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# An SEIRS Epidemic Model with Immigration and Vertical Transmission

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***Authors' contributions***

*This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.*

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## Abstract

The study indicates that we should improve the model by introducing the immigration rate in the model to control the spread of disease. An SEIRS epidemic model with Immigration and Vertical Transmission and analyzed the steady state and stability of the equilibrium points. The model equations were solved analytically. The stability of the both equilibrium are proved by Routh-Hurwitz criteria. We see that if the basic reproductive number $R_0 < 1$ then the disease free equilibrium is locally asymptotically stable and if $R_0 > 1$ the endemic equilibrium will be locally asymptotically stable.

*Keywords: Mathematical modeling; immigration rate; vertical transmission; stability analysis; routh-hurwitz criteria.*

## 1 Intoduction

Mathematical modeling is an important tool to understand and predict the spread of infectious diseases. In this process, rate of incidence plays a crucial role. Many infectious diseases in nature transmit through both horizontal and vertical modes. For many human diseases such as Hepatitis B, and AIDS, the infected hosts stay in a latent period before becoming infectious [1,2,3].

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Epidemiology is basically a population biology discipline concerned with public health and it is heavily influenced by mathematical theory. Study of infectious disease by the means of mathematical modelling provides the behaviour of the diseases. Mathematical models can design how infectious diseases progress to show the likely outcome of an epidemic and help inform public health issues. Most commonly used effective methods to control the spread of disease are vaccination, treatment. The fighting with infectious diseases has a long history and great progresses had been achieved, especially during the twenty century. First epidemiological model was formulated by Daniel Bernoulli in 1760 for smallpox. More complex mathematical studies of deterministic and compartmental epidemic models were undertaken by Kermack and Mckendrick. In 1927 Kermack and Mckendrick formulated a well known and well recognized deterministic compartment model, to study the outbreak of Black Death in London (1665-1666), and outbreak of plague in Mumbai (1906). This model was successful in predicting behavior of outbreaks very similar to that observed in recorded epidemics.

Several epidemic models with varying population size are analyzed mathematically by Busenberg, Van den Driesscha, Busenberg and Hadeler [4,5,6]. A number of models have been developed in response to various different infectious disease [7].

Hethcote, H.W. [8] showed that solution always approach equilibrium points for an ordinary differential equation SIR model thus periodic solution were ruled out. Different types of epidemic models have been studied and analyzed by various epidemiologists Trottier [9] proposed a verity of deterministic model of infection diseases. In this paper, we have use some terminology mentioned in the paper of Bava et al. [10], Michael et al. [11], and Sen et al. [12].

In this paper, we explore the result of Payal Joshi et al. [13] and consider an SEIRS model by allowing recovered hosts to return to the susceptible class (S) with Immigration rate. We analyzed and discussed about the stability for the system of differential equations by Routh- Hurwitz criterion and found that the model is locally asymptotically stable.

# 2 Mathematical Model

The total population is divided into four parts as susceptible, exposed (in the latent period), infectious, and recovered, with the densities respectively denoted by S(t), E(t), I(t), and R(t). The natural birth and death rates are assumed to be identical and denoted by ‘b’. It is also assumed that the total population density is constant; S(t)+ E(t)+ I(t)+ R(t)= 1.

The following is a summary of the notation used:

N= Total population
S=Susceptible
E= Exposed individuals in the latent period
I=Infective
R= Removed with immunity
$\delta$ = Immigration rate
$\lambda$=Contact or infection rate
B= Natural birth rate which identical to death rate
p= Fraction of infected newborns from the exposed class
q=Fraction of infected newborns from the infectious class
$\varepsilon$= Rate at which the exposed individuals become infected
$\gamma$= Rate at which the recovered individuals lose immunity and return to the susceptible class
$R_0$ = Basic reproduction number
The model can be described by following system of equations:

$$\frac{dS}{dt} = b - \lambda IS - pbE - qbI - bS + \gamma R + \delta$$

$$\frac{\mathrm{dE}}{\mathrm{dt}} = \lambda \mathrm{IS} + \mathrm{pbE} + \mathrm{qbI} - (\varepsilon + \mathrm{b})\mathrm{E}$$

$$\frac{dI}{dt} = \varepsilon E - (\gamma + b)I \qquad (2.1)$$

$$\frac{dR}{dt} = \gamma I - bR - \gamma R$$

# 3 Stability Analysis

From the system of equations (2.1) setting the time derivative of S, E, I, R equals to zero, then

b - λIS – pbE – qbI – bS + γR+ δ = 0

λIS + pbE + qbI – (ε + b) E = 0

εE – (γ + b) I = 0

γI – bR - γR = 0

After solving we get two equilibrium points $E_0$ ($\frac{b+\delta}{b}$, 0, 0, 0) which is the disease free equilibrium points of the system and a unique endemic equilibrium points of the system is $E^* = (S^*, E^*, I^*, R^*)$, where

$$S^* = \frac{(\gamma + b)}{\lambda\varepsilon}\left[\varepsilon + b - pb - \frac{qb\varepsilon}{\varepsilon + b}\right]$$

