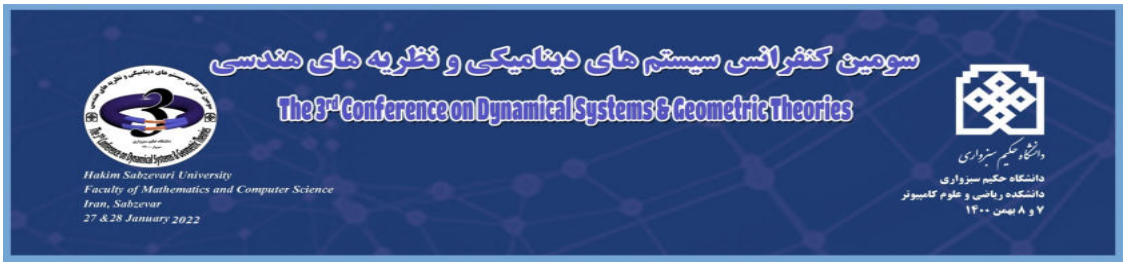

A Study on Epidemic Models; Stability and Basic Reproduction Number

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Abstract. Over the past century, mathematical modeling has made the connection between important public health questions and the basic parameters of infection for a proper understanding of the spread of disease has been used. Nowdays, every scientist and researcher knows the importance and appreciation of dynamical systems and differential equations in ecology, biology, medicine, epidemiology and etc. The major topic in epidemiology is when time a disease is epidemic, endemic or pandemic. This is usually done by finding the basic reproduction number, R_0. In this paper, we study SIR and SEIR models. In continuation after finding equilibrium point, we prove three theorems which analyzes locally and globally asymptotically stability and backward bifurcation.

Keywords: Stability, Basic reproduction number, Backward bifurcation.

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1. Introduction

We first give a brief literature to the modeling of epidemics; more thorough descriptions may be found in [1,5]. One of the early triumphs of mathematical epidemiology was the formulation of a simple model by Kermack and McKendrick (1927) whose predictions are very similar to this behavior, observed in countless epidemics. The Kermack-Mendrick model is a compartmental model based on relatively simple assumptions on the rates of flow between different classes of members of the population and there is a threshold quantity which is called the basic reproduction number and denoted by R_0 which determines whether there is an epidemic [3].

2. Modeling

The special case of the model proposed by Kermack and McKendrick in 1927 which is the starting point for our study of epidemic models is as follows:

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$$
\begin{aligned}
S^{'} &= -\beta SI, \\
I^{'} &= \beta SI - \alpha I, \\
R^{'} &= \alpha I.
\end{aligned} \tag{1}
$$

In this model, we assume that $S(t)$ denotes the number of individuals who are susceptible to the disease, that is, who are not infected at time t. $I(t)$ denotes the number of infected individuals, assumed infectious and able to spread the disease by contact with susceptibles. $R(t)$ denotes the number of individuals who have been infected and then removed from the possibility of being infected again or of spreading infection. In this model infected neighbors recover at rate α and infected neighbors transmit infection at rate β and it is based on the following assumptions:
(i) An average member of the population makes contact sufficient to transmit infection with βN others per unit time, where N represents total population size (mass action incidence).
(ii) Infectives leave the infective class at rate I per unit time.
(iii) There is no entry into or departure from the population, except possibly through death from the disease.
(iv) There are no any disease deaths, and the total population size is a constant N.
In many infectious diseases there is an exposed period after the transmission of infection from susceptibles to potentially infective members but before these potential infectives develop symptoms and can transmit infection. Cosider the $SEIR$ model with some infectivity in the exposed period, to incorporate an exposed period with mean exposed period $\frac{1}{\kappa}$, we add an exposed class E and use compartmentsS, E, I, R and total population size $N = S + E + I + R$ to give a generalization of the epidemic model (1) as follows:

$$
\begin{aligned}
S^{'} &= -\beta SI, \\
E^{'} &= \beta SI - \kappa E, \\
I^{'} &= \kappa E - \alpha I.
\end{aligned} \tag{2}
$$

