A Discrete Susceptible - Infected Epidemic Model

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Abstract.

In this paper, we propose a discrete-time SI epidemic model described by difference equations. The basic reproductive number R_0 of a discrete SI epidemic model is computed and the dynamical behavior of the model is studied. The stability of the disease free equilibrium and the endemic equilibrium are demonstrated. Numerical simulations are performed to illustrate the theoretical results.

I. INTRODUCTION

Mathematical models are important tools in analyzing the spread, dynamical evolution and control of infectious diseases. Also they provide great insight into disease spreading. Early modelling contributions for infectious disease spread were often for specific diseases. For example Bernoulli (1760) aimed at evaluating the effectiveness a certain technique of variolation against smallpox, and Ross (1911) modelled the transmission of malaria. One of the first more general and rigorous study was made by Kermack and McKendrick (1927).

The basic reproduction number is the number of cases generated by one infective over the period of infectivity when that infective is introduced into a large population of susceptibles. The ratio R_0 is of fundamental importance. More precisely, the basic reproduction number is defined. The basic reproduction number is the number of cases generated by one infective over the period of infectivity when that infective is introduced into a large population of susceptibles. More precisely, the basic reproduction number is defined.

II. FORMULATION OF THE MODEL EQUILIBRIA

An important research subject in mathematical epidemiology is the global stability of the equilibrium states of the epidemic models. There is an increasing interest in the study and application of discrete epidemic models. Allen et al. have studied some discrete-time SI, SIR, and SIS epidemic models ^{[2, 4, 6].} Most research works on discrete epidemic models concern the definition of the basic reproductive number, the global stability of the disease free equilibrium, the persistence of diseases, the existence and local stability of endemic equilibria, the existence of flip bifurcation and Hopf bifurcation. The results on the global stability of the disease free interest of the endemic equilibrium are quite few for discrete epidemic models. We consider

the simple SI model of an infectious pathogen which divides the host population into two groups: susceptible hosts (who are not infected with the pathogen but can get infected), S, and infectious hosts (who are infected with the pathogen I. There exists a vast literature on continuous epidemic models ^[1, 5]. The epidemic model we will consider is a nonlinear system of ordinary difference equations. In this section, we analyze the following discrete SI epidemic model.

$$S(n+1) = A - \frac{\beta S(n)I(n)}{S(n) + I(n)} + (1 - \mu)S(n) + \phi I(n)$$
(1)
$$I(n+1) = \frac{\beta S(n)I(n)}{S(n) + I(n)} + [1 - (\alpha + \mu + \phi)]I(n)$$

Here $A, \beta, \mu, \gamma, \alpha > 0$ and the initial conditions are S(0), I(0) > 0. The parameters have the following meaning: μ is the death rate, β is the average number of contacts perinfective per day,

 Γ is the recovery rate, and α is the death rate of infectives caused by the disease. The system ^[1] always has a disease-free equilibrium $E_0 = (\frac{A}{\mu}, 0)$ and an endemic equilibrium E_0 is called the

disease free equilibrium since I class is empty.

III.DYNAMIC BEHAVIOR OF THE MODEL AND NUMERICAL SIMULATIONS

The basic reproduction number R_0 is the number of secondary cases which one case would produce in a completely susceptible population. It depends on the duration of the infectious period, the probability of infecting a susceptible individual during one contact, and the number of new susceptible individuals contacted per unit of time. Also R_0 may vary considerably for different infectious diseases. This section deals with the stability of equilibria. For the discrete time model, stability of the equilibrium solution requires the dominant eigenvalue to have magnitude less thanone. For the system described by equations ^{[1],} this reduces to requiring all roots of the following equation to lie in the unit circle ^{[7].} The local stability analysis of the model can be carried out by computing the Jacobian matrixcorresponding to each equilibrium point. We first determine the stability of the system. The Jacobian matrix of system ^[1] is

$$J(S,I) = \begin{pmatrix} -\frac{\beta I^2}{(S+I)^2} + (1-\mu) & -\frac{\beta S^2}{(S+I)^2} + \phi \\ \frac{\beta I^2}{(S+I)^2} & \frac{\beta S^2}{(S+I)^2} + [1-(\alpha+\mu+\phi)] \end{pmatrix} (2)$$

DISEASE FREE EQUILIBRIUM

To determine if there is an epidemic, we look at the stability of the disease free equilibrium. At DFE, the matrix of the linearization is given by $J(E_0) = \begin{pmatrix} 1-\mu & -\beta+\phi \\ 0 & \beta+1-(\alpha+\mu+\phi) \end{pmatrix}$ The eigen values of the matrix $J(E_0)$ are $\lambda_1 = 1-\mu$ and $\lambda_2 = \beta+1-(\alpha+\mu+\phi)$. The basic reproductive number, R_0 is fundamental in the study of epidemiological models. Here the basic reproductive number $R_0 = \frac{\beta}{(\alpha+\mu+\phi)} < 1$. 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. We choose the parameter values A=0.015; β =0.027; μ =0.031; ϕ =0.035; α =0.0056.

