Global Journal of Pure and Applied Mathematics.
ISSN 0973-1768 Volume 21, Number 2 (2025), pp. 299-308

http://www.ripublication.com/gjpam.htm

Global Dynamics of SEIRS Epidemic Model with Immigration and Vertical Transmission

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Abstract

In this paper we improve our SEIRS epidemic model with immigration and vertical transmission for an infectious disease that spread in the host population vertically. The total population assumed to have constant density with bilinear mass –action incidence. Local and Global stability are determined by Basic Reproduction number R0 (p,q), where p and q are fraction of infected newborn from the exposed and infected classes respectively. If the $R0(p,q) \leq 1$, then disease free equilibrium is globally stable and disease always dies out . If $R0(p,q) > 1$, then endemic equilibrium exist and is globally stable in the interior of the feasible region and disease persists at endemic equilibrium state, if it initially exists. Numerical simulation of the model is investigated.
Keywords: SEIRS Epidemic Model, Vertical Transmission, Global stability, endemic equilibrium ,Dulac –Plus Poincare bendoxin theorem.

Introduction

Mathematical modeling plays an important role to spread and control of an infectious disease. First epidemiology model was formulated by Daniel Bernouli in 1760 for smallpox. In 1927 kermack and mckendrick[7] formulated, well know and well recognized deterministic compartment model(SIR). Mathematical model can design how infectious disease progress to show the likely outcome of an epidemic and help inform public health issue. Infectious diseases are caused by organism. Such as bacteria, virus, protozoa and fungi . Which enter infect a host organism. In infectious disease incidence rate play an important role. These infection organism passed through one individual host to another host individuals in this way spreading the infection throughout the host population. A number of models have been developed in represent to various different infectious diseases [10]. Busenberg, van den Driesscha, Busenberg and Hadeler are analyzed[1,2,3] serval epidemic model with varying population size . Many infectious diseases in nature transmit through both horizontal

and vertical model. Horizontal Transmission occurs through direct or indirect physical contact with infectious hosts , or may be through disease vector. Vertical transmission is the direct transmission of a disease from an infective parent to an newly born or unborn offspring . These include such as rubella, herpes simplex, hepatitis B, hepatitis C, Chagas disease, zika virus and AIDS. Babies born of pregnant women who are infected with a particular virus are at risk of contracting that virus from the parents. Busenberg and cook[4] discussed a variety of disease transmission of both vertically and horizontally, and gave comprehensive survey of the mathematical analysis of compartmental model that also incorporate vertical transmission. In [4] a standard SIR compartment model with vertical transmission describe by assuming a fraction q of the offspring from the infectious (I) class are infectious at birth, and hence a birth flux qbI, enter the I class, and the remaining birth, (b-qbI), enters the susceptible (S) class. In this SIR model assuming that there is no latent period, then infected host instantaneously become infectious. But some human infectious disease hepatitis B, AIDS and Chagas ,the infected hosts stay in a latent period before becoming infectious[9]. In SEIRS model with vertical transmission it is possible to assume that a fraction of p offspring of infected hosts (both E and I) are infected at birth , and adult infected hosts, will stay in latent period before becoming infectious and birth flux enter in E class[11].

In this paper we assumed an SEIRS model with immigration and vertical transmission. We divided total host population into four compartment susceptible individuals S(t),exposed individuals E(t), infectious individuals I(t), and recovered individual R(t). We assume that recovered individual loss their immunity and again go to the susceptible class. The birth and death rate are identical and it is denoted by b and we are assume that immigration in susceptible class and it denoted by δ .

The incidence is taken λIS which is a bilinear mass incidence represent horizontal transmission to take the form direct contact between infectious and susceptible host. For the vertical transmission that a fraction p and a fraction q of the offspring from exposed and infectious classes respectively are both in E class. In some vertical transmitted infectious disease their no permanent recovery like Chagas disease, Herpes simplex so our model is more appropriate to this type of infectious disease.

Mathematical Model Formulation

We divided total population into four compartment model susceptible, exposed (in the latent period), infectious and recovered with the density respectively denoted by S(t), E(t), I(t) and R(t). The natural birth and death rate are assumed to be identical and denoted by b.

