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Dynamics of a stochastic tuberculosis model with antibiotic resistance

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ABSTRACT

In this paper, we study a stochastic tuberculosis model with antibiotic resistance. By constructing a suitable stochastic Lyapunov function, we establish sufficient conditions for the existence and uniqueness of an ergodic stationary distribution of the positive solutions to the model. Moreover, we obtain sufficient conditions for extinction of the disease. The existence of a stationary distribution implies stochastic weak stability.

1. Introduction

In recent years, mathematical models have been regarded as a powerful tool in understanding the dynamic spread of tuberculosis (TB) (see e.g. [1–7]) and it has been one of the most major public health problems facing society today. Tuberculosis is a bacterial disease with about one third of the world human population as its reservoir (see e.g. [8,9]) and it remains the leading cause of death by an infectious disease in the world. As we know, tuberculosis is caused by Mycobacterium tuberculosis. The disease is most commonly transmitted from a person suffering from infectious tuberculosis to other persons by infected droplets created when the person with active TB coughs or sneezes.

Antibiotic resistance in pathogenic bacteria can be defined microbiologically or clinically. Microbiological resistance is the presence of a genetically determined resistance mechanism, categorizing the pathogen as resistant or susceptible based on the application of a set cut-off in a phenotypic laboratory text while clinical resistance is a level of antimicrobial activity that is correlated with a high likelihood of therapeutic failure [10]. Antibiotics resistance has accompanied with the introduction of antibiotics since shortly after penicillin was introduced [11]. Due to continuous evolution of new species, multi-antibiotic resistant bacteria has been considered as serious threat to public health and these bacterial strains have already presented in different bacteria species and resulting in increased patient mortality [12]. As we know, incomplete treatment of patients with infectious TB can not only lead to relapse but also to the development of antibiotic resistant TB. Due to its sociological importance, the study of the spread of TB using mathematical models has received much attention (see e.g. [3–5,13]). Especially, Castillo-Chavez and Feng [3] formulated one-strain transmission model to study the dynamics of TB. Their model takes the following form

$$\begin{cases} \dfrac{dS}{dt} = \Lambda - \dfrac{\beta cSI}{N} - \mu S, \\ \dfrac{dL}{dt} = \dfrac{\beta cSI}{N} - (\mu + k + r_1)L + \dfrac{\beta' cTI}{N}, \\ \dfrac{dI}{dt} = kL - (\mu + d)I - r_2 I, \\ \dfrac{dT}{dt} = r_1 L + r_2 I - \dfrac{\beta' cTI}{N} - \mu T, \\ N = S + L + I + T, \end{cases} \tag{1.1}$$

where the host population is divided into the following epidemiological class or subgroups: Susceptibles (S), Latent (L, infected but not infectious), Infectious (I) and (effectively) Treated (T) individuals, N denotes the total population, Λ denotes the recruitment rate; β and β' are rate of transmission that susceptible and treated

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individuals become infected by one infectious individual per contact per unit of time, respectively; c denotes the per-capita contact rate; μ represents the per-capita natural death rate of S, L, I and T, respectively; k is the rate at which an individual leaves the latent class by becoming infectious; d denotes the per-capita disease induced death rate, r_1 and r_2 denote per-capita treatment rates. The parameters involved in system (1.1) are positive constants. The basic reproduction number for system (1.1) is $\mathscr{R}_0 = (\frac{\beta c}{\mu+d+r_2})(\frac{k}{\mu+k+r_1})$ which determines the epidemic occurs or not. If $\mathscr{R}_0 < 1$, system (1.1) has a unique disease-free equilibrium $E^0 = (S^0, 0, 0, 0) = (\frac{\Lambda}{\mu}, 0, 0, 0)$ and it is globally asymptotically stable in the invariant set Γ. While if $\mathscr{R}_0 > 1$, then model (1.1) has two possible equilibria, i.e., the disease-free equilibrium E^0 and the unique positive endemic equilibrium $E^* = (S^*, L^*, I^*, T^*)$, E^0 is unstable and E^* is locally asymptotically stable, where $\Gamma = \{(S, L, I, T) : S > 0, L > 0, I > 0, T > 0, S + L + I + T \le \frac{\Lambda}{\mu}\}$. These results can be found in the literature [3].

Moreover, in an ecosystem, epidemic models are always affected by the environmental noise (see e.g. [14–18]). For human disease related epidemics, the nature of epidemic growth and spread is random due to the unpredictability in person-to-person contacts [19]. Hence the variability and randomness of the environment is fed through the state of the epidemic [20]. In epidemic dynamics, stochastic models may be a more appropriate way of modeling epidemics in many circumstances (see e.g. [21–24]). For instance, stochastic models are able to take care of randomness of infectious contacts occurring in the latent and infectious periods [25]. It also has been shown that some stochastic epidemic models can provide an additional degree of realism in comparison with their deterministic counterparts (see e.g. [14,26–28]). Particularly, Allee et al. [14] revealed that stochastic model should suit the question of disease extinction better. Herwaarden et al. [26] suggested that an endemic equilibrium in a deterministic model can disappear in its corresponding stochastic system due to stochastic fluctuations. And Näsell [27] formulated stochastic models to show that some stochastic models are a better approach to describe epidemics for a large range of realistic parameter values in comparison with their deterministic counterparts.

