Communication in Mathematical Modeling and Applications

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Stability analysis of infectious diseases model in a dynamic population

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Received: 24 July 2018, Accepted: 25 December 2018
Published online: 31 December 2018.

Abstract: The stability analysis of infectious disease model in a dynamic population is studied.The recruitment rate into the susceptible population is introduced since the population is dynamic thereby allowing a varying pouplation as a result of migration and birth.The model exhibited two equilibria: the disease free and endemic. The local stability of the model is asymptotically stable when $R_0 < 1$ and unstable when $R_0 > 1$. The global stability analysis of the disease free shows that the system is globally stable when the first derivative of Lyapunov function is negative.

Keywords: Basic Reproduction Number, dynamic population, asymptotically stable , Lyapunov function, equilibrium point.

1 Introduction

Infectious disease cause a rapid change in the population of any community. They cause morbidity and mortality in the population. Mathematical models play a significant role in studying the dynamical evolution and transmission of infectious diseases. Hongbin Guo [5] studied the global stability of SIR epidemic model with varying sub population. Zhang [8] did a study on the global stability of an SEI model with general contact rate. Guihua Li [4] studied global stability of a SEIR epidemic model in which the latent and incidence state were infective. Yu Zhang [8] examined the global stability of endemic equilibrium point of basic virus infection model with application to HBV infection. Xia Ma [6] studied the basic reproductive number R_0 of a discrete SIR epidemic model and its global stability. A.A Momoh [1] did a study on stability analysis of an infectious disease free equilibrium of Hepatitis B using MSEIR model to understand the transmission dynamics and control of HBV. Chunqing Wu [2] studied the global asymptotic stability for the disease - free equilibrium of a mathematical model for malaria transmission with two delays.

2 Model formulation

The population is divided into four (4) compartmental groups : The Susceptible population (S), the Exposed population (E), the Infected population (I) and the Recovered population (R). We introduced a recruitment rate Λ into the population

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which is dynamic i.e migration and birth are possible. The model is

$$\frac{dS(t)}{dt} = \Lambda - aS(t)I(t) - \mu S(t) + cR(t) \tag{1}$$
$$\frac{dE(t)}{dt} = aS(t)I(t) - \mu E(t) - bE(t) - \delta E(t) \tag{2}$$
$$\frac{dI(t)}{dt} = \delta E(t) - bI(t) - eI(t) - \mu I(t) \tag{3}$$
$$\frac{dR(t)}{dt} = bI(t) + bE(t) - cR(t) - \mu R(t), \tag{4}$$

where Λ= the recruitment rate at which the susceptible class is being populated,
a= the rate of infection,
b= the rate of recovery,
c= the rate at which recovered humans progress back to the susceptible class,
e= disease induced death rate,
μ= Natural death rate,
δ=rate at which the exposed class move into the infected compartment.
Equations 1-4 will be referred to as system 5-8

3 Methodology

The equilibrium points were first considered to evaluate the disease free equilibrium point and the endemic point of the disease. At equilibrium, we set

$$\frac{dS}{dt} = \frac{dE}{dt} = \frac{dI}{dt} = \frac{dR}{dt} = 0$$

If the rate of change is Zero, that means the system is at equilibrium. Our work is to find out, at what points are the system 2 at equilibrium

$$\frac{dS}{dt} = \Lambda - aSI - \mu S + cR = 0, \tag{5}$$
$$\frac{dE}{dt} = aSI - (\mu + b + \delta)E = 0, \tag{6}$$
$$\frac{dI}{dt} = \delta E - (b + e + \mu)I = 0, \tag{7}$$
$$\frac{dR}{dt} = bI + bE - (c + \mu)R = 0, \tag{8}$$

solving these equations we have,

$$E = 0$$

the disease free equilibrium and the endemic point,

$$[S = \frac{(\mu + b + \delta)(b + e + \mu)}{a\delta} \tag{9}$$

Substituting these stationary points into the system of equations 5-8 to get values of S E I and R respectively. When $E = 0$,

Let $P^0 = (S^0, E^0, I^0, R^0) = (\frac{\Lambda}{\mu}, 0, 0, 0)$ and $P^* = (S^*, E^*, I^*, R^*)$ be the values for S,E,I,R when

$$S = \frac{(\mu + b + \delta)(b + e + \mu)}{a\delta}$$

substituting S in equation (1), we have,

$$E = \frac{(b + e + \mu)I}{\delta}, \tag{10}$$

$$R = b\left(\frac{\delta + (b + e + \mu)}{\delta(c + \mu)}\right) I, \tag{11}$$

$$I = \frac{(c + \mu)(\mu(\mu + b + \delta)(b + e + \mu) - a\Lambda\delta}{abc((\delta + b + e + \mu) - (c + \mu)(\mu + b + \delta)(b + e + \mu)}, \tag{12}$$

