



Analysis of a Discrete SEIR Epidemic Model

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Abstract: In this paper, we propose a discrete-time SEIR epidemic model described by difference equations. The basic reproductive number R_0 for the discrete SEIR model is computed and the dynamical behavior of the model is studied. The stability of both the disease-free and endemic equilibrium are derived. It is proved that the disease free equilibrium is asymptotically stable if $R_0 < 1$. Numerical simulations are performed to illustrate the impact of threshold value on epidemic.

Keywords: SEIR Model, Reproduction Number, Equilibrium Points, Difference Equation.

I. Introduction

History of mathematical models in epidemiology goes back to the eighteenth century (Bernoulli 1760). Great attention has been paid to the dynamics properties (including stable, unstable, persistent and oscillatory behavior) of the epidemic models. Most of the models in mathematical epidemiology are compartmental models, with the population being divided into compartments. Various epidemic models have been formulated and analyzed by many researchers. The classical susceptible-infected-recovered (SIR) model is a system consisting of three differential equations which assumes that the host population is constant [1, 3, 5]. Many infectious diseases in nature incubate inside the hosts for a period of time before the hosts become infectious. The basic SEIR model represents infection dynamics in a total population of size N . This is the simplest model for mass action transmission in a homogeneously-mixed host population. Transmission of infection from infectious to susceptible individuals is controlled by a contact term $\frac{\beta IS}{N}$. In this model, infected individuals move into the Exposed (not infectious) class after an average incubation period and subsequently through the infectious class. The model assumes that recovered individuals are immune from infection [1].

II. Model Formulation and Equilibria

In this section, we formulate a model for epidemic outbreaks with exposed class. In the construction of the SEIR model, we will divide the total population into four epidemiological classes which are susceptible (S), exposed (E) infectious (I) and recovered (R). Few authors studied discrete epidemic models [2, 4, 6] whereas there exists a vast literature on continuous epidemic models [1, 5]. In this section, we analyze the following reduced discrete SEIR epidemic model.

$$\begin{aligned} S(n+1) &= a - b \frac{S(n)I(n)}{S(n) + I(n)} + dI(n) + (1-c)S(n) \\ E(n+1) &= b \frac{S(n)I(n)}{S(n) + I(n)} + [1 - (f + c)]E(n) \\ I(n+1) &= fE(n) + [1 - (d + c)]I(n) \end{aligned} \quad (1)$$

Where $a, b, c, d, f > 0$ and the initial conditions are $S(0) \geq 0, E(0) \geq 0, I(0) \geq 0$. The parameters have the following meaning: 'a' represents recruitment rate of the population, 'c' is the death rate, 'b' is the constant rate at which the susceptible population is converted into the exposed population, 'd' is the recovery rate to susceptible population, and 'f' is the effective transmission co-efficient. The system (1) always has two equilibria: The first one, corresponding to a population with no infected individuals, is referred to henceforth as disease-free equilibrium $E_0 = \left(\frac{a}{c}, 0, 0\right)$ and the second equilibrium corresponds to the case in which there is a significant group of infectious individuals referred to as the epidemic equilibrium $E_1 = (S^*, E^*, I^*)$ where

$$S^* = \frac{af(f+c)(d+c)}{c(d+f)[bf-(d+c)(f+c)]+cbf^2}, \quad E^* = \frac{a(d+c)[bf-(f+c)(d+c)]}{c(d+f)[bf-(d+c)(f+c)]+cbf^2}, \quad \text{and}$$

$$I^* = \frac{af[bf-(f+c)(d+c)]}{c(d+f)[bf-(d+c)(f+c)]+cbf^2}.$$

III. Dynamic Behavior of the Model and Numerical Simulations

We derive a threshold value R_0 . An important technique for analyzing nonlinear systems qualitatively is the analysis of the behavior of the solutions near equilibrium points using linearization. For the discrete time model, stability of the equilibrium solution requires the dominant eigenvalue to have magnitude less than one. For the system described by equations (1), this reduces to requiring all roots of the following equation to lie in the unit circle. The local stability analysis of the model can be carried out by computing the Jacobian matrix corresponding to each equilibrium point. We first determine the stability of the system. The Jacobian matrix of system (1) is

$$\begin{pmatrix} -\frac{bI}{S+I} + \frac{bSI}{(S+I)^2} + 1 - c & 0 & -\frac{bI}{S+I} + \frac{bSI}{(S+I)^2} + d \\ \frac{bI}{S+I} - \frac{bSI}{(S+I)^2} & 1 - f - c & \frac{bI}{S+I} - \frac{bSI}{(S+I)^2} \\ 0 & f & 1 - a - d \end{pmatrix} \quad (2)$$