3. Main Results

Now, we consider the $SEIR$ model infectivity in the exposed stage,

$$
\begin{aligned}
S^{'} &= -\beta S(I + \epsilon E), \\
E^{'} &= \beta S(I + \epsilon E) - \kappa E, \\
I^{'} &= \kappa E - \alpha I, \\
R^{'} &= \alpha I.
\end{aligned} \tag{3}
$$

The analysis of this model is the same as the analysis of (1), but with I replaced by $E + I$. That is, instead of using the number of infectives as one of the variables, we use the total number of infected members, whether or not they are capable of transmitting infection. In some diseases there is some infectivity during the exposed period. This may be modeled by assuming infectivity reduced by a factor ε during the exposed period. Here, the disease

states are E and I, and hence the Jacobin matrix is as follows:

$$J = \begin{bmatrix} \epsilon\beta N - \kappa & \beta N \\ \kappa & -\alpha \end{bmatrix}$$

So the next generation matrix obtanied by the following matrices

$$F = \begin{bmatrix} \epsilon\beta N & \beta N \\ 0 & 0 \end{bmatrix}, \qquad V = \begin{bmatrix} \kappa & 0 \\ -\kappa & \alpha \end{bmatrix}$$

the matrix $K = FV^{-1}$ is referred to as the next generation matrix for the system at the disease-free equilibrium. Since FV^{-1} has rank 1, it has only one nonzero eigenvalue, and since the trace of the matrix is equal to the sum of the eigenvalues, we see that

$$R_0 = \frac{\varepsilon\beta N}{\kappa} + \frac{\beta N}{\alpha},$$

the element in the first row and first column FV^{-1}. If all of new infections are in a single compartment, as the case here, the basic reproduction number is the trace of the matrix FV^{-1}. There are some situations in $R_0 < 1$ in which it is possible to show that the asymptotic stability of the disease-free equilibrium is global, that is, all solutions approach the disease-free equilibrium, only those with initial values sufficiently close to this equilibrium.

System (3) has a continuum of disease-free equilibria (DFE), given by: $E_0 = (N, 0, 0)$ and the next generation operator method can be used to analyse the asymptotic stability property of the DFE.

THEOREM 3.1. *Assume that the disease transmission model is given by*

$$\begin{aligned} x_i^{'} &= f_i(x, y) - v_i(x, y) && i = 1, ..., n \\ y_j^{'} &= g_j(x, y) && j = 1, ..., m \end{aligned} \tag{4}$$

The diseasefree equilibrium of (3.1) is locally asymptotically stable if $R_0 < 1$, but unstable if $R_0 > 1$.

PROOF. Let F and V be as defined as above, and let J_{21} and J_{22} be the matrices of partial derivatives of g with respect to x and y evaluated at the disease-free equilibrium. The Jacobian matrix for the linearization of the system about the disease-free equilibrium has the block structure

$$J = \begin{bmatrix} F - V & 0 \\ J_{21} & J_{22} \end{bmatrix}$$

The disease-free equilibrium is locally asymptotically stable if the eigenvalues of the Jacobian matrix all have negative real parts. Since the eigenvalues of J are those of $(F - V)$ andJ_{22}, and the latter all have negative real parts by assumption, the diseasefree equilibrium is locally asymptotically stable if all eigenvalues of $(F - V)$ have negative real parts. By the assumptions on F and V , F is nonnegative and V is a nonsingular M-matrix. Hence, all eigenvalues of $(F-V)$ have negative real parts if and only if $\rho(FV^{-1}) < 1$. It follows that the disease-free equilibrium is locally asymptotically stable if $R_0 = \rho(FV^{-1}) < 1$.

