Coexistence results for a spatial stochastic epidemic model

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Abstract. *We introduce a spatial stochastic model for infectious diseases, such as influenza, that do not confer immunity and from which one usually recovers. We prove the existence of an endemic state in any dimension for any strictly positive value of the recovery rate. This is in sharp contrast with what happens for the model with no recovery in $d = 1$ for which it is known that the disease dies out for all parameters values.*

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1. Introduction. Spatial stochastic models for the transmission of infectious diseases have been studied since at least Bartlett (1957). In this paper we consider a model that generalizes several of the models previously studied, see Mollison (1977), Kuulasmaa (1982), Sato, Matsuda and Sasaki (1994), Andjel and Schinazi (1996). We call the following model the *basic spatial epidemic*. It is a continuous time stochastic process on $\mathbf{Z}^d$ where there is at most one individual per site. Healthy individuals give birth to healthy individuals on empty nearest neighbor sites, infected individuals infect their healthy nearest neighbors and individuals die at certain rates. We say that an endemic state is possible if there exists a stationary measure for the process with infected and healthy individuals. The existence of an endemic state (this is also called a coexistence result) has not been proved for the basic spatial epidemic. The problem of showing coexistence for this model seems mathematically challenging. However, coexistence results have been obtained for modified models. In particular, Durrett and Neuhauser (1991) show coexistence for a model in which births of healthy individuals occur spontaneously, see also Andjel and Schinazi (1996). Schinazi (1996) and (2000) proves coexistence for models in which infected individuals may give birth to healthy or infected individuals.

In this paper we allow infected individuals to recover (they still may die). We propose a (very naive) model for diseases such as influenza for which we believe that this is the first spatial stochastic model. We show that for any stricly positive value of the recovery rate an endemic state in any dimension is possible for appropriate values of the other parameters. This is in sharp contrast to what happens for the basic spatial epidemic for which it is known that there can be no coexistence in $d = 1$, see Mollison (1977) and Andjel and Schinazi (1996).

2. The spatial stochastic model. We consider a continuous time spatial stochastic model on $\mathbf{Z}^d$ where each site may be in one of three states: 0, 1 or 2. State 0 corresponds to an empty site, state 1 to a site with a healthy individual and state 2 to a site with an infected individual. There is at most one individual per site.

If the model is in configuration η, let $n_1(x, \eta)$ and $n_2(x, \eta)$ be the number of nearest neighbors of x (among the $2d$ nearest neighbors of x) that are in state 1 and in state 2,

respectively. Assume that the model is in configuration η, then the state at a given site x evolves as follows:

$$0 \to 1 \text{ at rate } \lambda_1 n_1(x, \eta)$$

$$1 \to 2 \text{ at rate } \lambda_2 n_2(x, \eta)$$

$$2 \to 1 \text{ at rate } r$$

$$1 \to 0 \text{ at rate } \delta_1$$

$$2 \to 0 \text{ at rate } \delta_2$$

In words, healthy individuals give birth on empty nearest neighbor sites at rate λ_1. Infected individuals infect nearest neighbors that are healthy at rate λ_2. Infected individuals recover at rate r (and are immediately susceptible to the disease again). Finally, healthy and infected individuals die at rate δ_1 and δ_2, respectively. What we have called the basic spatial epidemic is the special case $r = 0$.

In the absence of infected individuals we have a population of 0's and 1's only. In this particular case, the system evolves as

$$0 \to 1 \text{ at rate } \lambda_1 n_1(x, \eta)$$

$$1 \to 0 \text{ at rate } \delta_1$$

The model above is called a contact process. It is known that it has critical value $\lambda_c(d)$ (that depends on the dimension d of the grid $\mathbf{Z}^d$) such that if $\lambda_1/\delta_1 \leq \lambda_c(d)$ then the 1's die out while if $\lambda_1/\delta_1 > \lambda_c(d)$ then there is a positive probability that there will be 1's at all times if the process starts with at least one 1. We will denote $\lambda_c(1) = \lambda_c$. For more on the contact process, see for instance Liggett (1999). We are now ready to state our results.

Theorem 1. *Assume that $r > 0$, $\lambda_1 > 0$ and that λ_2 is such that $\lambda_2/r > \lambda_c$ (the critical value for the one-dimensional contact process). There exists a constant $c > 0$ (depending on r, λ_1, λ_2) such that if $\delta_1 < c$ and $\delta_2 < c$ then*

(a) Starting with any initial configuration on $\mathbf{Z}^d$ ($d \geq 1$) with at least one healthy and one infected individual there is a positive probability that healthy and infected individuals will exist at all times.