and the basic reproduction number of the model using the next generation matrix $G = FV^{-1}$ where F is the matrix of the newly created infection, V is the matrix of transferred infection is given as V^{-1} is the inverse of matrix V, so,

$$F_i = \begin{pmatrix} aSI \\ 0 \\ 0 \end{pmatrix}, i = 1, 2, 3,$$

$$V_i = \begin{pmatrix} (\mu + b + \delta)E \\ (b + e + \mu)I - \delta E \\ (c + \mu)R - bI - bE \end{pmatrix}, i = 1, 2, 3,$$

$$F = \begin{pmatrix} \frac{\partial f_1}{\partial E}\Big|_{P^o} & \frac{\partial f_1}{\partial I}\Big|_{P^o} & \frac{\partial f_1}{\partial R}\Big|_{P^o} \\ \frac{\partial f_2}{\partial E}\Big|_{P^o} & \frac{\partial f_2}{\partial I}\Big|_{P^o} & \frac{\partial f_2}{\partial R}\Big|_{P^o} \\ \frac{\partial f_3}{\partial E}\Big|_{P^o} & \frac{\partial f_3}{\partial I}\Big|_{P^o} & \frac{\partial f_3}{\partial R}\Big|_{P^o} \end{pmatrix} = \begin{pmatrix} 0 & \frac{a\Lambda}{\mu} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix},$$

$$f_1 = aSI, f_2 = f_3 = 0,$$

$$V = \begin{pmatrix} (\mu + b + \delta) & 0 & 0 \\ -\delta & (b + e + \mu) & 0 \\ -b & -b & (c + \mu) \end{pmatrix},$$

$$G = \begin{pmatrix} \frac{a\Lambda\delta(c+\mu)}{\mu(\mu+b+\delta)(b+e+\mu)} & \frac{a\Lambda}{\mu(b+e+\mu)} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}.$$

The dominant eigenvalue of G is the basic reproduction number denoted by R_0, i.e $|G - \lambda I| = 0$ where I is the identity matrix. So,

$$R_0 = \frac{a\Lambda\delta}{\mu(\mu + b + \delta)(b + e + \mu)} \tag{13}$$

3.1 Local stability analysis of the Disease free equilibrium

Theorem 1. *The disease-free equilibrium of system (5-8) is locally asymptotic stable if $R_0 < 1$ otherwise unstable.*

Proof. The Jacobian matrix of system (5-8) at P^0

$$J = \begin{pmatrix} aI-\mu & 0 & -as & c \\ aI & -(\mu+b+\delta) & as & 0 \\ 0 & \delta & -(b+e+\mu) & 0 \\ 0 & b & b & -(c+\mu) \end{pmatrix},$$

at

$$p^0 = (S^0, E^0, I^0, R^0) = (\frac{\Lambda}{\mu}, 0, 0, 0).$$

Therefore, the characteristic equation is given by

$$\left|J(P^0) - \lambda I\right| = 0 (10)$$

and solving this gives,

$$(\lambda_1 + \mu) = 0, \quad (\lambda_2 + (c+\mu)) = 0$$

and

$$\lambda^2 + (2b+e+2\mu+\delta)\lambda + (\mu+b+\delta)(b+e+\mu)(1-R_0) = 0. \tag{14}$$

If $R_0 < 1$, then by Descarte's rule of signs, there is no sign change , hence, there are no positive roots of equation (14).

Furthermore, if λ is replaced by $-\lambda$ in equation (14).

$$\lambda^2 - (2b+e+2\mu+\delta)\lambda + (\mu+b+\delta)(b+e+\mu)(1-R_0) = 0 \tag{15}$$

If $R_0 < 1$, then equation (15) has two signs change, hence there are exactly two negative roots of equation (14) Therefore, P^0 is locally asymptotically stable if $R_0 < 1$. The result follows immediately that P^0 is unstable if $R_0 > 1$.

3.2 Global stability of disease-free equilibrium

In testing for the global stability of the disease free equilibrium of the model, We make use of Lyapunov function which says

$$L(E, I) = (\mu+b+\delta)I + \delta E. \tag{16}$$

If the first derivative of Lyapunov function is negative then the system (5-8) is globally stable thus, Differentiating equation (16) along the solutions of equations (2) and (3) at the disease free point

$$L' = (\mu+b+\delta)I' + \delta E'$$

we have,

$$\begin{aligned}(\mu+b+\delta)(\delta E-(b+e+\mu)I)+\delta(aSI-(\mu+b+\delta)E) &= (\mu+b+\delta)\delta E-(\mu+b+\delta)(b+e+\mu)I+\delta aSI\\ &\quad -(\mu+b+\delta)\delta E\\ &= \delta aSI-(\mu+b+\delta)(b+e+\mu)I\\ &= (\delta aS-(\mu+b+\delta)(b+e+\mu))I\\ &= (\mu+b+\delta)(b+e+\mu)\left(\frac{\delta aS}{(\mu+b+\delta)(b+e+\mu)}-1\right)I.\end{aligned}$$

