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An SEIR Epidemic Model with Diffusion

By

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Abstract

In this paper, we study an SEIR epidemic model with diffusion. The model is analyzed using stability theory of differential equations. Equilibrium points and conditions of local stability of the system are determined. Basic reproduction number of the model is computed by next generation matrix approach. It is observed that endemic equilibrium point exists only if basic reproduction number is greater than one otherwise disease vanishes from the system. Further, it is observed that diffusion plays a significant role in stability of the system.

Key words : diffusion, stability, epidemic, equilibrium point.

1. Introduction

An intensive worldwide effort is speeding up the developments in the establishment of a global surveillance network for combating emergent and re-emergent infectious diseases over the last years. Scientists from different fields extending from medicine and molecular biology to computer science and applied mathematics have made collective efforts for the rapid assessment of potentially urgent situations. Toward this aim mathematical modelling plays an important role that focus on predicting, assessing, and controlling potential outbreaks of such diseases. To better understand and model the dynamics of diseases, it is imperative to determine the impact of numerous variables ranging from the micro hostpathogen level to host-to-host interactions. Mathematical models have been proved helpful to study ecological, social, economic, and demographic impacts on the spread of infectious diseases. Among these diseases, most of the diseases are virus generated that range from mild or even asymptomatic infection to an acute fatal disease.

Many epidemiologists [1-6] have considered such types of diseases and modeled them to find control strategies. The standard (Kermack-McKendrick) epidemic models are the basic models that are used to study the dynamics of any

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disease. During the last three decades, there has been growing interest in the study of infectious diseases [1-12].In particular, Verma [12], studied a predator-prey eco-epidemiological SEI model. Predator population is assumed to contract disease, when they come into contact with infected prey population for their food. Author has done the mathematical analysis of the model for stability, persistence and impermanence. Basic reproduction number is also derived in the research article.

Present paper contains a separate class of exposed population in the basic SIR model. Moreover, to take into account the continuous movement of different individuals among the compartments, we include diffusion term in each equation.

2. Mathematical Model

We stratify total population $N(t)$ into four compartments: susceptible population $S(t)$, exposed population $E(t)$, infectious population $I(t)$ and recovered population $R(t)$. In addition, we assume that the population is homogeneous and closed. Therefore, at any time t, the total density $N(t)$ of the population is given by

$$N(t) = S(t) + E(t) + I(t) + R(t).$$

It is assumed that the influx of susceptible come from a single source, a constant recruitment rate A and they are removed by natural death at the death rate d. Moreover, it is assumed that the disease spread among the susceptible population through direct contact with the infectious host. It is further assumed that after infection, an individual stays in latent period before becoming infectious. The natural death rate d is assumed to be constant for all the compartments. The incidence term of infection from infectious to susceptible population is assumed to be bilinear, βIS, where β is the transmission coefficient of infection. μ is the rate of transfer from exposed to infectious class, such that $\frac{1}{\mu}$ is the mean latent period. Infectious population is assumed to be recovered at the rate, γ with the recovery period, $\frac{1}{\gamma}$.

Based on the above assumptions the classical SEIR model is given by:

$$\begin{aligned}
\frac{dS}{dt} &= A - \beta IS - dS, \\
\frac{dE}{dt} &= \beta IS - (d+\mu)E, \\
\frac{dI}{dt} &= \mu E - (d+\gamma)I, \\
\frac{dR}{dt} &= \gamma I - \mu R,
\end{aligned} \tag{1}$$

with the initial conditions $S(0) > 0$, $E(0) \geq 0$, $I(0) \geq 0$, $R(0) \geq 0$. Further, since value of R can be determined if S, E and I are known, hence we can omit last equation of the system (1). Now, considering the effect of diffusion in each compartment of the population and omitting the last equation, our model takes the following form:

$$\begin{aligned}
\frac{\partial S}{\partial t} &= A - \beta IS - dS + D_S \frac{\partial^2 S}{\partial x^2}, \\
\frac{\partial E}{\partial t} &= \beta IS - (d+\mu)E + D_E \frac{\partial^2 E}{\partial x^2}, \\
\frac{\partial I}{\partial t} &= \mu E - dI - \gamma I + D_I \frac{\partial^2 I}{\partial x^2},
\end{aligned} \tag{2}$$

where D_S, D_E and D_I are the diffusion coefficient of the susceptible, exposed, infectious population respectively.

