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Dynamical evolution of discrete epidemic models

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Abstract

The dynamical evolution of a deterministic epidemic model is studied. We model the system by taking into account an intermediate class of population, say infected, which after a latency period enter into the infectious class. A mortality rate induced by the disease is also considered. The system evolves towards a final state which may develop a catastrophic epidemic if small outbreaks of the disease emerge. The final size, the threshold and the severity of the epidemic are also analyzed and calculated for this model.

1. Introduction

Mathematical epidemic models have been used to calculate and describe the dynamical evolution of epidemics as well as their final sizes, threshold values and severity [1–3] the oldest model being due to Bernoulli [4]. A widely used model is the Kermack–McKendrik model [5], which studies a system of three populations: susceptible, infectious and removals. Our model is similar to this one, but we introduce discrete equations, a well-known approach in population dynamics [6]. In addition, we consider a fourth class, the infected population, characterized by a parameter γ related to the incubation period of the disease. Our model is not able to calculate the speed of propagation of the epidemic, which has been analyzed elsewhere [7], because diffusion effects are not considered. The effect of an incubation or latency period corresponds to a delay time, and this has recently been shown to be important with regard to the speed of propagation of epidemics [7], forest fires [8] and human migrations [9]. It is therefore important to analyze the influence of the incubation period of a disease on its

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threshold and final size, and this is the aim of the present paper. We also analyze the stability conditions of the first evolution of the epidemic, that is, we study the behavior of the epidemic around the final state when small outbreaks of the disease take place and observe a catastrophic effect on the population.

2. The discrete model

We propose in this work a discrete-time deterministic model for the study of the dynamical evolution of an epidemic taking into account a latency period, as well as a mortality rate induced by the disease. This model involves four populations: susceptible (x_n), infected (y_n), infectious (z_n) and removals (r_n). All of the susceptible individuals are nonimmune to the disease. The infected individuals are those nonimmune susceptibles who have caught the disease at some previous time, but they still cannot transmit it. After a latency period, the infected individuals leave to be infected and become infectious: they may thereafter transmit the disease. We also assume that the disease propagates by direct contact between a susceptible and an infectious, as occurs with viral diseases. We proceed now to develop the model. Let p denote the probability of effective transmission of the disease between any susceptible and any infectious during one sampling interval. So, $1-p$ is the probability to avoid the transmission and remain susceptible. The probability that a susceptible avoids becoming infected by all of the z_n infectious individuals during the sampling interval n is

$$q_n = (1-p)^{z_n} . \tag{2.1}$$

Therefore, the number of susceptibles in the next sampling interval $n+1$ will be the number of susceptibles which remain susceptible, namely $q_n x_n$. In consequence, we may write

$$x_{n+1} = (1-p)^{z_n} x_n . \tag{2.2}$$

We suppose that those individuals leaving the susceptible class enter entirely into the infected class. Furthermore, we assume that a proportion, say γ (related to the latency period τ), of the infected individuals remain infected at the end of each sampling interval. Then

$$y_{n+1} = [1-(1-p)^{z_n}]x_n + \gamma y_n . \tag{2.3}$$

The infectious individuals in the sampling interval $n+1$ are bz_n (b being the proportion of infectious individuals which remain infectious at the end of each sampling interval), plus the number of infected individuals which do not remain infected and in consequence become infectious. Then,

$$z_{n+1} = (1-\gamma)y_n + bz_n \tag{2.4}$$

and b may be viewed as the life expectancy. The parameter γ is related to the latency period: when the latency period is large the fraction of infected individuals which become infectious, $1-\gamma$, is small and vice versa, so $1-\gamma \sim \tau^{-1}$.

Finally, the removals in the interval $n+1$ are those of the period before plus the fraction of infectious individuals which die, so

$$r_{n+1} = r_n + (1-b)z_n \,. \tag{2.5}$$

The system under study is a set of nonlinear discrete equations given by

$$\begin{aligned} x_{n+1} &= (1-p)^{z_n} x_n \,, \\ y_{n+1} &= [1-(1-p)^{z_n}]x_n + \gamma y_n \,, \\ z_{n+1} &= (1-\gamma)y_n + bz_n \,, \\ r_{n+1} &= r_n + (1-b)z_n \,. \end{aligned} \tag{2.6}$$

One may observe that

$$x_{n+1} + y_{n+1} + z_{n+1} + r_{n+1} = x_n + y_n + z_n + r_n = 1 \,, \tag{2.7}$$

if we normalize the number of individuals.