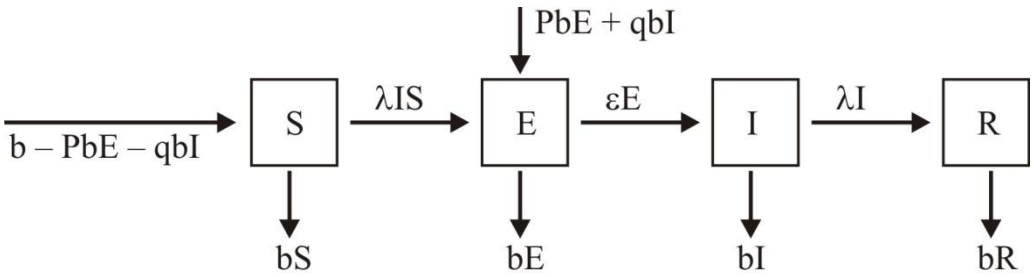

Figure-1: Transmission of disease

Table-1: Parameter with Description

Symbol	**Description**
N	Total population
S	Immigration rate
λ	Contact rate or Infection rate
b	Natural birth rate which identical to death rate
P	Fraction of infected new born from the exposed class
q	Fraction of infected new born from the infectious class
ϵ	Rate at which the exposed individuals become infected
γ	Rate at which the infected Individuals is recovered
α	Rate at which the recovered individuals lose immunity and return to the susceptible class
Ro (p,q)	Basic Reproduction

The proposed model can be described by system to differential equations.

$$\begin{aligned} S' &= b - \lambda IS - pbE - qbI - bs + \alpha R \\ E' &= \lambda IS + PbE + qbI - (\varepsilon + b)E \\ I' &= \varepsilon E - (\gamma + b)I \\ R' &= \gamma I - bR \end{aligned} \tag{2.1}$$

The incidence rate λIS is of the bilinear mass-action Incidence. The horizontal transmission is assumed to take the form the direct contact between infectious and susceptible hosts. The vertical transmission, we assume a fraction P from exposed

class and a fraction q from infectious class, are born into the exposed class. The birth flux into the susceptible class is given by $b - pbE - qbI$ where,

$$0 \leq p \leq 1 \ \& \ 0 \leq q \leq 1$$

2.1positivety: solution of the model (2.1) together with initial conditions.

$$S(0) > 0, E(0) \geq 0, I(0) \geq 0, R(0) \geq 0$$

are always a positive that is the model $S(t), E(t), I(t) \ \& \ R(t)$ are positive for all t.

For system (1) feasible region

N = S + E + I + R

$$N'(t) = (b + \delta) - bN$$

Which exhibits N(t) is moving towards $\frac{b+\delta}{b}$ as the time becomes infinitely large

$$\Omega = \left\{(S,E,I,R) \in R_{+}^{4} : S + E + I + R = \frac{b+\delta}{b}\right\} \quad ...(2.2)$$

Lemma 2.1:

The set $\Omega = (S,E,I,R) \in R_{+}^{4}: 0 \leq S,E,I,S,\ S + E + I + R \leq \frac{b+\delta}{b}\}$ is Positively invariant region for the proposed model .

Basic Reproduction Number

Basic reproduction number is defined as the number of newly infective individuals caused by a single infective Individuals and it is denoted by $R_0(p, q)$ with help of Next generation matrix [5], we calculate basic reproduction number of the system (2.1).

For the system (2.1) always a disease free-equilibrium $P_0(S_0, 0, 0, 0)$.

Where $S_0 = \frac{b+\delta}{b}$, let $X = [E,I]^T$

Then $$\frac{dx}{dt} = F(x) - V(x)$$

$$F(x) = [\lambda SI, \ \ 0]^T, V(x) = [-pbE - qbI + (\varepsilon + b)E, \ \ -\varepsilon E + (\gamma + b)I]^T$$

Jacobian matrix of F(x) and V(x) at disease -free equilibrium point P_0 are respectively.

$$f(x)_{p_0} = \begin{bmatrix} 0 & \frac{\lambda(b+\delta)}{b} \\ 0 & 0 \end{bmatrix}, V(x)_{P_0} = \begin{bmatrix} -pb + (\varepsilon + b) & -qb \\ -\varepsilon & (\gamma + b) \end{bmatrix}$$

Then basic reproduction number is the spectral radius of the $\rho(fv^{-1})$.