3. Boundedness and Dissipative Analysis

To analyze the existence and stability of the equilibrium points, we find the region of attraction in the following theorem.

Theorem. All the solutions of the system (2) are bounded and dissipative.

Proof. Let us define a function $W = S + E + I$. From (2), we have

$$\frac{dW}{dt} = A - dS - dE - dI - \gamma I \leq A - d(S + E + I).$$

Let us choose $\delta > 0$, such that

$$\begin{aligned}
\frac{dW}{dt} + \delta W &\leq A - d(S+E+I) + \delta(S+E+I) \\
&= A - (d-\delta)S - (d-\delta)E - (d-\delta)I.
\end{aligned}$$

If $\delta < d$, then we have $\frac{dW}{dt} + \delta W \leq A$.

Applying the theory of differential inequality, we get $0 \leq W \leq \frac{A}{\delta} + W(S_0, E_0, I_0)$, for $t \to \infty$, $0 \leq W \leq \frac{A}{\delta}$. Therefore, all the solutions of system (2) enter into the region $B = \{(S, E, I); W \leq \frac{A}{\delta} + \epsilon, \text{ for any } \epsilon > 0\}$.

Hence, the system (2) is bounded.

Now, we prove that the system (2) is dissipative. If $(S(t), E(t), I(t))$ be any solution with initial conditions $S(0) > 0$, $E(0) > 0$, $I(0) > 0$, then we conclude from $\frac{dS}{dt} \leq A - dS$ and standard comparison theorem that $\lim_{t\to\infty} \text{Sup} S(t) \leq \frac{A}{d}$. Similarly we can prove for $E(t)$ and $I(t)$.

Hence, the system (2) is dissipative.

4. Basic Reproduction Number

Basic reproduction number is a significant metric in mathematical epidemiology, denoted by R_0. It is defined as the number of secondary infections produced by a single infected in a completely susceptible population. It determines whether the disease will spread in the population or vanish. If $R_0 > 1$ disease spreads in the population whereas if $R_0 < 1$ disease vanishes. Although its value does not clearly states the severity of disease yet its higher value confirms that it will be difficult to control the disease as the population required to get infected for developing herd immunity, given by $1 - \frac{1}{R_0}$ gets higher.

Here, we will use Next Generation Matrix (NGM) approach given in Driessche [13] to determine the basic reproduction number. For this, we arrange the equations of system (2) beginning with the exposed population. The method is a direct application of lemma 1 in Driessche [13]. The decomposition of the model into components $\Re_1$ and $\Re_2$ leads to a system of the form $X = \Re_1 - \Re_2$, where

$$\Re_1 = \begin{bmatrix} \beta IS \\ 0 \\ -\beta IS \\ 0 \end{bmatrix}, \qquad \Re_2 = \begin{bmatrix} (d+\mu)E \\ -\mu E + (d+\gamma)I \\ -A + dS \\ -\gamma I + \mu R \end{bmatrix}$$

and $X = \left[\frac{dE}{dt}, \frac{dI}{dt}, \frac{dS}{dt}, \frac{dR}{dt}\right]$.