If $R_0 < 1$, then the epidemic cannot maintain itself because each individual, on average, infects less than one member of the population. The epidemic equilibrium is then unstable, while the infection-free equilibrium point is locally stable. Also, if $R_0 > 1$, then on average, each infected individual infects more than one other member of the population and a self-sustaining group of infectious individuals will propagate. A simple linear analysis shows that in this case, the epidemic equilibrium point is locally stable, while the infection-free equilibrium point is unstable.

A. Disease Free Equilibrium

At the disease-free equilibrium, the matrix of the linearization is given by

$$J(E_0) = \begin{pmatrix} 1 - c & 0 & -b + d \\ 0 & 1 - (f + c) & b \\ 0 & f & 1 - (d + c) \end{pmatrix}$$

The Eigen values of the matrix $J(E_0)$ are $\lambda_1 = 1 - c$ and $\lambda_{2,3} = \frac{2(1-c) - (f+d)}{2} \pm \sqrt{(f-d)^2 + 4fb}$.

We obtain the explicit expression for the basic reproduction number R_0 . Then, it is shown that the disease-free equilibrium is locally and globally asymptotically stable if $R_0 < 1$. In this case, the disease always dies out. The basic reproductive number for our model is $R_0 = \frac{fb}{(d+c)(f+c)}$.

Lemma.1 Let $F(\lambda) = \lambda^2 + B\lambda + C$. Suppose that $F(1) > 0$, λ_1 and λ_2 are two roots of $F(\lambda) = 0$. Then $|\lambda_1| < 1$ and $|\lambda_2| < 1$ if and only if $F(-1) > 0$ and $C < 1$.

Theorem.1 If $R_0 < 1$, then the disease free equilibrium $E_0 = \left(\frac{a}{c}, 0, 0\right)$ of the model (1) is asymptotically stable.

Proof.

The linearization matrix of (1) at the positive equilibrium $E_0 = \left(\frac{a}{c}, 0, 0\right)$ is given by

$$\begin{pmatrix} 1 - c & 0 & -b + d \\ 0 & 1 - (f + c) & b \\ 0 & f & 1 - (d + c) \end{pmatrix}$$

The characteristic equation of matrix is

$$P(\lambda) = (1 - c - \lambda)[(1 - f - c - \lambda)(1 - d - c - \lambda) - fb]$$

We see that the equation $P(\lambda) = 0$ has an Eigen value $0 < \lambda_1 = 1 - c < 1$.

Therefore, in order to determine the stability of the positive equilibrium of model (1), we discuss the nature roots of the characteristic equation,

$$P(\lambda) = \lambda^2 - \lambda(2 - 2c - f - d) + (f + c)(d + c) + (1 - 2c - f - d) - fb$$

When $R_0 < 1$ the calculation yields,

$$P(1) = (f + c)(d + c) - fb > 0$$

$$P(-1) = 2[2(1 - c) - (f + d)] + (f + c)(d + c) - fb > 0 \text{ when } 2(1 - c) - (f + d) > 0$$

$$\frac{f + d}{2(1 - c)} < 1 \text{ and } c < 1$$

Furthermore, we have, Constant term $= 1 + (f + c)(d + c) - (f + c) - (d + c) - fb < 1$ with

$$(f + c)(d + c) - fb < f + c + d + c$$

$$f + d + 2c > 0$$

The Jury Criterion implies that the roots λ_2 and λ_3 of equation $P(\lambda) = 0$, satisfy $|\lambda_2| < 1$ and $|\lambda_3| < 1$.

B. Numerical Examples

Example.1 We choose the parameter values $a = 0.05$; $b = 0.006$; $c = 0.075$; $d = 0.025$; $f = 0.05$; $t = 50$ Here

$$R_0 = \frac{fb}{(d + c)(f + c)} = 0.024 < 1; \text{ so the equilibrium point } E_0 \text{ is globally stable, see fig - 1.}$$

