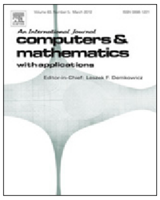
Contents lists available at ScienceDirect

Computers and Mathematics with Applications

journal homepage: www.elsevier.com/locate/camwa



An age-structured SIR epidemic model with fixed incubation period of infection

Vitalii Akimenko

Faculty of Cybernetics and Computer Science, T. Shevchenko National University of Kyiv, Volodymyrska 64, 01030 Kyiv, Ukraine

ARTICLE INFO

Article history:
Received 9 September 2016
Received in revised form 12 January 2017
Accepted 28 January 2017
Available online xxxx

Keywords:
SIR epidemic model
Age-structured model
Population dynamics
Asymptotical stability

ABSTRACT

This paper is devoted to the study of an age-structured SIR epidemic system on the basis of the model of polycyclic population dynamics of susceptible, infected and recovered individuals. This model was considered as a nonlinear competitive system of three initial–boundary value problems for the nonlinear transport equations with non-local integral boundary conditions and discrete time delay (fixed incubation period of infection). It was obtained the explicit recurrent formulae for computing the traveling wave solution of such system provided the model parameters (coefficients of equations and initial values) satisfy the restrictions that guarantee the existence and uniqueness of continuous solution. Using some insignificant simplifications the age-structured SIR model was reduced to the nonlinear autonomous system of delay ODE. It was studied the dimensionless indicators and conditions of existence of trivial disease-free equilibrium, two non-trivial endemic equilibriums for the incurable and curable infection-induced diseases, respectively. By carrying out an analysis of the local asymptotical stability of the solution of such system we obtain the restrictions for the time delay that guarantee the stability of solutions in the neighborhood of equilibriums. The numerous simulations of dynamics of SIR population illustrate the results of theoretical analysis.

1. Introduction

Advanced continuous age-structured models of population dynamics play an important role in the study of complex epidemic processes since they provide the theoretical analysis and practical insights into the epidemiology of infection-induced diseases. In particular, the age-structured epidemic models have been used to realistically describe all life stages of individuals in susceptible, infected and recovered (SIR) subpopulations (subclasses of population) such as birth, aging, fertility, death, intercohort interaction and transition of individuals between subpopulations to determine how the characteristics of these processes affect the outcomes and consequences of epidemiological processes. The first class of SIR models was presented in the mathematical theory of epidemics in the pioneer works of Kermack and McKendrick [1–3]. The SIR models with vital dynamics (births and deaths) named "endemic models" [4,5] were studied and developed mostly on the basis of continuous age-structured models in the numerous works of Diekmann and Heesterbeek [6], Brauer and Castillo-Chavez [4,7], Iannelli [8], Hethcote [5], Hoppensteadt [9], Webb [10,11], and others [12–19], the references cited therein. Most results on age-structured epidemic models focus on the analysis of existence and uniqueness of solution of non-linear competitive system of PDE, conditions of existence of trivial and endemic equilibriums, analysis of local and global asymptotical stability of solution in the neighborhood of equilibriums. The complexity of epidemic processes demands the consideration of new mathematical problems and challenges and study of new properties of existing models.

E-mail address: vitaliiakm@gmail.com.

http://dx.doi.org/10.1016/j.camwa.2017.01.022

Please cite this article in press as: V. Akimenko, An age-structured SIR epidemic model with fixed incubation period of infection, Computers and Mathematics with Applications (2017), http://dx.doi.org/10.1016/j.camwa.2017.01.022

In this paper we study the continuous age-structured *SIR* epidemic model which describes the vital dynamics of susceptible, infective and recovered individuals and is based on the competitive system of initial–boundary value problems for the nonlinear transport equations [12,13,7,6,14,11]. In constructing the mathematical model we assume that infection in population does not occur in the susceptibles directly after exposure to some pathogenic organism (infection) but at some later time with some time delay. The time elapsing from the instant of infection to the instant when first symptoms and signs of disease become apparent is called an "incubation time" and is often used in the *SIR* epidemic model with discrete or continuous time delay in [20–23]. We assume here that "incubation time" is known and fixed, and consider the equations of *SIR* epidemic model only with the discrete time delay. Such models can describe the dynamics of different epidemic diseases, for instance, hepatitis B (HBV) and E (HEV) [24], cholera [12], rubella [13], pertussis [18], and others.

Our first goal is to obtain the conditions of existence and uniqueness of solution and develop the explicit recurrent formulae for computing a traveling wave solution of the competitive system of initial–boundary value problems for the nonlinear transport equations with time delay. We use the well-known method of characteristics [25–28] of the theory of hyperbolic equations of first order in combination with the steps method of the theory of delay ODE [29–31]. The explicit form of solution obtained in the terms of integrals of the solution computed at the previous moments of time and of the coefficients of equation allows for obtaining the conditions for the coefficient of system which guarantee the existence and uniqueness of continuous solution of *SIR* epidemic model. The explicit recurrent algorithm derived in this paper is used in the numerical algorithm for computing the traveling wave solution at the nodes of difference lattice with high accuracy.