2.1. The threshold of the epidemic

The epidemic propagates if the infected or infectious individuals gain new recruits. If we consider the first step for the infectious individuals,

$$z_1 = (1-\gamma)y_0 + bz_0 \,.$$

In order to have $z_1 > z_0$, the following condition must be fulfilled:

$$y_0 > y_0^* \equiv \frac{(1-b)z_0}{1-\gamma} \,, \tag{2.8}$$

where y_0^* is the threshold value for the infected population. In the absence of any infectious individual ($z_0 = 0$), there is no threshold and the disease spreads. For $z_0 \neq 0$, the threshold decreases with increasing values of the parameter b, and vanishes for its maximum possible value $b=1$, as it was to be expected intuitively, because the disease will spread for sure in the absence of any removal from the infectious population. On the other hand, a large value of γ corresponds to a low latency period, which causes an increase in the threshold y_0^* for the epidemic not to die out. Thus, in contrast with the classical model [5], the one presented here predicts a dependence for the threshold on the incubation or latency period. As an application we take $x_0 = 0.8$, $y_0 = 0.1$, $z_0 = 0.1$, $r_0 = 0$, $p = 0.25$, $\gamma = 0.2$ and $b = \frac{1}{3}$ obtaining $y_0^* = 0.083$. The evolution of the epidemic in this case is plotted in Fig. 1. In this case, the threshold condition (2.8) is satisfied, so that the infection does spread and it eventually removes about 30% of the initial population. This result for the impact of the disease on the total population illustrates our model for a specific case. However, it is certainly relevant to approach this point in a more general way, and we tackle this point in the following section.

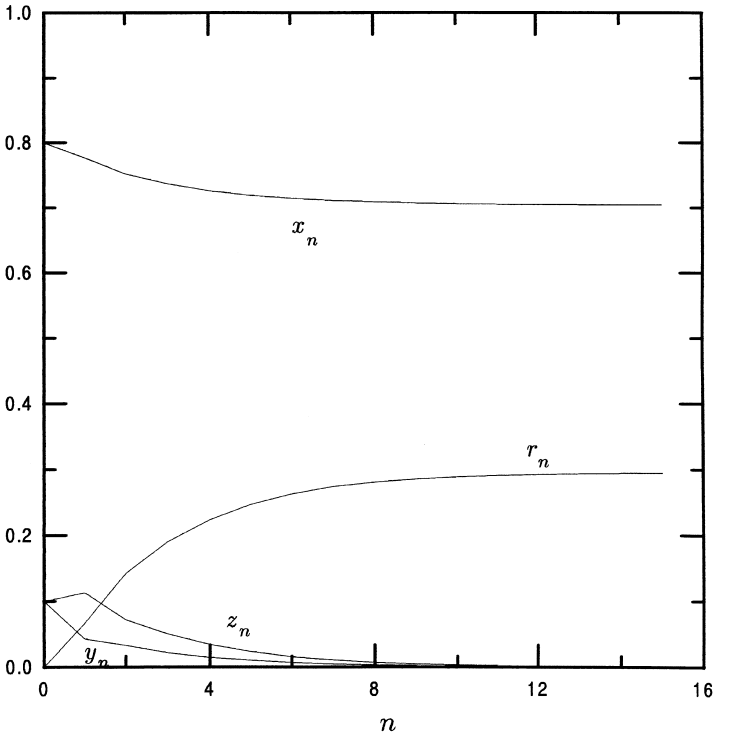

Fig. 1. Dynamical evolution of system (2.6) for $x_0 = 0.8, y_0 = z_0 = 0.1, r_0 = 0$ and $p = 0.25, \gamma = 0.2, b = \frac{1}{3}$. These initial conditions fulfill the threshold condition (2.8). One observes that the final size of the epidemic is 0 for infected and infectious populations, and 0.7 and 0.3 for susceptibles and removals, respectively.