Then ,

$$R_0(p,q) = \rho(fv^{-1}) = \frac{\lambda\varepsilon(b+\delta)}{b[(\varepsilon+b)(\gamma+b) - pb(\gamma+b) - qb\varepsilon]}$$

.....(2.3)

Equilibria of The System

To analysis the equilibrium of the system (2.1) setting the time derivatives of S,E,I,R. equal to zero, then

$$b - \lambda IS - pbE - qbI - bS + \alpha R + S = 0$$

$$\lambda IS + pbE + qbI - (\varepsilon + b)E = 0$$
$$\varepsilon E - (y + b)I = 0$$
$$yI - (b + \alpha)R = 0$$

After solving we get two equilibrium points one is disease free equilibrium $p_0\left(\frac{b+\delta}{b}, 0,0,0\right)$, and another is a unique endemic equilibrium points of the system (2.1) is $P_* = (S^*, E^*, I^*, R^*)$,

Where,

$$S^* = \frac{(\varepsilon + b)(y + b) - Pb(y + b) - qb\varepsilon}{\lambda\varepsilon}$$
$$E^* = \frac{y + b}{\varepsilon} I^*$$
$$R^* = \frac{y}{b + \alpha} I^* \qquad \text{.....(3.1)}$$
$$I^* = (R_0(p,q) - 1)\frac{(b+\alpha)b[(\varepsilon+b-pb)(y+b)-qb\varepsilon]}{\lambda((\varepsilon+b)(y+b)(b+\alpha)-\alpha y\varepsilon)}$$

It is easy to verify that $R_0(p,q) > 0$ for $0 \le p, q \le 1$

That P^* exists in Ω and is unique if and only if $R_0(p,q) > 1$.

Local Stability

To show the local stability of system (2.1) at disease free equilibrium point P_0. Let the Jacobian matrix of system (2.1) is

$$J(P_0) = \begin{bmatrix} -b-\psi & -pb & -\frac{\lambda(b+s)}{b} - qb & \alpha \\ 0 & Pb - (\varepsilon + b) - \psi & \frac{\lambda(b+s)}{b} + qb & 0 \\ 0 & \varepsilon & -(y + b) - \psi & 0 \\ 0 & 0 & y & -(b + \alpha) + \psi \end{bmatrix} = 0$$

From four Eigen value two are $\psi = -b$, $\psi = -(b + \alpha)$ and two Eigen values is obtained from the equation

$$\psi^2 + A_1\psi + A_0 = 0$$
$$A_1 = 2b + y + \varepsilon - pb > 0$$
$$A_0 = (y + b)(\varepsilon + b - pb) - \frac{\varepsilon\lambda(b + \delta)}{b} + \varepsilon qb^2$$
$$A_0 = 1 - R_0$$

Here if $R_0 < 1$ then all the three Eigen roots of the characteristics equation will have negative real part and if $R_0 > 1$, then two of its Eigen value are with negative real part and one with positive real part. This exhibits the following theorem:

***Theorem 3.1*:** The Disease – free-equilibrium is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.

To show the local stability of the system (2.1) at Endemic equilibrium at P_* .

Let the Jacobean matrix of system (2.1) is:

$$J(P_*) = \begin{bmatrix} -b-\lambda I^*-\psi & -pb & -\lambda S^*-qb & \alpha \\ \lambda I^* & Pb-(\varepsilon+b)-\psi & \lambda S^*+qb & 0 \\ 0 & \varepsilon & -(\gamma+b)-\psi & 0 \\ 0 & 0 & \gamma & -(b+\alpha)-\psi \end{bmatrix}$$

and the characteristics equation of the Jacobian matrix is

$$\psi^4 + A_3\psi^3 + A_2\psi^2 + A_1\psi + A_0 = 0 \qquad .....(3.1.2)$$

where,

$$A_3 = 4b + \gamma + \alpha + \varepsilon - pb + \lambda I^*$$

$$A_2 = (b+\alpha)(b+\lambda I^*) + (2b+\alpha+\lambda I^*)(2b+\varepsilon+\gamma+pb) + (\varepsilon+b-pb)(\gamma+b) - \varepsilon(\lambda S^* + qb) + \lambda PbI^*$$

