Nonlinear Analysis: Real World Applications 30 (2016) 16–31

Contents lists available at ScienceDirect

Nonlinear Analysis: Real World Applications

www.elsevier.com/locate/nonrwa

Global analysis of an SIR epidemic model with infection age and saturated incidence

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HIGHLIGHTS

- An SIR epidemic model with infection age and saturated incidence is studied.
- The basic reproduction number is obtained.
- A threshold dynamics is established.
- The main tool is the Lyapunov functional technique.

ARTICLE INFO

Article history:
Received 9 December 2014
Received in revised form 7 October 2015
Accepted 1 November 2015
Available online 9 December 2015

Keywords:
SIR model
Infection age
Saturated incidence
Global stability
Lyapunov functional
Fluctuation lemma

ABSTRACT

Epidemic models with infection age have been extensively studied in the recent decades. Unfortunately, the incidence rate used is the bilinear one. As incidence rate plays an important role in disease transmission, in this paper, we study an SIR epidemic model with infection age and saturated incidence. We establish a threshold dynamics by applying the fluctuation lemma and Lyapunov functional. Roughly, if the basic reproduction number is less than 1, then the disease-free equilibrium is globally asymptotically stable; while if the basic reproduction number is larger than 1, then the endemic equilibrium is globally asymptotically stable in the set with initial infectivity.

1. Introduction

Mathematical models describing the dynamics of infectious diseases are of great public health importance because the mathematics helps to devise effective mechanisms for controlling their spread. Most of such models are compartmental models, whose baseline assumption is that individuals in each class are homogeneous. For instance, infectious individuals are equally infectious during their period of infectivity.

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http://dx.doi.org/10.1016/j.nonrwa.2015.11.001
1468-1218/

This assumption is reasonable in modeling communicable diseases such as influenza and sexually transmitted diseases. However, infectivity experiments on HIV/AIDS epidemic recognized the importance of variable infectivity in the transmission dynamics of infectious diseases [1]. Stage-structured models described by ordinary differential equations (ODEs) have been proposed to incorporate this kind of phenomena. To be more realistic and relevant, these ODE models can be generalized with continuous age assumption by introducing infection age (the time passed since infected). Here, we just name a few of the recent works, [2–9].

A crucial issue in the study of the spread of an infectious disease is how it is transmitted, which depends on both the population behavior and the infectivity of the disease [10]. Mathematically, these two aspects are captured in the incidence rate of a disease, defined as the average number of new cases of a disease per unit time. Bilinear and standard incidence rates have been frequently used in classical epidemic models. But nonlinearity in the incidence rates has been observed in disease transmission dynamics, for example, by Capasso and Serio [11] in the study of cholera epidemic spread in Bari in 1973, and by Brown and Hasibuan [12] in the study of infection of the two-spotted spider mites. Hence it has been suggested that the standard bilinear incidence rate shall be modified into a nonlinear incidence rate by many authors. When the incidence rate is assumed to have a more general nonlinear form, the model can exhibit a wide range of dynamical behavior. A saturated incidence rate $f(I)S$ was introduced by Capasso and Serio [11] and some other forms of nonlinear incidence rates were proposed and studied (see, for example, some are mentioned in Naresh et al. [13]).

So far, works on epidemic models with infection age and nonlinear incidence are very scarce and we could hardly find any in the literature. This motivates us to study an SIR model with infection age and saturated incidence. More precisely, the population is divided into three classes, the susceptible $S(t)$, the infected $i(t,a)$ at time t with infection age a, and the removed $R(t)$. The removed is assumed to have permanent immunity and hence we only need to consider the evolution of S and i. The model is built based on the following hypotheses.

(a) There is a constant recruitment rate $\Lambda > 0$ for the susceptible and the natural death rate of the susceptible is $\mu_1 > 0$.
(b) The transmission coefficient of the infected with infection age a is $\beta(a)$ and the death rate of it is $\mu_2(a)$ (which includes the natural death, disease related death and removed rate).
(c) The incidence rate at time t and at infection age a is $S(t)f(i(t,a))$.

With these hypotheses, we can obtain the following SIR model with infection age and saturated incidence,

$$\begin{cases} \dfrac{dS(t)}{dt} = \Lambda - \mu_1 S(t) - S(t)\displaystyle\int_0^\infty \beta(a) f(i(t,a))da, \\ \dfrac{\partial i(t,a)}{\partial t} + \dfrac{\partial i(t,a)}{\partial a} = -\mu_2(a) i(t,a), \\ i(t,0) = S(t)\displaystyle\int_0^\infty \beta(a) f(i(t,a))da, \\ S(0) = S_0 \geq 0, \qquad i(0,\cdot) = i_0 \in L^1_+, \end{cases} \tag{1.1}$$

where L^1_+ is the set of all integrable functions from $(0,\infty)$ into $\mathbb{R}_+ = [0,\infty)$. The total infectivity $S(t)\int_0^\infty \beta(a) f(i(t,a))da$ is reasonable and is inspired by that in Enatsu and Nakata [14], for instance, since latent period can be included in infection age by assuming the transmission coefficient to be zero.

In the sequel, we make the following assumptions.

(A1) β is a bounded and uniformly continuous function from $\mathbb{R}_+$ to $\mathbb{R}_+$, and μ_2 is a bounded function on $\mathbb{R}_+$ satisfying $\mu_2(a) \geq \mu_1$ for $a \in \mathbb{R}_+$.
(A2) For $x \in \mathbb{R}_+$, $f(x) \geq 0$ with equality if and only if $x = 0$, $f'(x) \geq 0$, and $f''(x) \leq 0$.