Since the infected compartments are E and I, at the disease-free equilibrium point, we define

$$R_1 = \left[\frac{\partial(\Re_1)_l}{\partial x_j}\right], R_2 = \left[\frac{\partial(\Re_2)_l}{\partial x_j}\right] \quad \text{for} \quad 1 \le l, j \le 2 \quad \text{giving}$$

$$R_1 = \begin{bmatrix} 0 & \beta\frac{A}{d} \\ 0 & 0 \end{bmatrix} \quad \text{and} \quad R_2 = \begin{bmatrix} d+\mu & 0 \\ -\mu & d+\gamma \end{bmatrix}.$$

Note that R_1 is non-negative, R_2 is a non-singular M-matrix, its inverse, ${R_2}^{-1}$ is non-negative and $R_1{R_2}^{-1}$ is non-negative. According to Diekmann [14], $R_1{R_2}^{-1}$ is the next generation matrix. In this case, if

$$A = R_1 R_2^{-1} = \frac{1}{(d+\mu)(d+\gamma)} \begin{bmatrix} \frac{\beta A}{d}\mu & \frac{\beta A}{d}(d+\mu) \\ 0 & 0 \end{bmatrix}$$

then, the spectral radius of A is given by $\lambda = \frac{\beta A \mu}{d(d+\mu)(d+\gamma)}$.

Hence, basic reproduction number is given by $R_0 = \frac{\beta A \mu}{d(d+\mu)(d+\gamma)}$.

5. Equilibrium Analysis

An equilibrium point of a dynamical system is a value of the state variables where the state variables do not change. In other words, we may define an equilibrium point of the system as a solution that does not change with time. This means if the systems starts at an equilibrium, the state will remain at the equilibrium forever.

System (2) has two equilibrium points, disease free equilibrium point $E_1 = \left(\frac{A}{d}, 0, 0\right)$ and endemic equilibrium point $E_2 = (\hat{S}, \hat{E}, \hat{I})$, where

$$\hat{S} = \frac{(d+\mu)(d+\gamma)}{\beta\mu}, \qquad \hat{E} = \frac{(d+\gamma)}{\mu}\left(\frac{A\beta\mu - d(d+\gamma)(d+\mu)}{\beta(d+\mu)(d+\gamma)}\right),$$

$$\hat{I} = \frac{A\beta\mu - d(d+\gamma)(d+\mu)}{\beta(d+\mu)(d+\gamma)}.$$

Remark. It is observed that E_2 exist if and only if $A\beta\mu > d(d+\mu)(d+\gamma)$. That is, if $R_0 > 1$, the pathogen is able to invade the susceptible population and disease spreads among the population. However, if $R_0 < 1$, endemic equilibrium point does not exist and infection dies out.

6. Stability Analysis

It is important to discuss the local stability of equilibrium points as practically initial data is not known and we wish to find the impact of small perturbation in the equilibrium points on the system. To study the local stability of system, we find the variational matrix of system. Stability of an equilibrium point is determined by the signs of the real parts of the eigenvalues of the variational matrix.

To determine stability conditions for disease free equilibrium point $E_1(\bar{S}, 0, 0)$, we linearize the system of equations given by (2) about E_1 by substituting $S = s + \bar{S}, E = e + 0$ and $I = i + 0$. After substitution and neglecting non-linear terms we obtain the following set of differential equations linear in s, e and i:

$$\begin{aligned}
\frac{\partial s}{\partial t} &= -\beta i\bar{S} - ds + D_S\frac{\partial^2 s}{\partial x^2},\\
\frac{\partial e}{\partial t} &= \beta i\bar{S} - (d+\mu)e + D_E\frac{\partial^2 e}{\partial x^2},\\
\frac{\partial i}{\partial t} &= \mu e - (d+\gamma)i + D_I\frac{\partial^2 i}{\partial x^2}.
\end{aligned} \tag{3}$$

Let us assume the solution of system (3) as

$$s = \alpha_1 e^{\sigma t} \cos p_1 x, \qquad e = \alpha_2 e^{\sigma t} \cos p_1 x, \qquad i = \alpha_3 e^{\sigma t} \cos p_1 x,$$

where $\alpha_1, \alpha_2, \alpha_3$ and σ are constants, p_1 is another constant known as the wave number of perturbations.