At the disease free,

$$S=S^0=\frac{\Lambda}{\mu}=(\mu+b+\delta)(b+e+\mu)\left(\frac{\delta a\Lambda}{\mu(\mu+b+\delta)(b+e+\mu)}-1\right)I$$

solving this at the disease free point, we have,

$$S=S^0=\frac{\Lambda}{\mu}=(\mu+b+\delta)(b+e+\mu)\left(\frac{\delta a\Lambda}{\mu(\mu+b+\delta)(b+e+\mu)}-1\right)I,$$

Therefore, $L'=(\mu+b+\delta)(b+e+\mu)(R_0-1)I$, $L'<0$ whenever $R_0<1$ and $I>0$, furthermore, $L'=0$ whenever $R_0=1$ and or $I\geq 0$, $L'\leq 0$ if $R_0\leq 1$ and $I\geq 0$, which shows the system (5-8) is globally stable.

4 Analysis and conclusion

Using the data of 1995 Ebola outbreak in Kikwit Zaire cited in Zach Yarus [9] we have , the results of numerical simulations of the dynamical behaviour of system 2 as presented by using Maple 18 and with the parameter values from Zach Yarus (2012).

The Variation of total population when $R_0>1$

To know how the total population will look like if the reproduction number $R_0>1$, in the figure 1 below, the infected population increased as the susceptible individuals decreased and the exposed decreased. It implies that, efforts must be intensified to control the most sensitive parameters which are the transmission rate of the disease and the recruitment rate into the susceptible population since it is a dynamic population so that the reproduction number can be brought below 1, so that the disease can die out. Figure 2 is when the reproduction number $R_0<1$ which means the effect of the disease has greatly reduced in the long run because the reproduction number has been brought below 1 which means the disease will die out in the long run and the total population will be free of the disease.

Competing interests

The authors declare that they have no competing interests.

Authors' contributions

All authors have contributed to all parts of the article. All authors read and approved the final manuscript.

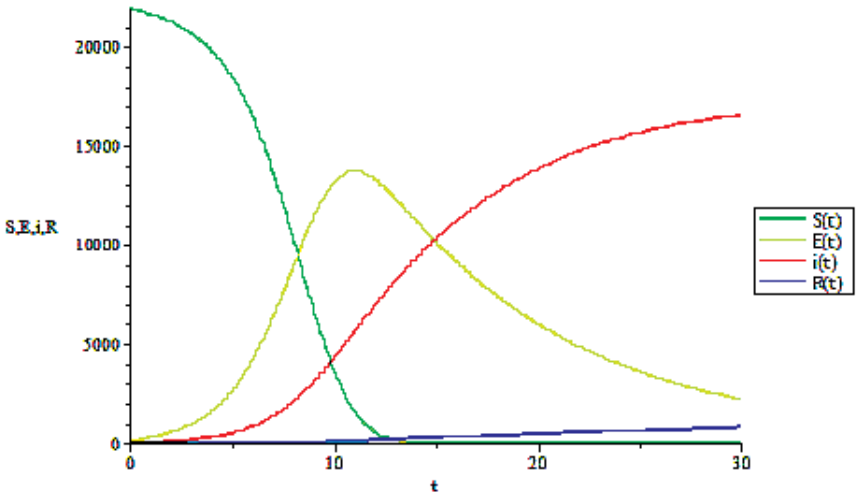

Fig. 1: Variation of the total population against time for R_0 greater then 1.

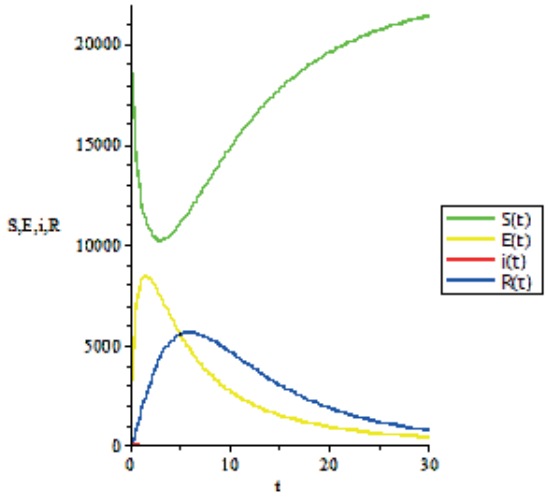

Fig. 2: Variation of the total population against time e when $R(0) < 1$.

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