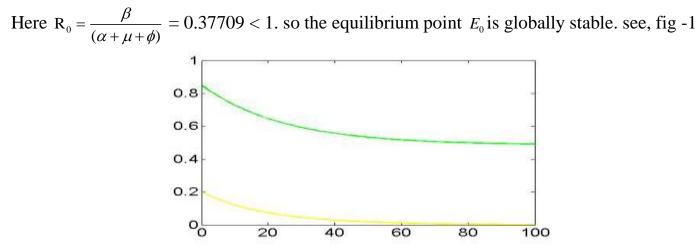


Fig-1 time plot and phase digram for the system (1) with $R_0 < 1$

Thus the disease free equilibrium of ^[1] is asymptotically stable when $R_0 < 1$. In the following figure, the effect of the parameter β on the disease dynamics (infection) is demonstrated.

Example 2.Choose the parameter A=0.015; β =0.07; μ =0.001; ϕ =0.015; α =0.0056.here R₀ = $\frac{\beta}{(\alpha + \mu + \phi)}$ = 3.2407 > 1.so the equilibrium point E₀ is asymptotically stable. see, fig -2

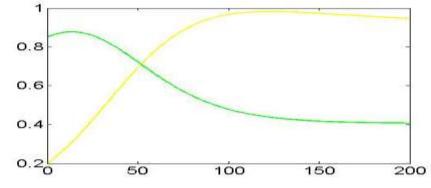
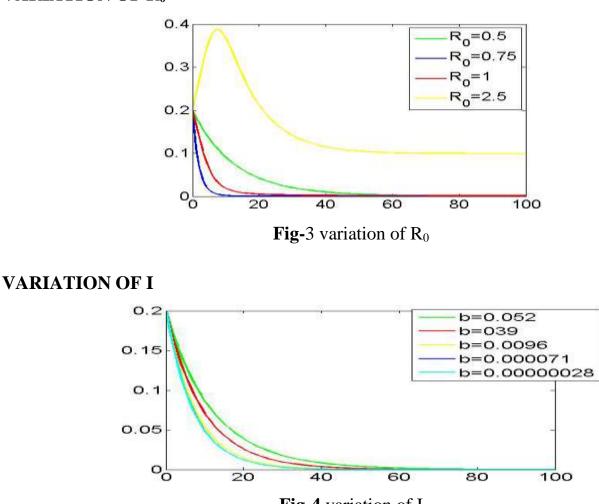


Fig-1 time plot and phase digram for the system (1) with $R_0>1$

When $R_0 > 1$, the average number of a new infection by an infected individual is more than one. Hence the disease may keep persistent in the population. The discrete SI model considered in this paper is simple, but it exhibits rich and complicated dynamical behavior. The analytical findings are confirmed with numerical simulations.



VARIATION OF R₀

Fig-4 variation of I

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

Proof:

The linearization matrix of (1) at the positive equilibrium $E_0 = (\frac{A}{\mu}, 0)$ is given by The characteristic equation of matrix is $J(E_0) = \begin{pmatrix} 1-\mu & -\beta+\phi \\ 0 & \beta+1-(\alpha+\mu+\phi) \end{pmatrix}$

 $\phi(\lambda) = \lambda^2 + \lambda(-2 + 2\mu - \beta + \alpha + \phi) + \mu^2 + \mu(-1 - \beta + \alpha + \phi) + 1 + \beta - (\alpha + \mu + \phi)$

We see that the equation $\phi(\lambda) = 0$ has an eigen value $0 < \lambda_1 = 1 - \mu < 1$

Therefore, in order to determine the stability of the positive equilibrium of model (1), we discuss the roots of the following equation, when $R_0 < 1$, the calculation yields,

$$\phi_1(1) = \mu^2 + \mu(-\beta + \alpha + \phi) > 0$$

$$\phi_1(-1) = 2(2 + \beta - \alpha - \phi - 2\mu) + \mu^2 + \mu(-\beta + \alpha + \phi) > 0$$

Furthermore, the constant term satisfies,

$$\mu^{2} + \mu(-1 - \beta + \alpha + \phi) + 1 + \beta - (\alpha + \mu + \phi)$$
$$\mu^{2} + \mu(-1 - \beta + \alpha + \phi) + 1 + \beta < (\alpha + \mu + \phi)$$
$$c = (\alpha + \mu + \phi) > 0$$

The jury criterion implies that the roots λ_2 nd of equation $\phi_1(\lambda) = 0$, satisfy $|\lambda_2| = 1$.

The linearization theory implies that the positive equilibrium $E_0 = (\frac{A}{\mu}, 0)$ of the system (1) is asymptotically stable if $R_0 < 1$.

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