Nonlinear Analysis: Real World Applications 28 (2016) 192–207

Contents lists available at ScienceDirect

Nonlinear Analysis: Real World Applications

www.elsevier.com/locate/nonrwa

Biological consistency of an epidemic model with both vertical and horizontal transmissions

B.E. Ainseba[a], S.M. Bouguima[b], S. Fekih[c,*]

[a] Institute of Mathematics, University of Bordeaux, UMR CNRS 5251, 3 ter place de la Victoire, 33076 Bordeaux Cedex, France

[b] Laboratoire: Systèmes Dynamiques et Applications, Faculty of Sciences, Department of Mathematics, University of Tlemcen, Algeria

[c] Faculty of Sciences, Departement of Mathématics, University of Tlemcen, Algeria

ARTICLE INFO

Article history:
Received 11 April 2015
Accepted 27 September 2015
Available online 11 November 2015

Keywords:
SIS epidemic models
Age-structure
Reaction diffusion
Vertical transmission
Global existence
Positivity

ABSTRACT

A system of nonlinear integro-differential equations is investigated. The model describes an age structured S.I.S system of a disease with horizontal and vertical transmission. Global well-posedness is proved in L^1space. The method is based on the contraction fixed point theorem. We exhibit a closed subset of a Banach space, on which a certain mapping is a strict contraction.

1. Introduction

One process that characterizes many infectious diseases is vertical transmission. It is defined as the infection of newborns by their mother. For instance, vertical transmission is the main cause of HIV infection in children. The study of HIV/AIDS transmission is of great interest for scientists. Mathematical models play an important role for understanding the dynamics of infectious diseases. In this paper, we consider well-posedness of an epidemic model describing an SIS system with vertical and horizontal transmission. They are called SIS models because the susceptible individual become infective and then susceptible again, upon recovery from infection.

Suppose that Ω is a regular bounded in $\mathbb{R}^n$, $n \geqslant 1$. Let a^+ be the maximum age of the individuals. The population is divided into two groups: infected population $u(a,t,x)$, and susceptible population $v\,(a,t,x)$,

* Corresponding author.
E-mail addresses: bedreddine.ainseba@u-bordeaux2.fr (B.E. Ainseba), bouguima@yahoo.fr (S.M. Bouguima), si_fekih@yahoo.fr (S. Fekih).

http://dx.doi.org/10.1016/j.nonrwa.2015.09.010
1468-1218/

depending on chronological age $a \in [0, a^+)$, time $t \in [0, T)$, for some $T > 0$, and position $x \in \Omega$. The total population of infected individuals at time t and position $x \in \Omega$ is

$$P_1(t,x) = \int_0^{a^+} u(a,t,x)da.$$

Similarly, the total population of susceptible individuals at time t and position $x \in \Omega$ is

$$P_2(t,x) = \int_0^{a^+} v(a,t,x)da.$$

Let

$$P(t,x) = \int_0^{a^+} u(a,t,x) + v(a,t,x)da = P_1(t,x) + P_2(t,x).$$

The functions $\mu_u(a)$ and $\mu_v(a)$ denote the death rate for the infected and the susceptible individuals respectively, and $\beta_u(a,t,x,P_1,P_2)$, $\beta_v(a,t,x,P_1,P_2)$ are the corresponding birth rate. The vertical transmission to newborns is

$$\begin{aligned} u(0,t,x) &= \lambda \int_0^{a^+} \beta_u(a,t,x,P_1,P_2)\, u(a,t,x)\, da, \\ v(0,t,x) &= \int_0^{a^+} \beta_v(a,t,x,P_1,P_2)\, v(a,t,x) + (1-\lambda)\, \beta_u(a,t,x,P_1,P_2)\, u(a,t,x)\, da. \end{aligned}$$

This means that a fraction $(1-\lambda)$ of the offspring from infective parents are susceptible, and a fraction $\lambda \in (0,1]$ are infective. Let $\gamma(a,t,x,P_1,P_2)$ be the force of infection rate and $\delta(a,t,x)$ the recovery rate.

The change rate of the infected population density u is given by

$$\begin{aligned} Du(a,t,x) &= \lim_{\Delta t \to 0} \frac{u(a+\Delta t, t+\Delta t, x) - u(a,t,x)}{\Delta t} \\ &= \lim_{\Delta t \to 0} \frac{u(a+\Delta t, t+\Delta t, x) - u(a, t+\Delta t, x)}{\Delta t} - \frac{u(a, t+\Delta t, x) - u(a,t,x)}{\Delta t} \\ &= \lim_{\Delta t \to 0} \left[u_a(a, t+\Delta t, x) + u_t(a,t,x)\right] \\ &= u_a(a,t,x) + u_t(a,t,x). \end{aligned}$$

A similar expression defines the change rate of the susceptible population density $v(a,t,x)$. Hence,

$$Dv(a,t,x) = v_a(a,t,x) + v_t(a,t,x).$$

Assume that the susceptible and the infected populations move randomly, described as a Brownian motion. Then the model describing the relation between $u(a,t,x)$ and $v(a,t,x)$ on the domain $Q = [0,a^+) \times [0,T) \times \Omega$ is given by

$$\begin{cases} \partial_t u + \partial_a u + \mu_u(a)\, u = d_1 \Delta_x u + \gamma(a,t,x,P_1,P_2)\, v - \delta(a,t,x)\, u \\ \partial_t v + \partial_a v + \mu_v(a)\, v = d_2 \Delta_x v - \gamma(a,t,x,P_1,P_2)\, v + \delta(a,t,x)\, u \\ u(0,t,x) = \lambda \displaystyle\int_0^{a^+} \beta_u(a,t,x,P_1,P_2)\, u(a,t,x)\, da \\ v(0,t,x) = \displaystyle\int_0^{a^+} \beta_v(a,t,x,P_1,P_2)\, v(a,t,x) + (1-\lambda)\, \beta_u(a,t,x,P_1,P_2)\, u(a,t,x)\, da \end{cases} \tag{1}$$

The model is to be analyzed under non-zero initial conditions

$$\begin{cases} u(a,0,x) = u_0(a,x) & \text{on } \left[0,a^+\right) \times \Omega \\ v(a,0,x) = v_0(a,x) & \text{on } \left[0,a^+\right) \times \Omega \end{cases}$$