The variational matrix about $E_1(\bar{S}, 0, 0)$ is given by

$$V(E_1) = \begin{bmatrix} -d - D_S\, p_1^2 & 0 & -\beta\bar{S} \\ 0 & -d - \mu - D_E\, p_1^2 & \beta\bar{S} \\ 0 & \mu & -d - \gamma - D_I\, p_1^2 \end{bmatrix}$$

whose two eigenvalues can be obtained from the equation

$$\lambda^2 + \lambda(2d + \mu + \gamma + D_E\, p_1^2 + D_I\, p_1^2) + (d + \mu + D_E\, p_1^2)(d + \gamma + D_I\, p_1^2) - \beta\bar{S}\mu = 0,$$

and the third eigenvalue is $-d - D_S\, p_1^2$.

Clearly, we conclude that E_1 is stable or unstable according as

$$\beta\bar{S}\mu < \text{ or } > (d + \mu + D_E\, p_1^2)(d + \gamma + D_I\, p_1^2).$$

Similarly, to determine stability conditions for endemic equilibrium point $E_2(\hat{S}, \hat{E}, \hat{I})$, we linearize the system of equations given by (2) about E_2 by substituting $S = s + \hat{S}, E = e + \hat{E}$ and $I = i + \hat{I}$. After substitution and neglecting non-linear terms we obtain the following set of differential equations linear in s, e and i:

$$\begin{aligned} \frac{\partial s}{\partial t} &= -\beta i\hat{S} - \beta s\hat{I} - ds - D_S \frac{\partial^2 s}{\partial x^2} \\ \frac{\partial e}{\partial t} &= \beta i\hat{S} + \beta s\hat{I} - (d + \mu)e - D_E \frac{\partial^2 e}{\partial x^2}, \\ \frac{\partial i}{\partial t} &= \mu e - (d + \gamma)i - D_I \frac{\partial^2 i}{\partial x^2}. \end{aligned} \tag{4}$$

The variational matrix about $E_2(\hat{S}, \hat{E}, \hat{I})$ is given by

$$V(E_2) = \begin{bmatrix} -\beta\hat{I} - d - D_S\, p_1^2 & 0 & -\beta\hat{S} \\ \beta\hat{I} & -d - \mu - D_E\, p_1^2 & \beta\hat{S} \\ 0 & \mu & -d - \gamma - D_I\, p_1^2 \end{bmatrix}.$$

Eigenvalues corresponding to above variational matrix can be obtained from

$$\lambda^3 + A_1\lambda^2 + A_2\lambda + A_3 = 0$$

where

$$A_1 = 3d + \mu + \gamma + \beta\hat{I} + (D_E + D_I + D_S)p_1^2,$$

$$A_2 = (2d + \mu + \gamma + 2D_E\, p_1^2)(\beta\hat{I} + d + D_S\, p_1^2) + \{(d + \mu + D_E\, p_1^2)(d + \gamma + D_I\, p_1^2) - \beta\hat{S}\mu\},$$

$$A_3 = (\beta\hat{I} + d + D_S\, p_1^2)\{(d + \mu + D_E\, p_1^2)(d + \alpha + D_I\, p_1^2) - \beta\hat{S}\mu\} + \beta^2\hat{S}\hat{I}\mu.$$

By Routh-Hurwitz criteria, we conclude that the eigen values of $V(E_2)$ are negative and hence endemic equilibrium point E_2 is asymptotically stable if $A_1 > 0$, $A_3 > 0$ and $A_1A_2 - A_3 > 0$.

7. Results and Discussion

We have studied the effect of diffusion on the SEIR model by considering the migration of population in each compartment. The system is analyzed for its equilibria and their stability. System has two equilibrium points. Basic reproduction number of the model is computed using next generation matrix method. Conditions of local asymptotic stability of disease free and endemic equilibrium points are computed and it is observed that the diffusion term has an important role in defining the stability conditions of the system.

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