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Infection Spread in a Discrete SEIR Model

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Abstract. The dynamics of SEIR epidemic model is explored in this paper. Discrete-time SEIR epidemic model described by difference equations is proposed. The basic reproduction number of the discrete SEIR model that determines disease extinction and disease survival is computed. The stability the disease free equilibrium is demonstrated. Numerical simulations are performed to illustrate the theoretical results.

Keywords: SEIR, SIR

I. INTRODUCTION

The modeling of epidemics has been the object of a vast number of studies over the past century. The desire to understand their mechanism has led to the formulation of various models which make possible the simulation of events for which laboratory experiments cannot be conducted easily. In recent years, various epidemic models have been proposed and explored to prevent and control the spread of the infectious diseases, such as measles, tuberculosis, flu and ebola [1, 3, 4]. In the theoretical studies of epidemic dynamical models, there are two kinds of mathematical models: the continuous-time models described by differential equations and the discrete-time models described by difference equations [2, 7]. Analysis of steady states of the model and the stability for the epidemic model is of a great importance as it can help our society and direct us to determine and forecast the development trend of infection. The analytical results can be used to describe the spread characteristics of infectious diseases, predict the status of the infection and evaluate the efficiency of the control strategies.

II. FORMULATION OF THE MODEL AND EQUILIBRIA

In recent years, many researchers studied SEIR epidemic models. S, E, I and R are the fractions of the population in each state. The host population is divided into three epidemiological classes: the susceptibles S, the exposed E the infectives I, and the removed/recovered R. Few authors studied discrete epidemic models [2, 5, 7] where as there exists a vast literature on continuous epidemic models [6]. In this section, we analyze the following discrete SIR epidemic model.

$$\begin{aligned} S(n+1) &= b - hS(n)I(n) - pbE(n) + S(n) - qbI(n) - bS(n) \\ E(n+1) &= hS(n)I(n) + qbI(n) - (\varepsilon + b)E(n) + E(n) \\ I(n+1) &= \varepsilon E(n) - (\gamma + b)I(n) + I(n) \\ R(n+1) &= \gamma I(n) - bR(n) + R(n) \end{aligned} \quad (1)$$

where $b, h, p, q, \varepsilon, \gamma > 0$ and the initial conditions are $S(0) > 0, E(0) > 0, I(0) > 0, R(0) > 0$ We can study (1) in the following feasible region:

$$\sum = \{(S, E, R, I) \in R_+^4 : S + E + I + R = 1\}$$

The parameter $\varepsilon > 0$ is the rate at which the exposed individuals become infectious, $\gamma \geq 0$ is the rate at which the infectious individuals recover, and b is birth rate.

When $\gamma = 0$, there is no recovery from the disease, and model (1) reduces to SEI model.

$$\begin{aligned} S(n+1) &= b - hS(n)I(n) - pbE(n) + S(n) - qbI(n) - bS(n) \\ E(n+1) &= hS(n)I(n) + qbI(n) - (\varepsilon + b)E(n) + E(n) \\ I(n+1) &= \varepsilon E(n) - (\gamma + b)I(n) + I(n) \end{aligned} \quad (2)$$

The system (2) always has a disease-free equilibrium $E_0 = (1, 0, 0)$ and an endemic equilibrium $E_1 = (S^*, E^*, I^*)$, where $S^* = \frac{(\varepsilon + b)(\gamma + b) - qb\varepsilon}{h\varepsilon}, E^* = \frac{-b[(\varepsilon + b)(\gamma + b) - \varepsilon(qb + h)]}{\varepsilon h(b + \varepsilon + pb)}$ and $I^* = \frac{-b[(\varepsilon + b)(\gamma + b) - \varepsilon(qb + h)]}{h(\gamma + b)(b + \varepsilon + pb)}$. E_0 is called the disease free equilibrium since E and I classes are empty.