$$A_1 = (b+\alpha)(b+\lambda I^*)(2b+\varepsilon+\gamma+pb) + (2b+\alpha+\lambda I^*)(\varepsilon+b-pb)(\gamma+b) + \lambda PbI^*(2b+\alpha+\gamma) - \varepsilon(\lambda S^*+qb)(2b+\alpha)$$

$$A_0 = (b+\alpha)(\gamma+\alpha)[(b+\lambda I^*)(\varepsilon+b) - Pb^2] - \gamma\varepsilon\alpha\lambda I^* - \varepsilon(\lambda S + qb)(b+\alpha)(b+\lambda I^*) + \lambda I^*\varepsilon(b+\alpha)(\lambda S^*+qb)$$

$$= (b+\alpha)(\gamma+\alpha)[(b+\lambda I^*)(\varepsilon+b) - Pb^2] - \gamma\varepsilon\alpha + dI^* - b(b+\alpha)(\lambda S^*+qb)\varepsilon - \gamma\varepsilon\alpha\lambda I^*$$

By Routh Hurwitz criterion, the system (2.1) is locally stable if $A_1 > 0, A_3 > 0, A_2 > 0$ and $A_3 \cdot A_2 \cdot A_1 > A_1^2 + A_3^2 \cdot A_0$. Thus $P*$ is locally asymptotically stable. This exbiti following theorem

Theorem 3.1.2: The endemic equilibrium P^* is locally asymptotically stable at $R_0 > 1$.

3.2 Global Stability

To analyze the global stability of the disease free equilibrium at P_0.

We construct a Lyapunov function [12].

$$L = \varepsilon E + (\varepsilon + b - Pb)$$

$$\Rightarrow L' = \varepsilon E' + (\varepsilon + b - Pb)I'$$

$$= \varepsilon[\lambda IS + PbE + qbI - (\varepsilon+b)E] + (\varepsilon+b-Pb)(\varepsilon E - (\gamma+b)I)$$

$$= \lambda\varepsilon IS - b\left[(b+\gamma)(b+\varepsilon-Pb) - qb\varepsilon\right]I$$

$$= b[(b+\gamma)(b+\varepsilon-Pb) - qb\varepsilon][R_0(P,q)S - 1]I \qquad .....(3.2.1)$$

$L' = 0$ if and only if I = 0 or $R_0(p,q) = 1$ and S = 1, then the largest compact Invariance set in $\{(s,E,I,R) \in \pi : L' = 0\}$ is the singleton $\{P_0\}$. If $L' < 0$ if

$R_0(p,q)<1$then $P_0$is largest Invariant set in (S, E, I, R) $\in \Omega$. So by Lypunov-Lasalle invariance principle [8]. The disease. Free equilibrium P_0 is Globally Asymptotically stable. Then following theorem exhibit.

Theorem 3.2.1: If $R_0 < 1$, the P_0 is Globally Asymptotically stable.
Now, for global stability at endemic equilibrium we use Dulac plus poincare Bendixson theorem [8] as.

$H(S,E,I,R) = \frac{1}{S,E,I,R}$,where, S > 0, E > 0, I > 0, R >0

$$\psi_1 = b - \lambda IS - PbE - qbI - bs + \alpha R + \delta$$
$$\psi_2 = \lambda IS + PbE + qbI - (\varepsilon + b)E$$
$$\psi_3 = \varepsilon E - (\gamma + b)I$$
$$\psi_4 = \gamma I - bR - \alpha R$$

$$\nabla(H.F) = \frac{1}{S,E,I,R}\left\{\frac{\partial(H.\psi_1)}{\partial S} + \frac{\partial(H.\psi_2)}{\partial E} + \frac{\partial(H.\psi_3)}{\partial I} + \frac{\partial(H.\psi_4)}{\partial R}\right\}$$

$$= \frac{-b}{S^2EIR} + \frac{Pb}{S^2IR} + \frac{qb}{S^2ER} - \frac{\alpha}{S^2EI} - \frac{\delta}{S^2EIR}$$
$$\frac{-\lambda}{E^2R} - \frac{qb}{SE^2R} - \frac{\varepsilon}{SI^2R} - \frac{\gamma}{SEIR^2}$$

....(3.2.2)

$$\nabla(H_1F) < 0$$

Hence by Dulac criterion, there is no closed orbit in the first quadrant. Then the endemic equilibrium is Globally asymptotically stable.