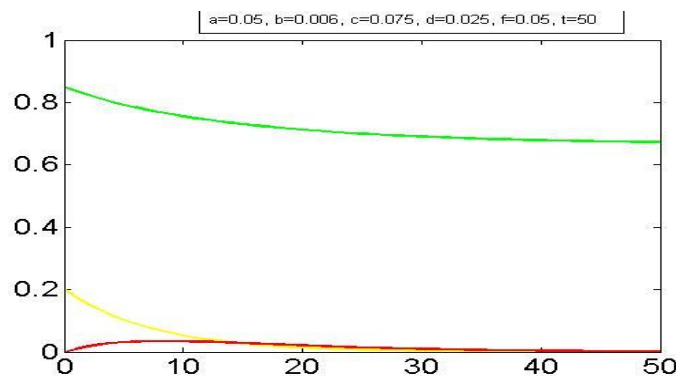


Figure 1. Time plot and Phase diagram for the system (1) with $R_0 < 1$

Thus the disease free equilibrium of (1) is asymptotically stable when $R_0 < 1$.

Example 2. When $R_0 > 1$, there exists unique endemic equilibrium which is stable under certain conditions. In order to show E_1 is stable when $R_0 > 1$ we choose $a = 0.005$; $b = 0.073$; $c = 0.0056$; $d = 0.023$; $f = 0.0234$; $t = 500$ Here

$$R_0 = \frac{fb}{(d + c)(f + c)} = 2.05956 > 1, \text{ see fig - 2.}$$

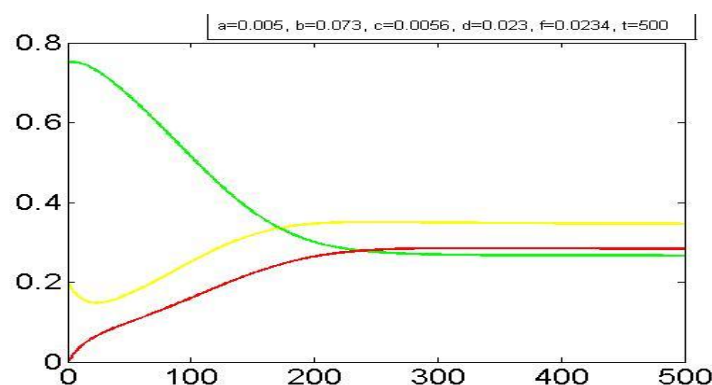


Figure 2. Time plot and Phase diagram for the system (1) with $R_0 > 1$

Example 3. In this example we choose to illustrate the impact of the parameter b on the infective class.

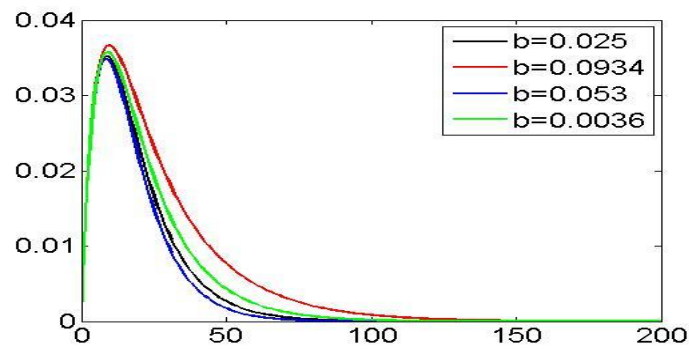


Figure 3. Impact on $I(n)$

Example 4. The effect of R_0 on disease propagation is demonstrated by taking several values of $R_0 = 0.599$; 0.75130; 1.0550; 1.52627; 2.3904; 3.0. Here $R_0 = \frac{fb}{(d+c)(f+c)}$.

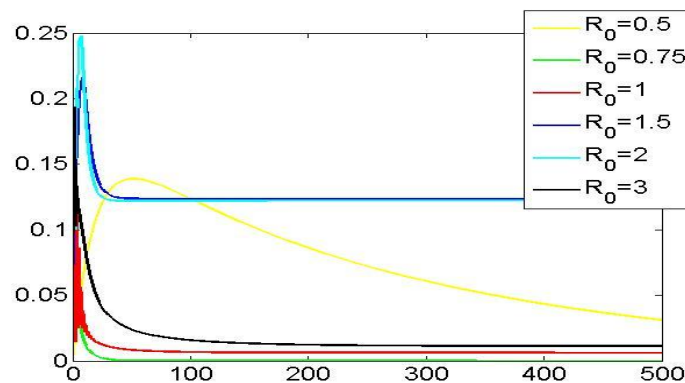


Figure 4. Impact of R_0

In this paper, we formulated a discrete version of SEI model to describe disease transmission. Reproduction number is computed based on linearization theory and its effects on extinction and persistence are demonstrated.

IV. References

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