III. DYNAMIC BEHAVIOR OF THE MODEL AND NUMERICAL SIMULATIONS

In this section, we will examine the local stability of the equilibria by analyzing the eigenvalues of the Jacobian matrix at the equilibria. For the system described by equations (2), using Routh-Hurwitz criterion, this reduces to requiring all roots of the following equation to lie in the unit circle [9]. 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 (2) is

$$\begin{pmatrix} -hI+1-b & -pb & -hS-qb \\ hI & 1-\varepsilon-b & hS+qb \\ 0 & \varepsilon & 1-\gamma-b \end{pmatrix} \qquad (3)$$

3.1. Disease Free Equilibrium.

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

$$J(E_0)=\begin{pmatrix} 1-b & -pb & -h-qb \\ 0 & 1-\varepsilon-b & h+qb \\ 0 & \varepsilon & 1-\gamma-b \end{pmatrix}$$

The Eigen values of the matrix $J(E_0)$ are $\lambda_1 = 1-b$ and $\lambda_{2,3} = \frac{2(1-b)-(\varepsilon+\gamma)}{2} \pm \frac{1}{2}\sqrt{(\varepsilon-\gamma)^2+4\varepsilon(bq+h)}$.

The basic reproductive number R_0 is fundamental in the study of epidemiological models. Here the basic reproductive number $R_0 = \frac{\varepsilon(bq+h)}{(b+\gamma)(b+\varepsilon)}$. The epidemic spreads when $R_0 > 1$ and dies out when $R_0 < 1$. If $R_0 < 1$, the disease-free equilibrium E_0 is stable.

Example 1. To demonstrate the theoretical results obtained in this paper, we will give some numerical simulations. The solutions are calculated and plotted using MATLAB. We consider the hypothetical set of parameter values $b = 0.852, h = 0.41, p = c = 0.031,\ q = d = 0.4,\ \gamma = f = 0.095,\ \varepsilon = f = 0.1$ and initial condition $(S,E,I) = (0.55, 0.15, 0, 1)$. Here $R_0 = \frac{\varepsilon(bq+h)}{(b+\gamma)(b+\varepsilon)}$ = 0.08327 < 1 so the equilibrium point E_0 is globally stable, see fig -1.

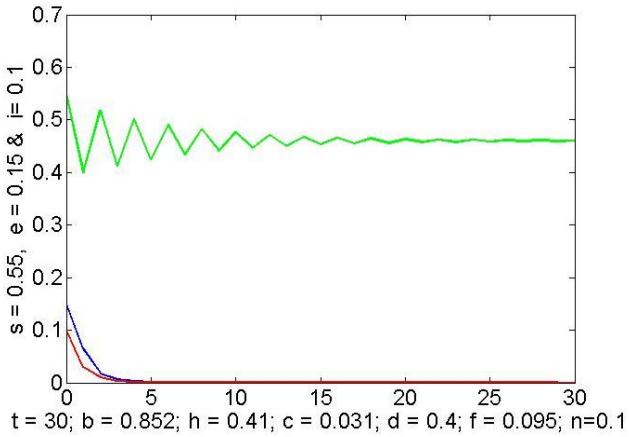

Figure 1. Time plot and Phase diagram for the system (1) with $R_0 < 1$.

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

Example 2. We choose the parameter values $b = 0.078, h = 0.999, p = c = 0.0000019,\ q = d = 0.32, \gamma = f = 0.00000026, \varepsilon = f = 0.24$ and initial condition $(S,E,I) = (0.55, 0.15, 0, 1)$ Here $R_0 = \frac{\varepsilon(bq+h)}{(b+\gamma)(b+\varepsilon)}$ = 9.9076592 > 1 so the equilibrium point E_0 is asymptotically stable, see fig - 2.

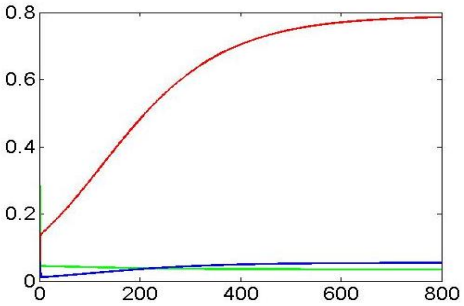

Figure 2. Time plot and Phase diagram for the system (1) with $R_0 > 1$

Example 3. We obtained the vales of R_0 = 0.877, 0.999, 0.504, 7.3, 9.907. Here $R_0 = \dfrac{\varepsilon(bq+h)}{(b+\gamma)(b+\varepsilon)}$.