3. The final size of the epidemic

One of the most important characteristic parameters of an epidemic is the final size of the population. Let $(x_\infty, y_\infty, z_\infty, r_\infty)$ be the final state of the population. The parameters with the subindex ∞ denote the final size of each population. The final state is the critical or fixed point of system (2.6) and fulfills the relation

$$x_\infty + y_\infty + z_\infty + r_\infty = 1\,, \tag{3.1}$$

where the final size of the susceptible population is defined by

$$x_\infty = \lim_{n\to\infty} x_n\,,$$

and equivalently for the other individuals. It is easy to prove that x_∞ always exists: from Eqs. (2.6) we observe that $0 < x_{n+1} < x_n$, so $\{x_n\}$ is a nonincreasing sequence that is bounded from below. Therefore, the limit always exists.

In the limit $n \to \infty$, $x_{n+1} \to x_n$ and, assuming that $\gamma \neq 0$ and $b \neq 0$, from Eqs. (2.6) and (3.1) one may note that

$$y_\infty = z_\infty = 0\,,$$

$$r_\infty = 1 - x_\infty\,, \tag{3.2}$$

where x_∞ and r_∞ must be determined. From system (2.6) one gets for the first two steps

$$x_1 = x_0(1-p)^{z_0}\,,$$

$$x_2 = x_0(1-p)^{z_0+z_1}\,,$$

then, by induction one finds that

$$x_n = x_0(1-p)^{\sum_{i=0}^{n-1} z_i}\,. \tag{3.3}$$

On the other hand, one also gets

$$r_1 = r_0 + (1-b)z_0\,,$$

$$r_2 = r_0 + (1-b)(z_0+z_1)$$

and

$$r_n = r_0 + (1-b)\sum_{i=0}^{n-1} z_i\,. \tag{3.4}$$

By combining (3.3) and (3.4) we have

$$x_n = x_0\alpha^{r_n - r_0}\,,$$

where we have defined the auxiliary parameter

$$\alpha \equiv (1-p)^{1/(1-b)}\,,$$

and from $r_\infty = 1 - x_\infty$ we finally get

$$\alpha^{x_\infty} = \frac{\beta}{x_\infty}\,, \tag{3.5}$$

where

$$\beta \equiv x_0\alpha^{1-r_0}\,.$$

Eq. (3.5) is a transcendent equation which must be solved numerically to find the final size x_∞. Another characteristic parameter related to the epidemic is the severity of the epidemic which may be defined as

$$S \equiv \frac{x_0 - x_\infty}{x_0}\,.$$

So, Eq. (3.5) may be written as

$$1 - S = (1-p)^{(1-x_0(1-S)-r_0)/1-b}\,.$$

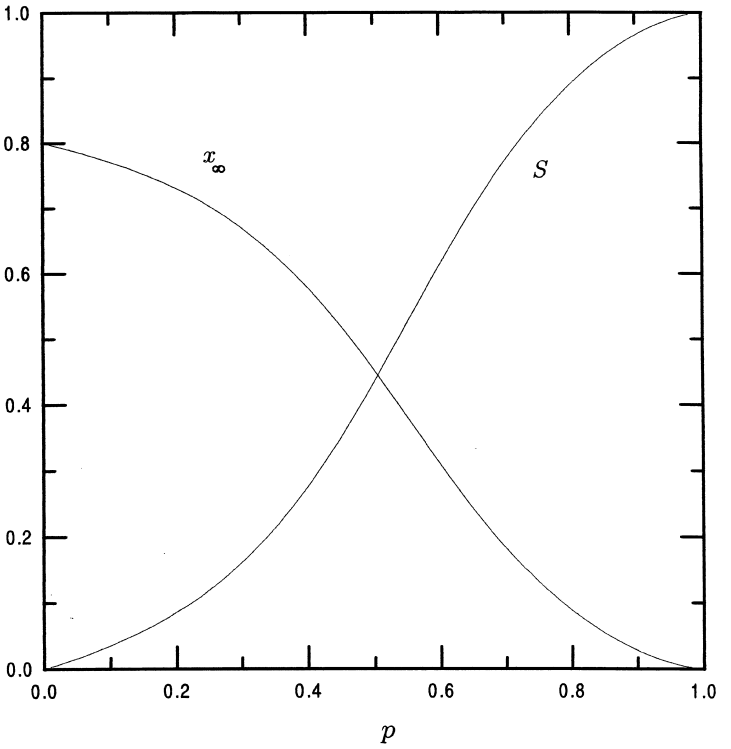

Fig. 2. Dependence of the final size of the susceptible population, and of the severity of the epidemic, on the probability of effective transmission. We have taken, also for this plot, $x_0 = 0.8, r_0 = 0$ and $\gamma = 0.2, b = \frac{1}{3}$.