Secondly, we carry out the stability analysis of autonomous system. For this purpose the *SIR* epidemic model is reduced to the autonomous competitive system of nonlinear ODE with discrete time delay under some insignificant simplifications. After that the dimensionless indicators and conditions of existence of trivial and non-trivial endemic equilibriums of the *SIR* epidemic system are derived. We obtain the conditions of existence of two nontrivial endemic equilibriums for incurable and curable infection-induced diseases. In all cases we derive the dimensionless indicators and conditions of local asymptotical stability of solutions of autonomous *SIR* epidemic model in the neighborhoods of nontrivial equilibriums. Finally, the numerous simulations of dynamics of SIR population at the neighborhood of both nontrivial equilibriums illustrate the results of theoretical analysis for the different values of dimensionless indicators and time delay. The conclusion remarks are given in the last section.

2. Nonlinear age-structured *SIR* epidemic model of population dynamics with discrete time delays

We consider the age-structured *SIR* epidemic model which describes the dynamics of three interactive subpopulations (subclasses): susceptibles ($i = 1$), infected ($i = 2$) and recovered ($i = 3$) individuals. The vital dynamics of this model is schematically presented in Fig. 1. The individuals of each subpopulation pass two stages of aging. In the first, maturing stage individual births, ages with time, can die or reach the maximum age of maturing x_p which is considered as initial age of individual's reproduction. Matured individuals of the second proliferating stage (in age $x > x_p$) in each ith subclass can be divided into μ_i new individuals, can age, die or live up to the maximal age x_d. Susceptibles, infectives and recovers belong to the reproductive subpopulations in proliferating stage. Some fraction of individuals of all subpopulations can give birth for new individuals in susceptible subpopulation ($i = 1$) and in the same time some fraction of individuals of infective subpopulation can reproduce the individuals of their own subpopulation ($i = 2$). Within the framework of the considered model, the biological parameters of individuals, such as natural death rate and birth modulus, are different for each subpopulation.

Let $S(x,t), I(x,t), R(x,t)$ denote the age-specific population densities of the susceptibles, infectives and recovers at age x and time t in the domain $\bar{\Omega} = \{(x,\ t) : \ 0 \le x \le x_d,\ 0 \le t \le T\}$. The number of susceptibles, infectives and recovers in population is given as $N_S(t) = \int_0^{x_d} S(x,t)dx$, $N_I(t) = \int_0^{x_d} I(x,t)dx$, $N_R(t) = \int_0^{x_d} R(x,t)da$, respectively, and the number of all individuals in population is $N(t) = N_S(t) + N_I(t) + N_R(t)$. In constructing the mathematical model we assume that infection in population does not occur in the susceptibles directly after exposure but at some later time with delay $\tau = \text{const} > 0$. This parameter is named as an "incubation period of infection". Considered *SIR* epidemic model of population dynamics is represented via a system of initial–boundary value problems for nonlinear delay transport equations:

$$S_t + S_x = -\left(\tilde{\alpha}_1(x,t) + \sigma\tilde{\theta}_1(x,t)\right) S(x,t) - \lambda_0\,(x, t-\tau)S(x,t), \quad (x,t) \in \Omega, \tag{1}$$

$$I_t + I_x = -\left(\tilde{\alpha}_2(x,t) + \sigma\tilde{\theta}_2(x,t)\right) I(x,t) + \lambda_0\,(x, t-\tau)S(x,t) - \gamma_2(x,t)I(x,t), \quad (x,t) \in \Omega, \tag{2}$$

$$R_t + R_x = -\left(\tilde{\alpha}_3(x,t) + \sigma\tilde{\theta}_3(x,t)\right) R(x,t) + \gamma_2(x,t)I(x,t), \quad (x,t) \in \Omega, \tag{3}$$

$$S(x,0) = S_0(x), \quad x \in [0, x_d]\,, \tag{4}$$

$$S(0,t) = \int_{x_p}^{x_d} \left(\mu_1\theta_1(x,t)S(x,t) + \mu_2(1-q(x,t))\theta_2(x,t)I(x,t) + \mu_3\theta_3(x,t)R(x,t)\right) dx, \quad t \in (0,T)\,, \tag{5}$$

$$I(x,t) = I_0(x,t), \quad x \in [0, x_d]\,,\ t \in [-\tau, 0]\,, \tag{6}$$

Please cite this article in press as: V. Akimenko, An age-structured SIR epidemic model with fixed incubation period of infection, Computers and Mathematics with Applications (2017), http://dx.doi.org/10.1016/j.camwa.2017.01.022