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A stochastic SIS epidemic model incorporating media coverage in a two patch setting

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ABSTRACT

In this paper, we investigate the stochastic disease dynamics of an *SIS* epidemic model on two patches incorporating media coverage. We give the global existence and positivity of the solutions, and the sufficient conditions for almost surely exponentially stability of the disease-free equilibrium, which means that the disease will be stochastic extinction. Furthermore, we perform some numerical simulations to validate the analytical finding.

1. Introduction

Populations worldwide have incurred significant losses from outbreaks infectious disease both in terms of morbidity and mortality as well as social and economic costs [1]. As a result, a wide range of tools, including media coverage, have been deployed in an effort to control the epidemic diseases spreading [2–7]. And various models have been used to study different aspects of diseases spreading [8–20].

In fact, media coverage of health related events has become so important that several surveillance systems now rely on active trolling of Internet news media and blogs to detect emerging disease threats [21]. And media coverage plays an important role in helping both the government authority make interventions to contain the disease and people's response to the disease [22–28].

On the other hand, environmental variations have a critical influence on the development of an epidemic [29]. For disease spreading, the nature of epidemic growth and spread is inherently random due to the unpredictability of person-to-person contacts [30] and population is subject to a continuous spectrum of disturbances [31,32]. And in epidemic dynamics, stochastic differential equation (SDE) models may be a more appropriate way of modeling epidemics in many circumstances and many realistic stochastic epidemic models can be derived based on their deterministic formulations [28,29,33–43]. But to our knowledge, the research on the dynamics of SIS epidemic model incorporating media coverage with random perturbation seems rare.

The aim of this paper is to consider the effect of environment fluctuations on the disease spreading incorporating media coverage. The paper is organized as follows. In Section 2, we derive a stochastic differential SIS model incorporating media coverage. In Section 3, we give the conditions of global existence of the solutions and the stochastic extinction of the model. In Section 4, we provide some numerical examples to support our analytic results. In the last section, we provide a brief discussion and summary of main results.

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2. Model derivation

Let $S(t)$ and $I(t)$ be the number of susceptible and infective individuals at time t, respectively. In the absence of media coverage, we assume a classic standard (or proportional) incidence, with the rate at which new infections arise given by $\frac{\beta SI}{S+I}$, β being the infection coefficient. In the presence of media coverage, social distancing mechanisms come into effect. The reporting by media is assumed to be an increasing function of the number of infectious cases present, as a consequence at the contact rate between susceptible and infectious individuals there is a decreasing function of the number of infectious cases present. We take similar non-linear functions as in [2] and denote the effective contact rate as

$$\beta_i(I_i) = a_i - b_i f(I_i)$$

where a_i is the maximal effective contact rate between the susceptible and infectious in patch i and b_i is the maximal reduced effective contact rate due to mass media alert in the presence of infectious. We here assume that $a_i \geq b_i$ and choose a simple "media coverage function" for $f(I_i) = \frac{I_i}{1+I_i}$. It follows from the work of Sun et al. [21] that the basic *SIS* metapopulation system under consideration is then

$$\begin{cases} \dfrac{dS_1}{dt} = \Lambda_1 - \left(a_1 - \dfrac{b_1 I_1}{1+I_1}\right)\dfrac{S_1 I_1}{S_1+I_1} + \gamma_1 I_1 - \mu S_1 - m_{12}S_1 + m_{21}S_2, \\ \dfrac{dI_1}{dt} = \left(a_1 - \dfrac{b_1 I_1}{1+I_1}\right)\dfrac{S_1 I_1}{S_1+I_1} - (\mu+\gamma_1)I_1 - m_{12}I_1 + m_{21}I_2, \\ \dfrac{dS_2}{dt} = \Lambda_2 - \left(a_2 - \dfrac{b_2 I_2}{1+I_2}\right)\dfrac{S_2 I_2}{S_2+I_2} + \gamma_2 I_2 - \mu S_2 + m_{12}S_1 - m_{21}S_2, \\ \dfrac{dI_2}{dt} = \left(a_2 - \dfrac{b_2 I_2}{1+I_2}\right)\dfrac{S_2 I_2}{S_2+I_2} - (\mu+\gamma_2)I_2 + m_{12}I_1 - m_{21}I_2, \end{cases} \tag{1}$$

under initial conditions

$$\begin{aligned} &S_1(0), S_2(0) \geq 0, \quad S_1(0) + S_2(0) > 0, \\ &I_1(0), I_2(0) \geq 0, \quad I_1(0) + I_2(0) > 0. \end{aligned} \tag{2}$$

In model (1), Λ_i is the (constant) recruitment into patch $i = 1, 2$. The parameter m_{ij} $(i, j = 1, 2, i \neq j)$ is the travel rate from patch i to patch j, and we assume that the travel rates for susceptible and infective individuals are the same, i.e., the disease is not severe enough to impede travel. γ_i is the individuals' rate of recovery due to natural causes or treatment, and μ the natural death rate in two patch. Because most diseases that fit within the framework of an *SIS* model are benign, and we ignore disease-induced death. The population in patch i is denoted by $N_i = S_i + I_i$ and the total population is $N = N_1 + N_2$.

Model (1) has a disease-free equilibrium $E_0 = (S_{10}, I_{10}, S_{20}, I_{20}) = (S_1^*, 0, S_2^*, 0)$, where

$$S_1^* = \frac{\Lambda_1\mu + m_{21}(\Lambda_1+\Lambda_2)}{\mu(\mu+m_{12}+m_{21})}, \qquad S_2^* = \frac{\Lambda_2\mu + m_{12}(\Lambda_1+\Lambda_2)}{\mu(\mu+m_{12}+m_{21})}. \tag{3}$$

For model (1), the basic reproduction number

$$R_0 := \rho(FV^{-1}) \tag{4}$$

is the threshold of the system for an epidemic to occur. Here $\rho(A)$ is the spectral of matric A and

$$F = \begin{pmatrix} a_1 & 0 \\ 0 & a_2 \end{pmatrix}, \quad V = \begin{pmatrix} m_{12}+\gamma_1+\mu & -m_{21} \\ -m_{12} & m_{21}+\gamma_2+\mu \end{pmatrix}.$$

By some computations, we obtain

$$R_0 = \frac{A + \sqrt{A^2 - 4a_1a_2B}}{2B},$$

where

$$\begin{aligned} A &= \mu(a_1+a_2) + a_1\gamma_2 + a_2\gamma_1 + a_1m_{21} + a_2m_{12}, \\ B &= (m_{12}+\gamma_1+\mu)(m_{21}+\gamma_2+\mu) - m_{12}m_{21}. \end{aligned}$$

The disease-free equilibrium is globally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$. The endemic equilibrium is unique and globally asymptotically stable if $R_0 > 1$. These results of model (1) were studied in [21].

There are different possible approaches to including random effects in the model, both from a biological and mathematical perspective [44], we adopt the approach by Mao et al. [36], where the authors had demonstrated that one or more system parameter(s) can be perturbed stochastically with white noise term to derive environmentally perturbed system.