If we take the same values as in Fig. 1 we get for the final size $x_\infty \simeq 0.7$, $r_\infty \simeq 0.3$ and the severity is $S = 0.125$. We note that these results are in agreement with the asymptotic behavior in Fig. 1. We can also plot the final size x_∞ and the severity S in terms of the probability of effective transmission p. This is shown in Fig. 2, where we observe that the final size of susceptible individuals decreases with increasing p, which means that the number of susceptibles at the end of the epidemic is lower the greater the probability of effective transmission is. This is as it should be, and corresponds to the fact that the severity increases with p. It is interesting to note that the parameter γ has no effect on the final size of the epidemic (see Eq. (3.5)). We therefore conclude that although the inclusion of a latency period τ in the model has a very important effect on the threshold value y_0^* of the infected population for the epidemic to spread (see Eq. (2.8)), the severity of the epidemic is not affected by the value of τ.

4. Stability analysis of the final size

At the end of the epidemic one may countabilize its effects by means of the difference between the initial size and the final size of the populations. It has been observed

experimentally, however, that the final state may be sensible to small outbreaks of the disease [10]. In this sense it is interesting to analyze the evolution of the final size submitted to small deviations. This is the aim of this section. In order to analyze the stability conditions of the fixed point $(x_\infty, 0, 0, r_\infty)$, we must linearize system (2.6) around it. If we define the linearized matrix around the fixed points of system (2.6) by $\mathbb{L}$, and define $\|\mathbb{L}\| = \max\{|\mu_1|, |\mu_2|, |\mu_3|, |\mu_4|\}$ where μ_i, with $i = 1, 2, 3, 4$ are the eigenvalues of $\mathbb{L}$, the fixed point is stable if and only if $\|\mathbb{L}\| < 1$ and is unstable if $\|\mathbb{L}\| > 1$. After some algebra, one finds the Jacobian matrix given by

$$\mathbb{L} = \begin{pmatrix} 1 & 0 & x_\infty \ln(1-p) & 0 \\ 0 & \gamma & -x_\infty \ln(1-p) & 0 \\ 0 & 1-\gamma & b & 0 \\ 0 & 0 & 1-b & 1 \end{pmatrix} . \tag{4.1}$$

Evaluating the eigenvalues of $\mathbb{L}$ we find that the fixed point is unstable and small outbreaks of the disease generate a new epidemic if

$$x_\infty > x_\infty^* \equiv \frac{1-b}{\ln(1/1-p)} ,$$

otherwise we cannot predict the evolution of the epidemic. This condition together with Eq. (3.5) becomes, after assuming that $r_0 = 0$ and some algebra,

$$x_\infty e^{-1+(1/x_\infty)} < x_0 ,$$

but this inequality cannot be fulfilled. Therefore, the linear analysis of stability does not hold for this system and one must check the stability of the fixed point for the system $\mathbf{x}_{n+2} = \mathbf{F}(\mathbf{x}_n)$ or $\mathbf{x}_{n+3} = \mathbf{F}(\mathbf{x}_n)$ and so on, but in these cases our system repeats the same behavior and we cannot extract information about the stability. An alternative way to this study is to conserve the nonlinear part of the equations of the system by introducing a perturbation of the fixed point of the form

$$x_n = x_\infty + \varepsilon_n ,$$

$$y_n = \delta_n ,$$

$$z_n = \mu_n ,$$

$$r_n = r_\infty + \rho_n ,$$

where ε_n, δ_n, μ_n, and ρ_n symbolize the deviations from the fixed point $(x_\infty, 0, 0, r_\infty)$. Introducing this into (2.6) we get

$$\varepsilon_{n+1} = (1-p)^{\mu_n}(x_\infty + \varepsilon_n) - x_\infty ,$$

$$\delta_{n+1} = [1-(1-p)^{\mu_n}](x_\infty + \varepsilon_n) + \gamma\delta_n ,$$

