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Global convergence analysis of a class of epidemic models☆

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ABSTRACT

This paper addresses the global convergence of the epidemic models whose infected subsystems are monotone in the sense of Hirsch (1984). By invoking results from monotone system theory and nonlinear control theory, a simple method is proposed for determining the global asymptotic stability of a disease free equilibrium (DFE) and the global convergence to an endemic equilibrium (EE). Typical epidemic models are studied to illustrate the applicability of the proposed methodology.

1. Introduction

Many epidemic models have a disease free equilibrium (DFE) at which the population is not invaded by infectious diseases. To verify the stability performance of the DFE, a threshold parameter R_0 (known as the basic reproduction number) is needed, and the related analysis method has been widely used (see [1,2] and the references therein). In principle, these results only reveal the local dynamic properties since they are obtained by examining the linear approximation near the DFE. In the past literature, the powerful Lyapunov's direct method has also been systematically explored to determine the global asymptotic stability of a DFE or an endemic equilibrium (EE); see, for instance, [3–8] and [9].

On the study of epidemic models, there is a not too striking but clearly significant branch in which the monotone systems theory plays a role. The earliest work in this respect appears in [10], and is further interpreted from the viewpoint of monotone flow in [11]. According to [11], one of important properties of monotone systems is that, under suitable conditions, their solutions often converge to either the origin or a unique positive equilibrium. This observation has been helpful for dealing with some general compartment systems such as epidemic systems [12].

Due to the appealing properties of monotone systems, some approaches have been developed for decomposing biological systems into monotone subsystems, and much insight has been attained from the analysis of the interconnections of monotone subsystems using tools from control theory (see [13] and the references therein). Indeed, it should be a novel direction to combine the monotone systems theory with the stability analysis methods from control community. Note that the input-to-state stability (ISS) related robust stability criteria [14,15], the nonlinear small-gain theory [16] and other advanced theories [17] have been playing a decisive role in robust control designs. Among the above control theories, the

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so-called "converging input converging state" (CICS) stability theory, originated from the ISS framework, is quite suitable for determining the global convergence of the interconnected systems without using involved Lyapunov functions.

For the case that the infected subsystem possesses the monotone property and the non-infected subsystems can again be proved to be CICS stable, we in this paper provide a simple method for determining the global asymptotic stability (GAS) of the DFE and the global convergence to an EE. More specifically, using the monotone systems theory and the R_0 based stability theory, we deduce that the solutions of the infected subsystem converge to the origin when $R_0 < 1$, or converge to a positive equilibrium when $R_0 > 1$. Then, by the application of the CICS stability theory, we again conclude that the non-infected subsystem is globally convergent. In the detailed treatment, we will first check if the concerning model can be dealt with by the method in [1], then check if the infected subsystem has a monotone property and if the non-infected subsystem is CICS stable. In this way, we will establish a global convergence analysis method that differs from the existing ones, and obtain global convergence or global stability results rather than local ones.

The rest of the paper is organized as follows. In Section 2, we provide necessary mathematical preliminaries and introduce the related theorems by analyzing a SIS model. Then, in Section 3, we develop global variants of the local threshold criteria proposed in the present literature of mathematical biology. In Section 4, we study the global stability analysis problem for two epidemic models whose infected subsystems are monotone. In Section 5, numerical simulation results are presented to support the main theoretical results. Finally, concluding remarks are given in Section 6.

2. Preliminaries

2.1. Basic reproduction number

In this subsection, we outline the computation of the basic reproduction number. It is proposed in [1] and is powerful for determining the local stability analysis of a DFE.

Consider a heterogeneous population that can be grouped into n homogeneous compartments. Let $x=(x_1,\cdots, x_m,x_{m+1}, \cdots, x_n)^{\mathrm{T}}$ with x_i being the number of individuals in the$i$thcompartment, and without loss of generality assume that the first m compartments correspond to the infected individuals. In addition, define X_s as the disease-free set: $X_s = \{x \in \mathbb{R}^n, x \geq 0 | x_i = 0, i = 1, \ldots, m\}$.