In figures 3 and 4, we illustrate the effect of different values of R_0 and λ on the spread of infection.

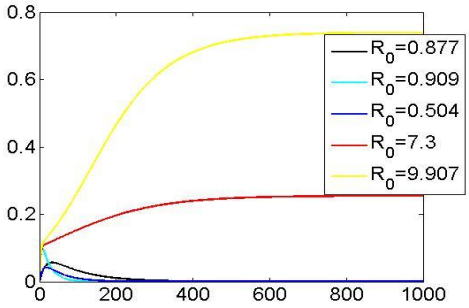

Figure 3. R_0 Variation

Variation of I

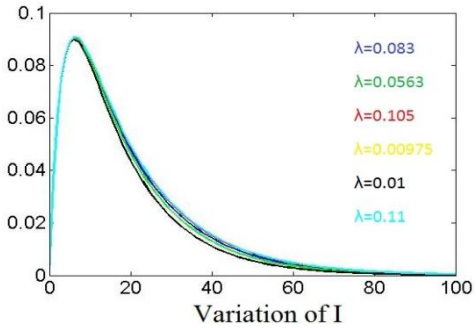

Figure 4. Variation of I

Lemma 1. Let $P(\lambda) = \lambda^2 + B\lambda + C$. Suppose that $P(1) > 0$, λ_1 and λ_2 are two roots of $P(\lambda) = 0$. 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 $E_0 = (1,0,0)$ of the model (2) is asymptotically stable.

Proof:

The linearization matrix of (2) at the positive equilibrium $E_0 = (1,0,0)$ is given by

$$J(E_0) = \begin{pmatrix} 1-b & -pb & -h-qb \\ 0 & 1-\varepsilon-b & h+qb \\ 0 & \varepsilon & 1-\gamma-b \end{pmatrix}$$

The characteristic equation of matrix is

$$P(\lambda) = (1-b-\lambda)\{(1-\varepsilon-b-\lambda)(1-\gamma-b-\lambda) - \varepsilon(h+qb)\}$$

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

Therefore, in order to determine the stability of the positive equilibrium of model (2), we discuss the roots of the following equation,

$$P(\lambda) = \lambda^2 - \lambda(2-2b-\gamma-\varepsilon) + (\varepsilon+b-1)(\gamma+b-1) - \varepsilon(h+qb)$$

When $R_0 < 1$ the calculation yields,

$$P(1) = 1 - 1(2-2b-\gamma-\varepsilon) + (\varepsilon+b-1)(\gamma+b-1) - \varepsilon(h+qb)$$

$$P(1) = (\varepsilon+b)(\gamma+b) - \varepsilon(h+qb) > 0 \text{ when } R_0 < 1$$

$$P(-1) = (-1)^2 - (-1)(2-2b-\gamma-\varepsilon) + (\varepsilon+b-1)(\gamma+b-1) - \varepsilon(h+qb)$$

$$P(-1) = 2[2(1-b) - (\gamma+\varepsilon)] + (\varepsilon+b)(\gamma+b) - \varepsilon(h+qb) > 0$$

when $2(1-b) - (\varepsilon+\gamma) > 0$

$$\frac{\varepsilon+\gamma}{2(1-b)} < 1 \text{ and } b < 1$$

Furthermore, the constant term satisfies,

$$\text{Constant terms(C)} = 1 - (\varepsilon+2b+\gamma) + (\varepsilon+b)(\gamma+b) - \varepsilon(h+qb) < 1$$

with the condition $\varepsilon + 2b + \gamma > 0$

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

The linearization theory implies that the positive equilibrium $E_0 = (1, 0, 0)$ of system (2) is asymptotically stable if $R_0 < 1$

IV. CONCLUSION

In this paper, we considered the discrete SEIR epidemic model. We have shown in this epidemic model, the basic reproduction number, which is the key concept in epidemiology, can be decreased below unity to eradicate the disease. We also illustrated that the equilibrium E_0 is stable, while E_1 is unstable by using the numerical simulation.

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