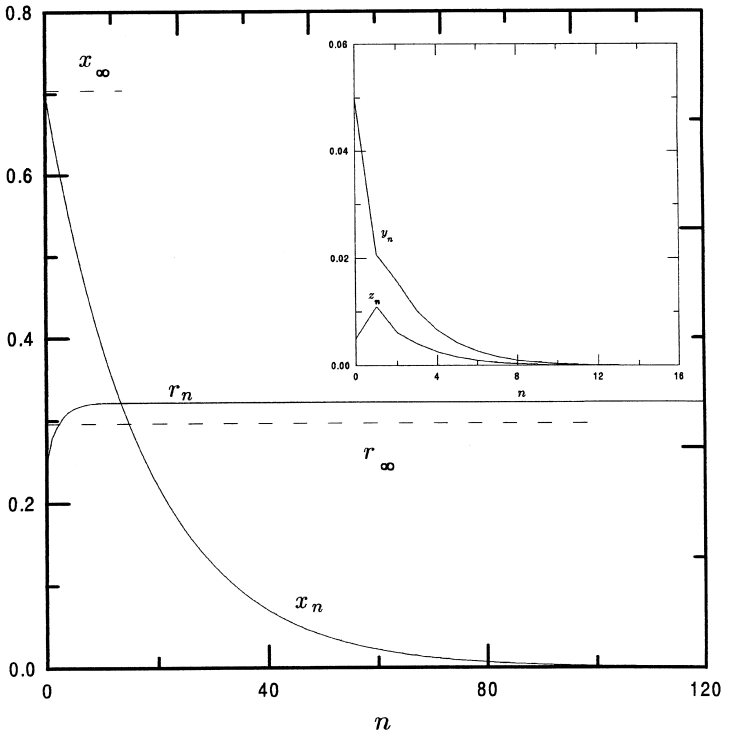

Fig. 3. This plot shows the dynamical evolution of the epidemic for an initial condition near the final state $(x_\infty, 0, 0, r_\infty)$. The larger window shows the behavior of susceptibles and removals, whereas the inset shows the evolution of the infected and infectious individuals. The catastrophic behavior is clear from the fact that x_∞ decreases continuously with increasing values of n.

$$\mu_{n+1} = (1-\gamma)\delta_n + b\mu_n\,,$$

$$\rho_{n+1} = \rho_n + (1-b)\mu_n\,, \tag{4.2}$$

where condition (2.7) may be rewritten as

$$\varepsilon_n + \delta_n + \mu_n + \rho_n = 0\,.$$

We choose as an application the same case as in the first section. The evolution starts around the fixed point (0.7,0,0,0.3) and evolves according to system (4.2). We have checked that for different initial perturbations $\varepsilon_0, \delta_0, \mu_0, \rho_0$ the system evolves in such a way that the susceptible, infected and infectious populations tend to zero, but the removals tend to a different value for different initial perturbations. This means that, in some sense, susceptible individuals and removals are unstable under small outbreaks of the disease but the infected and infectious populations are stable. From a practical point of view, this case describes the evolution of an epidemic which reaches a final state but a small outbreak of the disease develops a catastrophic behavior for the population. This behavior may be viewed in Fig. 3, where we present the evolution of the population near the final state from small initial perturbations.

5. Conclusions

We have studied a discrete deterministic epidemic model which takes into account an incubation period, introduced by an intermediate class (infected individuals), and a mortality rate induced by the disease. We have analyzed the characteristic parameters of an epidemic such as the threshold value, the final size and the severity of the disease and we have noted that the incubation period does not affect the latter two parameters. We have shown that the final size of the susceptible population is a nonincreasing function of the probability of effective transmission p and the severity is an increasing function of p. The stability analysis of the final state has been carried out and we have shown how small outbreaks of the disease may be catastrophic to the population, after the first evolution of the epidemic.

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