Theorem 3.2.2: If $R_0 > 1$, then P_* is Globally Asymptotically stable.

Basic Reproduction Number

To get better understanding of the Basic reproduction number $R_0(p,q)$ in (2.3). We write in Taylors Expansion as.

$$R_0(p,q) = R_0(1 + R + R^2 + ...),$$

....(4.1)

where $$R_0 = \frac{\lambda\varepsilon(b+\delta)}{b(b+\gamma)(b+\varepsilon)}$$ ....(4.2)

and $$R = R_p + R_q = \frac{Pb}{\varepsilon + b} + \frac{qb\varepsilon}{(\varepsilon + b)(\gamma + b)}$$

The R_0 in (4.2) is the basic reproduction number for the horizontal transmission it mean that number of secondary infectious contributed through horizontal infection by a single infectious host during the infective period in an entirely susceptible population [10].

Now rewrite as $$R_o.R_p = \frac{\lambda}{b}\cdot\frac{(b+\delta)}{b+\gamma}\cdot\frac{Pb}{\varepsilon+b}\cdot\frac{\varepsilon}{b+\varepsilon}$$

This describes as the mean infectious period $\frac{b+\delta}{b+\gamma}$, a single infective produces. $\frac{\lambda}{b}.\frac{b+\delta}{b+\gamma}$ latent hosts through direct contact. Each new latent host give $\frac{bp}{b+\varepsilon}$ latent offspring during the mean latent period. And a fraction $\frac{\varepsilon}{b+\varepsilon}$ it survives latency and becomes infectious.

Similarly ,we also rewrite R_0R_q as

$$R_0R_q = \frac{\lambda}{b}.\frac{b+\delta}{b+\gamma}.\frac{\varepsilon}{(b+\varepsilon)}.\frac{bq}{b+\gamma}.\frac{\varepsilon}{b+\varepsilon}$$

Which mean infectious period, a single infective produces $\frac{\lambda(b+\delta)}{b(b+\gamma)}$ latent hosts through direct contact. Each of these new infectious hosts gives $\frac{bq}{b+\gamma}$ latent offspring during the mean infectious period. Then $R_0\cdot R = R_0(R_p+R_q)$ represent the total contribution to the infective class made by the first generation offspring of our original infective. Similarly, R_0R^2 and the higher order term in (4.1) represent the contribution through vertical transmission in second generation.

Numerical simulation

We find the numerical solution of proposed model (2.1) by choosing the initial condition of population susceptible individuals S = 20, Exposed individuals E=10, Infectious individuals I=10, Recover individuals R=10. The parameter and their value for R_0 are λ = 1.3, b=.2, p=.75,q=.25, α=.05, δ= .09, ε=.9, γ=.4 and R_0= 0.8907. Figure 2 show the behaviour of distinct classes for $R_0 < 1$.