(b) There is a stationary measure for the spatial stochastic epidemic that concentrates on configurations with healthy and infected individuals.

Theorem 1 shows the existence of an endemic state for low virulence (that is, for low δ_2). Conversely, one can show that if the virulence is too high then an endemic state is not possible. This is what we do next.

Theorem 2. *For any $r \geq 0$ and any $\lambda_2 \geq 0$, if $\delta_2 > \frac{\lambda_2}{\lambda_c(d)} - r$ then the infected individuals die out in the following two senses. There is no stationary measure with infected individuals. Starting with finitely many infected individuals, with probability one there are no infected individuals after a finite random time.*

In particular, in $d = 1$ there can be no epidemic if $\frac{\lambda_2}{\lambda_c} < r$ and Theorem 1 tells us that epidemics are possible if $\frac{\lambda_2}{\lambda_c} > r$ and δ_2 and δ_1 are low enough.

3. The mean field model. We now consider the mean field model associated with our spatial stochastic epidemic. This is a model which is deterministic and non spatial. We like to think of it as a model where all individuals mix together. Since the spatial stochastic model above is rather rigid (infections and births occur at nearest neighbors) it is interesting to compare its behavior to the behavior of the mean field model.

Let $u_i \geq 0$ be the density of individuals in state i, for $i = 0, 1, 2$, in particular $u_0 + u_1 + u_2 = 1$. Assuming total mixing we get the following system of differential equations.

$$u_1' = \lambda_1 u_1 u_0 + r u_2 - \lambda_2 u_1 u_2 - \delta_1 u_1$$

$$u_2' = \lambda_2 u_1 u_2 - r u_2 - \delta_2 u_2$$

Note that there are two trivial equilibria $(u_1, u_2) = (0, 0)$ and $(u_1, u_2) = (1 - \delta_1/\lambda_1, 0)$, provided

$$\delta_1 < \lambda_1$$

The condition above is necessary and sufficient for the disease free population not to die out, a hypothesis that we assume. We now examine the stability of the equilibrium $(u_1, u_2) = (1 - \delta_1/\lambda_1, 0)$. The Jacobian of the system of differential equations at $(1 - \delta_1/\lambda_1, 0)$ is

$$\begin{pmatrix} -\lambda_1 + \delta_1 & -(\lambda_1 + \lambda_2)(1 - \delta_1/\lambda_1) + r \\ 0 & \lambda_2(1 - \delta_1/\lambda_1) - r - \delta_2 \end{pmatrix}$$

There are two eigenvalues: $-\lambda_1 + \delta_1$ and $\lambda_2(1 - \delta_1/\lambda_1) - r - \delta_2$. The first one is strictly negative. The second one is strictly positive if and only if

$$\delta_1/\lambda_1 + (r + \delta_2)/\lambda_2 < 1 \tag{3.1}$$

Thus, condition (3.1) is necessary and sufficient for the unstability of the disease free equilibrium $(1-\delta_1/\lambda_1, 0)$ (see for instance Hirsh and Smale (1974), p 181, p 187). Therefore, an epidemic is possible (in the sense that the disease free equilibrium is not stable) if and only if (3.1) holds.

4. Discussion. It is known that coexistence does not hold for the basic spatial epidemic ($r = 0$) when $d = 1$, see Mollison (1977) and Andjel and Schinazi (1996) (the argument there is written in the case $\delta_1 = 0$ but can easily be adapted for any $\delta_1 \geq 0$). Thus, our Theorem 1 shows that the introduction of a recovery rate (even a very small one) drastically changes the behavior of the model, at least in dimension one. We believe this is due to the fact that the recovery rate r in the spatial model adds some mixing. In particular, in $d = 1$ a block that has 2's at both endpoints and no 1's in between remains free of 1's until it disappears if $r = 0$. If $r > 0$ then 1's may appear inside a block of 2's and this gives more fuel to the epidemic. This picture is consistent with what happens to the mean field model: coexistence may occur for $r = 0$. This is so because everybody mixes with everybody else and r is not needed. Similarly, it is generally believed that coexistence holds for the basic spatial epidemic in $d \geq 2$ with $r = 0$, see Sato, Matsuda and Sasaki (1994). In $d \geq 2$ a block of 0's and 2's may split into several smaller blocks and that helps coexistence. Again this is consistent with our picture that mixing helps coexistence for this type of model. However, the reverse may happen for other types of models (see Schinazi (2003)).