Instability for $R_0 > 1$ can be established by a continuity argument. If $R_0 \leq 1$, then for any $\varepsilon \geq 0$, $((1+\varepsilon)I - FV^{-1})$ is a nonsingular M-matrix and by Lemma 3.1, $((1+\varepsilon)I - FV^{-1})^{-1} \geq 0$.
By Lemma 3.2, all eigenvalues of $((1+\varepsilon)V - F)$ have positive real parts. Since $\varepsilon > 0$ is arbitrary, and eigenvalues are continuous functions of the entries of the matrix, it follows that all eigenvalues of $(V - F)$ have nonnegative real parts. To reverse the argument, suppose all the eigenvalues of $(V - F)$ have nonnegative real parts. For any positive ε, $(V + \varepsilon I - F)$ is a nonsingular M-matrix, and by Lemma 3.2, $\rho(F(V + \varepsilon I)^{-1}) < 1$.
Again, since $\varepsilon > 0$ is arbitrary, it follows that $\rho(FV^{-1}) \leq 1$. Thus, $(F - V)$ has at least one eigenvalue with positive real part if and only if $\rho(FV^{-1}) > 1$, and the disease-free equilibrium is unstable whenever $R_0 > 1$.

□

For globally asymptotically stable theorem, we will say that a vector is nonnegative if each of its components is nonnegative, and that a matrix is if each of its entries is non-negative. We rewrite the system (4) as

$$\begin{aligned} x^{'} &= -Ax - \widehat{f}(x,y) \\ y_j^{'} &= g_j(x,y) \qquad\qquad\qquad j = 1, ..., m. \end{aligned} \tag{5}$$

THEOREM 3.2. *If -A is a nonsingular M-matrix and $\widehat{f} \geq 0$, if the assumptions on the model (4) are satisfied, and if $R_0 < 1$, then the disease-free equilibrium of (5) is globally asymptotically stable.*

PROOF. The variation of constants formula for the first equation of (4) gives

$$x(t) = e^{-tA}x(0) - \int_0^t e^{-(t-s)}\widehat{f}(x(s), y(s))ds.$$

It can be shown that $e^{-tA} \geq 0$ if $-A$ is an M-matrix. Because we have $-A = B - sI$ with $B \geq 0$,

$$e^{-tA} = e^{tB}e^{-stI} = e^{tB}e^{-st}I = e^{tB}e^{-st}$$

and $e^{tB} \geq 0$, since $B \geq 0$. This, together with the assumption that $f \geq 0$, implies that $0 \leq x(t) \leq e^{-tA}x(0)$ and since $e^{tA}x(0) \to 0$ as $t \to \infty$ follows that $t \to \infty$.
On other hand, there are another examples to show that the disease-free equilibrium may not be globally asymptotically stable if the condition $\widehat{f} \geq 0$ is not satisfied.

□

THEOREM 3.3. *Consider model (3). A backward bifurcation occurs at $R_0 = 1$.*

PROOF. the Jacobin matrix for system (3) at $E_0 = (N, 0, 0)$ is as follows:

$$J = \begin{bmatrix} \epsilon\beta_1 N - \kappa & \beta_1 N \\ \kappa & -\alpha \end{bmatrix}$$

Choosing β_1 as the bifuraction parameter, then $R_0 = 1$ and $\beta_1 = \dfrac{\kappa\alpha}{N(\epsilon\alpha + \kappa)}$

□

4. Conclusion

We have established that the simple Kermack-McKendrick epidemic model (3) has some basic properties:
(i) There is a basic reproduction number R_0 such that if $R_0 < 1$, the disease dies out while if $R_0 > 1$, there is an epidemic.
(ii) There is a relationship between the reproduction number and the final size of the epidemic, which is an equality if there are no disease deaths. And also, in epidemic models the disease-free equilibrium is asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.
(iii) In models for which endemic equilibria exist near the disease-free equilibrium for $R_0 < 1$ the bifurcation is called a backward bifurcation.

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