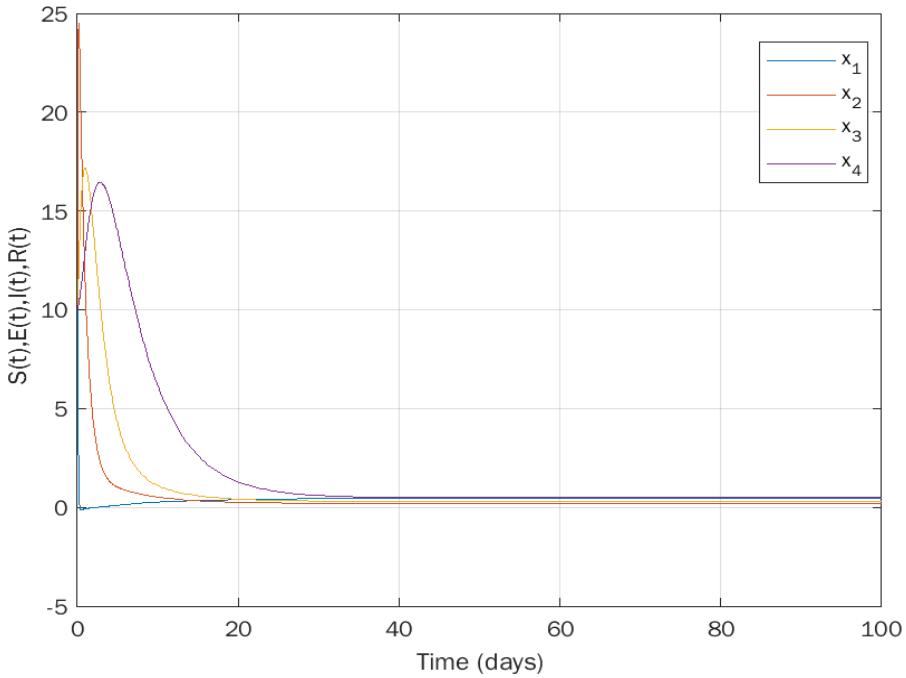

Figure 2: Represent that the disease will dies out with time

The parameter and their value for R_0 are λ = 1.3, b=.2, p=.75,q=.25, α=.05, δ= .9, ε=.9, γ=.4 and
R_0= 3.3784. Figure 3 show the behaviour of distinct classes for $R_0 > 1$.

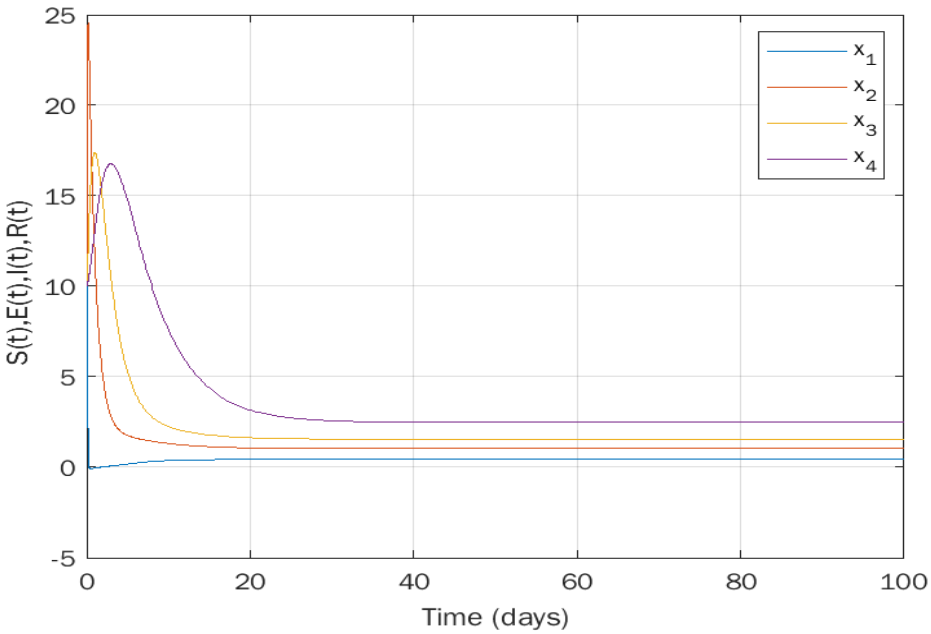

Figure 3: Represent that disease will persist in system for long time

Conclusion

We presented an SEIRS epidemic model for dynamics of vertically transmitted infectious disease with immigration. Bilinear incidence is assumed it show horizontal transmission between susceptible and infectious host. A vertical transmission is a fraction p of the newborn from exposed class and a fraction q of the newborns from infectious class are assumed to be infected at birth. The natural birth and death rate are identical and assuming that immunity is not permanent recover host loss their immunity and go to susceptible class.

A threshold parameter $R_0(p,q)$ is identified which completely determines the local and global dynamics of our SEIRS model. If $R_0(p,q) \leq 1$ then our model is globally stable in feasible region and disease will dies out .If $R_0(p,q) > 1$ there is a unique endemic equilibrium is globally stable in feasible region and disease persists at a constant endemic level if it initially present. More understanding about R_0 and $R_0(p,q)$ is analyze.

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