Condition (3.1) shows that whether or not an epidemic may occur, for the mean field model, depends on the density of healthy individuals in the disease free equilibrium. In particular, if δ_1/λ_1 approaches 1 (that is, the equilibrium density of healthy individuals approaches 0) then in order for (3.1) to be met $(r + \delta_2)/\lambda_2$ must approach 0 (that is, each infected individual must in average infect more and more people). We suspect that the same type of result holds for the spatial epidemic model but we dont know how to show it.

5. Proofs. We now give the so called graphical construction of the spatial stochastic process. Consider a collection of independent Poisson processes: $\{N_1^{x,y}, N_2^{x,y}, D_1^x, D_2^x, R^x :$

$x, y \in \mathbf{Z}^d, ||x-y|| = 1\}$. For x and y in $\mathbf{Z}^d$ such that $||x-y|| = 1$ let the intensities of $N_1^{x,y}$, $N_2^{x,y}$, D_1^x, D_2^x, R^x be λ_1, λ_2, δ_1, δ_2 and r, respectively. At every arrival time of D_1^x, if there is a 1 at x we put a 0 at x. Likewise at every arrival time of D_2^x, if there is a 2 at x we put a 0 at x. At an arrival time of $N_1^{x,y}$ if there is 1 at x and a 0 at y we put a 1 at y. At an arrival time of $N_2^{x,y}$ if there is 2 at x and a 1 at y we put a 2 at y. Finally, at the arrival times of R^x if there is a 2 at x we replace it by a 1.

In this way we obtain a version of our spatial epidemic model. The process is said to be *restricted* to a space-time region $\mathcal{A}$ if we only use the arrival times inside $\mathcal{A}$. For more on graphical constructions, see Liggett (1999).

Proof of Theorem 1

We prove Theorem 1 first in $d = 1$ and then we will explain how the same proof actually extends to any $d \geq 2$.

We define

$$\mathcal{L} = \{(m,n) \in \mathbf{Z}^2 : m+n \text{ is even}\}$$

$$B = (-4L, 4L) \times [0,T] \qquad B_{m,n} = (2mL, nT) + B$$

$$I = [-L, L] \qquad I_m = 2mL + I$$

where L, T are parameters to be chosen later. Let $k = [\sqrt{L}]$ (where $[a]$ is the integer part of a). We declare $(m,n) \in \mathcal{L}$ wet if at time nT there are no 0's in I_m and there are at least k 2's in I_m and if at time $(n+1)T$ there are no 0's in I_{m-1} and in I_{m+1} and at least k 2's in each of these intervals. Moreover, we require that the event just described occur for all possible states of the sites $-4L$ and $4L$ between times nT and $(n+1)T$. This is important to ensure a finite range of dependence for the percolation process defined on $\mathcal{L}$.

We will now show that by choosing L and T sufficiently large the probability of a site (m,n) being wet can be made arbitrarily close to 1. By translation invariance, it is enough to show this for the site (0,0).

There are three steps in this proof. In the first step we will show that starting with no 0's in I there will be no 0's in $(-4L, 4L)$ by a certain time T_1, with high probability. In the second step we will show that at time T_1 there are still many 2's in I. Finally, in the third step we will show that by a certain time T there are at least k 2's in I_1 and in I_{-1}.

We start by setting $\delta_1 = \delta_2 = 0$ in the box B. In particular a site that is occupied in B does not become empty again. Let R_t be the rightmost non empty site in $(-4L, 4L)$ at time t. We assume that there are no 0's in I at time 0, thus, $R_0 \geq L$. Under the assumption $\delta_1 = \delta_2 = 0$, R_t increases with time and never decreases. The rate at which R_t jumps to $R_t + 1$ depends on the state of the sites R_t, $R_t - 1$ and $R_t + 1$. By definition of R_t the state of $R_t + 1$ is 0 and the state at R_t cannot be 0. Since $\delta_1 = \delta_2 = 0$ the state at $R_t - 1$ cannot be 0 either. Thus, there are four possibilities for the states of $(R_t - 1, R_t)$. If, for instance $(R_t - 1, R_t) = (2, 2)$ then after a rate r exponential time we get that $(R_t - 1, R_t) = (2, 1)$ and after a rate λ_1 exponential time R_t jumps to $R_t + 1$ provided R_t is not infected by $R_t - 1$. Similarly for the other three possibilities for $(R_t - 1, R_t)$ we see that after a random time with finite mean R_t jumps to $R_t + 1$. Therefore, R_t is larger than a renewal process with finite mean renewal time. By the renewal theorem we get that there exists $a > 0$ such that almost surely

$$\liminf_{t \to \infty} \frac{R_t}{t} \geq a.$$

Thus, for any $\epsilon > 0$ there is an L large enough such that if $T_1 = 5L/(2a)$ then

$$P(R_{T_1} > 3L) \geq 1 - \epsilon.$$

The leftmost occupied site behaves in a symmetrical way. Therefore, the probability that all sites in $[-3L, 3L]$ are occupied at time T_1 is at least $1 - 2\epsilon$ if L is large enough.