$$E^* = \frac{(\gamma + b)^2\left((b + \delta)\lambda\varepsilon - b(\gamma + b)(\varepsilon + b - pb) + \varepsilon q b^2\right)}{\lambda\varepsilon\{(\varepsilon + b)(\gamma + b)^2 - \gamma^2\epsilon\}}$$

$$I^* = \frac{(\gamma + b)((b + \delta)\lambda\varepsilon - b(\gamma + b)(\varepsilon + b - pb) + \varepsilon q b^2)}{\lambda\{(\varepsilon + b)(\varepsilon + b)^2 - \gamma^2\epsilon\}}$$

$$R^* = \frac{\gamma\varepsilon E}{(\gamma + b)^2}$$

and $R_0 = \frac{b(\gamma+b)(\varepsilon+b)}{(b+\delta)\lambda\varepsilon}$ is the reproduction number.

# 4 Mathematical Analysis

## 4.1 Theorem

If $R_0 < 1$, the disease free equilibrium $E_0$ of system (2.1) is locally asymptotically stable and is unstable at $R_0 > 1$.

**Proof:** The Jacobian Matrix of the system (2.1) is

$$J = \begin{bmatrix} -b-\lambda I & -pb & -\lambda S - qb & \gamma \\ \lambda I & pb-(\varepsilon+b) & \lambda S + qb & 0 \\ 0 & \varepsilon & -(\gamma+b) & 0 \\ 0 & 0 & \gamma & -b-\gamma \end{bmatrix}$$

At the equilibrium point $E_0$ ( $\frac{b+\delta}{b}$ , 0, 0, 0), its characteristic equation is

$$\begin{vmatrix} -b-\Psi & -pb & -\frac{\lambda(b+\delta)}{b} - qb & \gamma \\ 0 & pb-(\varepsilon+b)-\Psi & \frac{\lambda(b+\delta)}{b} + qb & 0 \\ 0 & \varepsilon & -(\gamma+b)-\Psi & 0 \\ 0 & 0 & \gamma & -b-\gamma-\Psi \end{vmatrix} = 0$$

From four eigen values two is $\Psi_1 = -\mathrm{b}, \Psi_2 = -(\mathrm{b}+\gamma)$ and other two eigen values is obtained from the equation

$\Psi^2 + A_1\Psi + A_0 = 0$

where,

$A_1 = (\gamma + b) - pb + (\varepsilon + b)$

$A_0 = -\varepsilon(\frac{\lambda(b+\delta)}{b} + qb) - (\gamma + b)\, pb + (\gamma + b)\,(\varepsilon + b)$

it follows that

$$\Longrightarrow \frac{b(\gamma+b)(\varepsilon+b)}{(b+\delta)\lambda\varepsilon} < 1$$

$\Longrightarrow R_0 < 1.$

Thus, $A_0 > 0$ and $A_1 > 0$.

Therefore, all the Eigen values of the characteristic equation (2.3.1) are negative real parts. Hence the equilibrium $E_0$ is locally asymptotically stable.

## 4.2 Theorem

The endemic equilibrium E* of the system (2.1) is locally asymptotically stable.

Proof: The characterstics equation of the jacobian matrix

$$\Psi^4 + a_3\Psi^3 + a_2\Psi^2 + a_1\Psi + a_0 = 0$$

where,

$a_3 = \lambda I^* - pb + \varepsilon + 4b + 2\gamma$

$a_2 = (\gamma + b)^2 + 2(\gamma + b)(2b + \lambda I^* - pb + \varepsilon) - pb^2 + (\varepsilon + b)(b + \lambda I^*) - \varepsilon(\lambda S^* + qb)$

$a_1 = (\gamma + b)^2(2b + \lambda I^* - pb + \varepsilon) - 2(\gamma + b)(b + \lambda I^*).\big(pb - (\varepsilon + b)\big) - \varepsilon\gamma(\lambda S^* + qb)$

$a_0 = \varepsilon\gamma(\gamma + b)(\lambda S^* + qb) - (\gamma + b)^2\{\lambda I^* pb + (b + \lambda I^*).(pb - (\varepsilon + b))\}$

By Routh-Hurwitz Criterion, the system is locally stable if

$a_1 > 0$, $a_3 > 0$, $a_4 > 0$ and $a_1 a_2 a_3 > a_3^2 + a_1^2 a_4$.

Thus, E* is locally asymptotically stable.

# 5 Conclusions

One important goal of mathematical epidemiology is to understand how to control or exterminate diseases. Mathematical models are used extensively in the study of epidemiological and ecological phenomena. We all know that one of the main issues in the study of behavior of epidemics is the analysis of steady states of the model and their stability. If trivial or zero equilibrium is asymptotically stable, then, disease does not persist, whatever the initial number of infectives in population. In this paper we have carried out a compartment model with Immigration and Vertical Transmission and analyzed the steady state and stability of the equilibrium points.and observe that the basic reproduction number $R_0$ plays an important role to control the disease. It has been noted that when $R_0 < 1$ , the model has locally asymptotically stable and when $R_0 > 1$ disease is endemic.

# Competing Interests

Authors have declared that no competing interests exist.

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