There exist different approaches to introduce stochastic perturbations into the model, both from a mathematical and biological perspective [28,29]. In this paper, our approach to include stochastic perturbations is similar to that of Imhof and Walcher [16]. Here we assume that stochastic perturbations are of the white noise type which are proportional to S, L, I and T, influenced on the $\frac{dS}{dt}$, $\frac{dL}{dt}$, $\frac{dI}{dt}$ and $\frac{dT}{dt}$ in (1.1). Then corresponding to system (1.1), the stochastic version can be expressed as follows

$$\begin{cases} dS = \left[\Lambda - \dfrac{\beta cSI}{N} - \mu S\right]dt + \sigma_1 S dB_1(t), \\ dL = \left[\dfrac{\beta cSI}{N} - (\mu + k + r_1)L + \dfrac{\beta' cTI}{N}\right]dt + \sigma_2 L dB_2(t), \\ dI = [kL - (\mu + d)I - r_2 I]dt + \sigma_3 I dB_3(t), \\ dT = \left[r_1 L + r_2 I - \dfrac{\beta' cTI}{N} - \mu T\right]dt + \sigma_4 T dB_4(t), \end{cases} \tag{1.2}$$

where $B_i(t)$ are mutually independent standard Brownian motions with $B_i(0) = 0$, $\sigma_i^2 > 0$ denote the intensities of the white noise, $i = 1, 2, 3, 4$.

This paper is organized as follows. In Section 2, we give some known results, definition and lemma which will be used in the following analysis. In Section 3, we show that there exists a unique global positive solution of system (1.2). In Section 4, we prove that there is a unique ergodic stationary distribution of the positive solutions to system (1.2) under certain condition. In Section 5, we establish sufficient conditions for extinction of the disease. Finally, concluding remarks and future directions are provided to end this paper.

2. Preliminaries

In this section, we shall present some known results, definition and lemma which will be used later. Throughout this paper, unless otherwise specified, let $(\Omega, \mathcal{F}, \{\mathcal{F}_t\}_{t\ge 0}, \mathbb{P})$ be a complete probability space with a filtration $\{\mathcal{F}_t\}_{t\ge 0}$ satisfying the usual conditions (i.e., it is increasing and right continuous while $\mathcal{F}_0$ contains all $\mathbb{P}$-null sets) and we also let $B_i(t)$ be defined on the complete probability space, $i = 1, 2, 3, 4$. We introduce the following notations:

$$\mathbb{R}^d_+ = \{x = (x_1, \dots, x_d) \in \mathbb{R}^d : x_i > 0, 1 \le i \le d\} \text{ and}$$

$$\overline{\mathbb{R}}^d_+ = \{x = (x_1, \dots, x_d) \in \mathbb{R}^d : x_i \ge 0, 1 \le i \le d\}.$$

Then we give some basic theory in stochastic differential equations which is introduced in [15].

In general, consider the d-dimensional stochastic differential equation

$$dX(t) = f(X(t))dt + g(X(t))dB(t) \text{ for } t \ge t_0, \tag{2.1}$$

with the initial value $X(0) = X_0 \in \mathbb{R}^d$. $B(t)$ denotes a d-dimensional standard Brownian motion defined on the complete probability space $(\Omega, \mathcal{F}, \{\mathcal{F}_t\}_{t\ge 0}, \mathbb{P})$. Denote by $C^2(\mathbb{R}^d; \overline{\mathbb{R}}_+)$ the family of all nonnegative functions $V(X)$ defined on $\mathbb{R}^d$ such that they are continuously twice differentiable in X. The differential operator L of Eq. (2.1) is defined by [15]

$$L = \sum_{i=1}^{d} f_i(X, t)\frac{\partial}{\partial X_i} + \frac{1}{2}\sum_{i,j=1}^{d}[g^T(X, t)g(X, t)]_{ij}\frac{\partial^2}{\partial X_i \partial X_j}.$$

If L acts on a function $V \in C^2(\mathbb{R}^d; \overline{\mathbb{R}}_+)$, then

$$LV(X) = V_X(X)f(X) + \frac{1}{2}\text{trace}[g^T(X)V_{XX}(X)g(X)],$$

where $V_X = (\frac{\partial V}{\partial X_1}, \dots, \frac{\partial V}{\partial X_d})$, $V_{XX} = (\frac{\partial^2 V}{\partial X_i \partial X_j})_{d\times d}$. According to Itô's formula [15], if $X(t) \in \mathbb{R}^d$, then

$$dV(X(t)) = LV(X(t))dt + V_X(X(t))g(X(t))dB(t).$$

Definition 2.1 [30]. The transition probability function $P(s, x, t, A)$ is said to be time-homogeneous (and the corresponding Markov process is called time-homogeneous) if the function $P(s, x, t + s, A)$ is independent of s, where $0 \le s \le t$, $x \in \mathbb{R}^d$ and $A \in \mathcal{B}$ and $\mathcal{B}$ denotes the σ-algebra of Borel sets in $\mathbb{R}^d$.

Let $X(t)$ be a regular time-homogeneous Markov process in $\mathbb{R}^d$ described by the stochastic differential equation

$$dX(t) = f(X(t))dt + g(X(t))dB(t).$$

The diffusion matrix of the process $X(t)$ is defined as follows

$$A(x) = (a_{ij}(x)), \quad a_{ij}(x) = g^i(x)g^j(x).$$

Lemma 2.1 *[30]. The Markov process $X(t)$ has a unique ergodic stationary distribution $\pi(\cdot)$ if there exists a bounded open domain $D \subset \mathbb{R}^d$ with regular boundary Γ, having the following properties:*

A_1: there is a positive number M such that $\sum_{i,j=1}^{d} a_{ij}(x)\xi_i\xi_j \ge M|\xi|^2$, $x \in D$, $\xi \in \mathbb{R}^d$.

A_2: there exists a nonnegative C^2-function V such that LV is negative for any $\mathbb{R}^d \setminus D$.

3. Existence and uniqueness of the positive solution

To study the dynamical behavior of a tuberculosis model, the first concern is whether the solution is global and positive. The following result is regarded to the existence and uniqueness of the