We now start the second step of our proof. Part of it has already appeared somewhere else for a different model (see Schinazi (2001)) but we include it for the sake of completeness. We want to show that by time T_1 there are still plenty of 2's in I. Note that there are no 0's in I and that the death rates are taken equal to 0 in B. Therefore, the 2's restricted to I are a contact process with the following rates:

$$1 \to 2 \text{ at rate } \lambda_2 n_2(x, \eta)$$

$$2 \to 1 \text{ at rate } r$$

A special coupling shows that, given a certain number of 2's, the more spread out the initial configuration the more 2's it produces (see Theorem 1.9 (c) in Liggett (1985)). Since we know we have at least $k = [\sqrt{L}]$ 2's in I, to start with, the worst case scenario

(from the 2's point of view) is to start with an interval C that has length $k+1$ for which each site is occupied by a 2.

We now restrict the 2's to C, that is, we do not allow infection from outside to inside C. This can only decrease the number of 2's in C. We assume that $\lambda_2/r > \lambda_c$, therefore we have a supercritical contact process. Let τ^n be the (random) time it takes for a contact process to become extinct when restricted to $[-n,n]^d$ and starting with a particle on each site of $[-n,n]^d$. Mountford (1993)(see his Proposition 2.1) has shown that for a supercritical contact process we have

$$P(\tau^n \leq e^{dn}) < e^{-dn} \text{ for large } n.$$

At time 0 there is a 2 on each site of C, that is $k+1$ particles. Let M be the integer part of $k^{1/2}$. We partition C into M intervals, where each one is a translate of $[0,M]$. We run M contact processes each one restricted to one of the M sub-intervals of C. It is easy to see that at any time there are at least as many 2's in C than in the union of these sub-intervals. If by time T_1 none of the contact processes running on a sub-interval of C has died out then there are at least M particles (one per sub-interval) in C. Thus, the probability that there are at least M particles in C by time T_1 is at least

$$P(\tau^M \geq T_1)^M \geq P(\tau^M \geq e^M)^M \geq (1-e^{-M})^M.$$

The preceding probability can be made larger than $1-\epsilon$ provided L is large enough.

The last paragraph shows that, with probability at least $1-3\epsilon$, at time T_1 we have at least M 2's in I and no 0's in $[-3L,3L]$. Thereafter, the 2's evolve as a supercritical contact process in $[-3L,3L]$ (since we are assuming that $\delta_1 = \delta_2 = 0$ in B).

We now start the third and final step of this proof. It consists in showing that, with high probability, we will have at least k 2's in $[-3L,-L]$ and in $[L,3L]$ at a certain time T.

For any subset A of $\mathbf{Z}$, let η_t^A be a contact process starting with a 2 at each site of A and 1's everywhere else. Let $|\eta_t^A|$ be the number of 2's at time t. The key to the proof is the following result. There is $\alpha > 0$ such that for any A there are strictly positive constants C and γ such that

$$P(|\eta_t^A| \neq 0, \eta_t^A(x) \neq \eta_t^{\mathbf{Z}}(x)) \leq Ce^{-\gamma t}$$

for all $x = y + \alpha t$ where y is in A. In words, η_t^A is coupled to $\eta_t^{\mathbf{Z}}$ inside a linearly growing set. See (3.2) in Durrett and Schinazi (1993).

We can pick k large enough so that a contact process stating with at least $M = [\sqrt{k}]$ 2's has a survival probability of at least $1 - \epsilon$, see (1.9) in Liggett (1999) and Theorem 1.9 (c) in Liggett (1985).

Let $T_2 = \frac{9L}{2a}$, it is easy to see that if we take L large enough then the contact process starting with at least M 2's in $[-L, L]$, at time T_1, will be coupled to $\eta_t^{\mathbf{Z}}$ on $[-3L, 3L]$ with probability at least $1 - \epsilon$ at time $T = T_1 + T_2$. Moreover, it is not difficult to see that α is also the speed at which the rightmost and leftmost 2's travel. So by time T the contact process started inside $[-L, L]$ has not yet, with high probability, reached the boundary of $[-4L, 4L]$. That is, the contact process restricted to B and the unrestricted contact process are identical with probability at least $1 - \epsilon$, provided L is large enough, and the coupling above works for the restricted process as well.

