The phase diagram obtained by the simple and pair mean-field approximation as well as the numerical simulations are qualitatively similar. However, there are important quantitative changes. For instance, we have found that the H, I and C regions of the phase diagram obtained by numerical simulations are smaller than their counterpart obtained by pair mean-field approximations which in turn are smaller than those obtained by simple mean-field approximation.

**2. Model**

The stochastic lattice model is defined as follows. Each site of a regular lattice is either empty or occupied by a host that can be healthy or infected. A healthy host dies spontaneously with rate  $u_1$  and is born by a catalytic process with rate strength  $b_1$ . Analogously, an infected host dies spontaneously with rate  $u_2$  and is born by a catalytic process with rate strength  $b_2$ , a reaction related to vertical transmission. A healthy host becomes infected catalytically with rate strength  $\beta$ , a reaction understood as horizontal transmission. These reactions are illustrated in Fig. 1.

Denoting the state of site  $i$  by the stochastic variable  $\eta_i$ , then  $\eta_i$  takes the values 0, 1, or 2, according to whether the site is empty, occupied by a healthy host or occupied by an infected host. The possible transitions of the state of a given site  $i$  with the respective rates are as follows

|          |                   |                   |                   |                   |                   |
|----------|-------------------|-------------------|-------------------|-------------------|-------------------|
| Reaction | $0 \rightarrow 1$ | $1 \rightarrow 0$ | $0 \rightarrow 2$ | $2 \rightarrow 0$ | $1 \rightarrow 2$ |
| Rate     | $b_1 n_i$         | $u_1$             | $b_2 m_i$         | $u_2$             | $\beta m_i$       |

where  $n_i$  and  $m_i$  denote the number of healthy hosts and the number of infected hosts in the neighborhood of site  $i$ , respectively. The neighborhood of a site in a regular lattice is chosen to be its nearest neighbor sites. The model has five parameters:  $b_1, u_1, b_2, u_2$ , and  $\beta$ . Sometimes it will be convenient to use the parameters  $r_1$  and  $r_2$  defined by

$$r_1 = \frac{u_1}{b_1}, \quad \text{and} \quad r_2 = \frac{u_2}{b_2}. \tag{1}$$

When  $u_1 = u_2$ , the present stochastic model reduces to a particular case of the stochastic model introduced by Schinazi [17].

The transition rates above define a stochastic process characterized by a master equation, which gives the evolution of the probability distribution  $P(\eta)$  associated to the microscopic state of the system  $\eta = \{\eta_i\}$ . From the master equation it is possible to write down the time evolution of the several marginal probability distributions such as  $P(\eta_i)$ , the probability

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