Applied Mathematics Letters 84 (2018) 168–175

Contents lists available at ScienceDirect

Applied Mathematics Letters

www.elsevier.com/locate/aml

A stochastic SICA epidemic model for HIV transmission

Jasmina Djordjevic[a], Cristiana J. Silva[b], Delfim F.M. Torres[b,*]

[a] Faculty of Science and Mathematics, University of Niš, Višegradska 33, 18000 Niš, Serbia
[b] Center for Research and Development in Mathematics and Applications (CIDMA), Department of Mathematics, University of Aveiro, 3810-193 Aveiro, Portugal

ARTICLE INFO

Article history:
Received 22 January 2018
Received in revised form 3 May 2018
Accepted 3 May 2018
Available online 29 May 2018

Keywords:
SICA epidemic model
HIV infection
Stochastic differential equations
Brownian motion
Extinction and persistence

ABSTRACT

We propose a stochastic SICA epidemic model for HIV transmission, described by stochastic ordinary differential equations, and discuss its perturbation by environmental white noise. Existence and uniqueness of the global positive solution to the stochastic HIV system is proven, and conditions under which extinction and persistence in mean hold, are given. The theoretical results are illustrated via numerical simulations.

1. Introduction

Epidemics are, inevitably, affected by environmental white noise, which is an important component to be taken into account by mathematical models, providing an additional degree of realism in comparison to their deterministic counterparts [1]. Here, our aim is to improve the deterministic SICA epidemic model for HIV transmission recently proposed in [2,3], by considering environmental interactions. For that, we follow [1,4–8] and introduce stochastic noise in the form of a Brownian motion with positive intensity. The advantage of our model with respect to previous ones in [2,3] is that we assume fluctuations in the environment, manifesting in the transmission coefficient rate, thus making it more biologically realistic for the transmission dynamics of HIV/AIDS in a homogeneously mixing population of variable size.

The model subdivides human population into four mutually-exclusive compartments: susceptible individuals (S); HIV-infected individuals with no clinical symptoms of AIDS (the virus is living or developing in the individuals but without producing symptoms or only mild ones) but able to transmit HIV to other individuals (I); HIV-infected individuals under ART treatment (the so called chronic stage) with a viral load remaining low (C); and HIV-infected individuals with AIDS clinical symptoms (A). The total population at

---

[*] Corresponding author.
E-mail addresses: djordjevichristina@gmail.com (J. Djordjevic), cjoaosilva@ua.pt (C.J. Silva), delfim@ua.pt (D.F.M. Torres).

https://doi.org/10.1016/j.aml.2018.05.005

time t, denoted by $N(t)$, is given by $N(t) = S(t) + I(t) + C(t) + A(t)$. Using the same arguments as in [3], we consider a force of infection given by $\beta\,(I + \eta_C\, C + \eta_A A)$ with $\beta = \frac{\beta_0\,\mu}{\Lambda}$, where β_0 is the effective contact rate for HIV transmission. The modification parameter $\eta_A \geq 1$ accounts for the relative infectiousness of individuals with AIDS symptoms, in comparison to those infected with HIV with no AIDS symptoms. Individuals with AIDS symptoms are more infectious than HIV-infected individuals (pre-AIDS) because they have a higher viral load and there is a positive correlation between viral load and infectiousness [9]. On the other hand, $\eta_C \leq 1$ translates the partial restoration of immune function of individuals with HIV infection that use ART correctly [10]. All individuals suffer from natural death, at a constant rate μ. We also assume that HIV-infected individuals, with and without AIDS symptoms, have access to ART treatment. HIV-infected individuals with no AIDS symptoms I progress to the class of individuals with HIV infection under ART treatment C at a rate ϕ, and HIV-infected individuals with AIDS symptoms are treated for HIV at rate α. Individuals in the class C leave to the class I at a rate ω. Moreover, an HIV-infected individual with AIDS symptoms A that starts treatment moves to the class of HIV-infected individuals I, moving only to the chronic class C if the treatment is maintained. HIV-infected individuals I with no AIDS symptoms, which do not take ART treatment, progress to the AIDS class A at rate ρ. We assume that only HIV-infected individuals with AIDS symptoms A suffer from an AIDS induced death, at a rate d. Precisely, we consider the model

$$\begin{cases} dS(t) = [\Lambda - \beta\,(I(t) + \eta_C\, C(t) + \eta_A A(t))\, S(t) - \mu S(t)]\, dt, \\ dI(t) = [\beta\,(I(t) + \eta_C\, C(t) + \eta_A A(t))\, S(t) - \xi_3 I(t) + \alpha A(t) + \omega C(t)]\, dt, \\ dC(t) = [\phi I(t) - \xi_2 C(t)]\, dt, \\ dA(t) = [\rho\, I(t) - \xi_1 A(t)]\, dt, \end{cases} \tag{1}$$

where $\xi_1 = \alpha+\mu+d$, $\xi_2 = \omega+\mu$ and $\xi_3 = \rho+\phi+\mu$. Existence and uniqueness of solution to the deterministic model (1) is proved in [2,3], where it is shown that the system has one disease free equilibrium when the basic reproduction number is less than one and one endemic equilibrium when the basic reproduction number is greater than one. Local and global stability of the equilibrium points of (1) is also proved in [2,3]. Motivated by [5], we consider here fluctuations in the environment, which are assumed to manifest themselves as fluctuations in the parameter β, so that $\beta \to \beta + \sigma \dot{B}(t)$, where $B(t)$ is a standard Brownian motion with intensity $\sigma^2 > 0$. Our stochastic model takes then the following form:

$$\begin{cases} dS(t) = [\Lambda - \beta\,(I(t) + \eta_C\, C(t) + \eta_A A(t))\, S(t) - \mu S(t)]\, dt - \sigma\,(I(t) + \eta_C\, C(t) + \eta_A A(t))\, S(t) dB(t), \\ dI(t) = [\beta\,(I(t) + \eta_C\, C(t) + \eta_A A(t))\, S(t) - \xi_3 I(t) + \alpha A(t) + \omega C(t)]\, dt \\ \qquad\quad +\, \sigma\,(I(t) + \eta_C\, C(t) + \eta_A A(t))\, S(t) dB(t), \\ dC(t) = [\phi I(t) - \xi_2 C(t)]\, dt, \\ dA(t) = [\rho\, I(t) - \xi_1 A(t)]\, dt. \end{cases} \tag{2}$$

The paper is organized as follows: Section 2 is devoted to existence and uniqueness of a global positive solution to the Stochastic Differential Equation (SDE) (2) (cf. Theorem 2.1); Section 3 to conditions for the extinction of HIV within the population (cf. Theorem 3.1); and Section 4 to conditions for the persistence in mean of the disease (cf. Theorem 4.1). We end with Section 5, illustrating both theoretical results of extinction and persistence with numerical simulations.

2. Existence and uniqueness of a positive global solution

Throughout the paper, let $(\Omega, \mathcal{F}, \{\mathcal{F}\}_{t\geq 0}, \mathcal{P})$ be a complete probability space with filtration $\{\mathcal{F}\}_{t\geq 0}$, which is right continuous and such that $\mathcal{F}$ contains all $\mathcal{P}$-null sets. The scalar Brownian motion $B(t)$ of (2) is defined on the given probability space. Also, we denote $\mathbb{R}^4_+ = \left\{(x_1, x_2, x_3, x_4) | x_i > 0, i = \overline{1,4}\right\}$.