The process $\eta_t^{\mathbf{Z}}$ is known to be stochastically larger than the so called upper invariant measure of the contact process. The upper invariant measure of a supercritical contact process has positive density $\rho > 0$ of 2's. Moreover, since μ is ergodic (see Proposition 2.16 p 143 in Liggett (1985)) we have that

$$\lim_{L\to\infty} \frac{1}{2L+1} \sum_{x=-3L}^{x=-L} \eta(x) = \rho > 0$$

μ-almost everywhere. This shows that under μ there are at least k 2's in $[-L, L]$, with probability $1 - \epsilon$ if L is large enough. Since $\eta_t^{\mathbf{Z}}$ is coupled to the contact process restricted to B with probability at least $1 - \epsilon$, we get that for L large enough there are at least k 2's in $[-3L, -L]$ with probability at least $1 - 2\epsilon$ at time T. Similarly, we have at least k 2's in $[L, 3L]$ with probability at least $1 - 2\epsilon$ at time T.

For any $\epsilon > 0$ we may pick L (depending on ϵ and λ_2) large enough so that

$$P((0,0) \text{ is wet}) > 1 - 7\epsilon \text{ for } \delta_1 = \delta_2 = 0.$$

Since B is a finite space time box, we may pick $c > 0$ so that the probability that no flip from 1 to 0 and that no flip from 2 to 0 occur inside the box B is at least $1 - \epsilon$, for $\delta_1 < c$

and $\delta_2 < c$. Thus,

$$P((0,0) \text{ is wet}) > 1 - 8\epsilon \text{ for } \delta_1 < c \text{ and } \delta_2 < c.$$

Note that the event (m,n) is wet for the percolation model defined on $\mathcal{L}$ involves only a finite range of dependence. Standard percolation arguments show that we may take $\epsilon > 0$ small enough so that there is an infinite cluster of wet sites in $\mathcal{L}$ with positive probability. If we start the process with at least one 1 and at least one 2 then there is a positive probability of having at least k 2's in $[-L, L]$ by time 1. We then start the construction above and there is a positive probability of an infinite cluster of wet sites. This in turn guarantees that there will be 1's and 2's at all times and completes the proof of Theorem 1 (a) in $d = 1$.

The existence of a stationary distribution concentrating on configurations with 1's and 2's is a consequence of our comparison with oriented percolation. To see this, start the process with a 2 at each site and take Cesaro averages of the law of the process; extract a convergent subsequence of the Cesaro averages. Since our process is Feller, any limit is a stationary distribution. Since we start the process with infinitely many 2's we have infinitely many trials at our disposal to succeed in our construction of an infinite wet cluster for the oriented percolation on $\mathcal{L}$. We will eventually succeed since each trial has the same probability of success. Moreover, this infinite cluster has a positive density of wet sites, provided ϵ is small enough, so we get that the limit of the Cesaro average must have a positive density of 2's. This completes the proof of Theorem 1 (b) in $d = 1$.

For the proof of the Theorem in $d > 1$ we may embed the preceding 1-dimensional construction in $\mathbf{Z}^d$. The only difference is that the boundary of each $B_{m,n}$ is larger in $d > 1$ but this may only provoke the appearance of more 1's and 2's inside the box (since there are no deaths inside the box) and so the same construction will work in $d > 1$.

Proof of Theorem 2

We are going to couple the epidemic process to the contact process with rates:

$$1 \to 2 \text{ at rate } \lambda_2 n_2(x, \eta)$$

$$2 \to 1 \text{ at rate } \delta_2 + r$$

Fix an initial configuration for the epidemic model and to get the initial configuration for the contact process replace all the 0's by 1's. We construct the contact process above in the same probability space as the epidemic model by using some of the same Poisson processes used in the construction of the epidemic model. More precisely, we use the Poisson processes $N_2^{x,y}$, D_2^x and R^x that have rates λ_2, δ_2 and r, respectively. At the arrival times of D_2^x and R^x we put a 1 at x. At the arrival times of $N_2^{x,y}$, if there is a 2 at x and a 1 at y we put a 2 at y. It is easy to check that at all times the contact process has more 2's than the epidemic model in the sense that if there is a 2 at a site for the epdemic model there must be a 2 at the same site for the contact process. This is due to the fact that in the contact process 2's have more opportunities to infect their neighbors than in the epidemic model since there are no 0's in the contact process. Under the assumption of Theorem 2 this is a subcritical contact process and the 2's die out in the two senses stated in the theorem. Thanks to the coupling just described the 2's in the epidemic model must die out as well. This completes the the proof of Theorem 2.

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