In order to compute the basic reproduction number, let $\mathbb{F}_i(x)$ be the appearance rate of new infections in compartment i, $\mathbb{V}_i^-(x)$ be the transfer rate of individuals out of compartment i, and $\mathbb{V}_i^+(x)$ be the transfer rate of individuals into compartment i. Then, the disease transmission model can be described by

$$\dot{x}_i = f_i(x) = \mathbb{F}_i(x) - (\mathbb{V}_i^-(x) - \mathbb{V}_i^+(x)), \quad i = 1, \cdots, n$$

i.e.,

$$\begin{aligned} \dot{x} &= f(x) = \mathbb{F}(x) - (\mathbb{V}^-(x) - \mathbb{V}^+(x)) \\ f &= (f_1, \cdots, f_n)^{\mathrm{T}},\ \mathbb{F} = (\mathbb{F}_1, \cdots, \mathbb{F}_n)^{\mathrm{T}},\ \mathbb{V}^- = (\mathbb{V}_1^-, \cdots, \mathbb{V}_n^-)^{\mathrm{T}},\ \mathbb{V}^+ = (\mathbb{V}_1^+, \cdots, \mathbb{V}_n^+)^{\mathrm{T}}. \end{aligned} \tag{1}$$

The following conditions are needed for inferring the theoretical results of [1]:

(A1) If $x \geq 0$, then $\mathbb{F}_i, \mathbb{V}_i^+, \mathbb{V}_i^- \geq 0$ for $i=1, \cdots, n$;
(A2) If $x_i=0$, then $\mathbb{V}_i^- = 0$. In particular, if $x \in X_s$, then $\mathbb{V}_i^- = 0$ for $i=1, \cdots, m$;
(A3) $\mathbb{F}_i = 0$ if $i > m$;
(A4) If $x \in X_s$, then $\mathbb{F}_i = 0$ and $\mathbb{V}_i^+ = 0$ hold for $i=1, \cdots, m$;
(A5) If $\mathbb{F}(x)$ is set to zero, then all eigenvalues of $Df(x_0)$ have negative real parts, where $x_0 = (0, \cdots, 0, x^*_{m+1}, \cdots, x^*_n)^{\mathrm{T}}$ is a disease free equilibrium (DFE) of system (1) and $Df(x_0)$ is the Jacobian $[\partial f_i/\partial x_j]$ of f evaluated at the DFE x_0.

When system (1) satisfies conditions (A1)–(A5), $D\mathbb{F}(x_0)$ and $D(\mathbb{V}^- - \mathbb{V}^+)(x_0)$ can be partitioned as (Lemma 1 of [1])

$$D\mathbb{F}(x_0) = \begin{pmatrix} F & 0 \\ 0 & 0 \end{pmatrix}, \quad D(\mathbb{V}^- - \mathbb{V}^+)(x_0) = \begin{pmatrix} V & 0 \\ \times & \times \end{pmatrix}, \tag{2}$$

where

$$F = \left[\frac{\partial \mathbb{F}_i}{\partial x_j}(x_0)\right], \quad V = \left[\frac{\partial (\mathbb{V}_i^- - \mathbb{V}_i^+)}{\partial x_j}(x_0)\right], \quad 1 \leq i, j \leq m,$$

and $\times$ denotes the entry not needed in the subsequent computations.

Based on the above partition, then the basic reproduction number can be defined as $R_0 = \rho(FV^{-1})$, where $\rho(FV^{-1})$ denotes the spectral radius of FV^{-1}.

In the following, we analyze an example to show how we make a decomposition $(\mathbb{F}, \mathbb{V}^-, \mathbb{V}^+)$ and verify that the conditions (A1)–(A5) are fulfilled under the decomposition. Furthermore, we will show that the block partition in (2) does appear.