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Basic Reproductive Number of an Seivr Epidemic Model among Infants in a Vaccinated and Temporary Immune Protected Population

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ABSTRACT

In this article, we proposed an SEIVR mathematical model of the transmission dynamics of infectious diseases among infants taking into consideration passive immunization, treatment of the exposed infants at latent period and the infectious diseases treatment. The basic reproductive number of the mathematical model was obtained using the next generation matrix method. It is generally known that if the number is less than one, the infectious disease will die out with time and if it is greater than one, the disease will spread and become endemic in the community. The epidemiological interpretation of this threshold parameter (basic reproductive number) is connected to the local and global stability of a disease – free equilibrium.

Introduction

A disease is infectious if the causative agents whether a virus, bacterium, protozoan or toxin can be passed from one person (host) to another through modes of transmission such as direct physical contacts, aerial droplets, water or food, disease vectors, mother to newborns and so on. Disease infection begins with the transmission of the pathogen from the host to another [7]. After the pathogens invade the host body, they need to be able to evade or overcome the host immune response and be able to multiply or replicate. When the pathogens accumulate sufficiently large numbers and when they have reached the targeted organs, they begin to cause sufficient damage to the host body so that the host becomes symptomatic and the host is capable to transmit the pathogens to other host members of the community. The period from time of infection to time of showing symptoms is called the incubation period. The period from time of infection to time of being infectious is called the latent period. During the latent period, a host may or may not show symptoms but the host is not capable of transmitting pathogens to other hosts. When an infected host recovers from an infection, it usually maintains certain degree of immunity against reinfection from the same stain of pathogens. Dan and Zhongyi (2011) established and analyzed a deterministic mathematical model in their paper [1]. However, the integration of the recovered infants to the population was not incorporated into the mathematical model they established. In this paper, it is intended that the recovered infants class is incorporated into the mathematical model and the expression for the basic reproductive number of the mathematical model is obtained using the next generation matrix method. A quantity of central importance in epidemiology is the basic reproduction number, traditionally denoted as R_0 [3]. From time to time, people also call it the basic reproductive rate or ratio or the basic reproduction ration. For microparasitic infections, R_0 is defined as the mean number of secondary infections produced when one infected individual is introduced into a host population where everyone is susceptible. For most epidemiological models, an infection invades a fully susceptible host population if $R_0 > 1$ and dies out if $R_0 < 1$. If $R_0 > 1$ ($R_0 < 1$), then on average, each infectious infant produces more (less) than one new infection. Thus, the basic reproduction number R0 is a threshold quantity that determines when an infection invades a host population and when it does not [8].

Model Description

The SEIVR mathematical model is partitioned into compartments of susceptible infants class (S), the exposed infants class (E), the infected infants class (I), the vaccinated infant class (V) and the temporary recovered infants class (R). The immunized compartment changes due to the coming in of the immunized infants into the population where we assume that a proportion of Λ of the incoming infants are immunized against the infectious diseases. This compartment reduces due to the expiration of duration of vaccine efficacy at the rate ω and also by natural death at the rate of μ. The susceptible population increases due to the coming in of the infants from the immunized compartment as a result of the expiration of the duration of vaccine efficacy at the rate ω. The susceptible population also reduces due to the natural death rate μ and infection with contact rate of infection β. The population dynamics of the exposed infants class at the latent period grows with the incidence rate of $\beta SI(1+\alpha I)$. This class reduces by natural death rate μ and occasional breakdown of the exposed infants at the latent period into infectious class at the rate of σ. Also, the population dynamics of the infectious class grows with the past information of the infected given by α while this class reduces by the natural death rate μ and successful cure of the infectious diseases at the rate of τ by given the infected immunization.

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The vaccinated class denoted by V but because the efficacy of the vaccine is not one hundred percent such that it can wane at the rate of ω but the temporary recovered class increases with temporary immunity at the rate of δ which are transferred back to the susceptible class and decreases by natural death rate μ [5]. The schematic description of the model is shown in the Fig. 1 below.

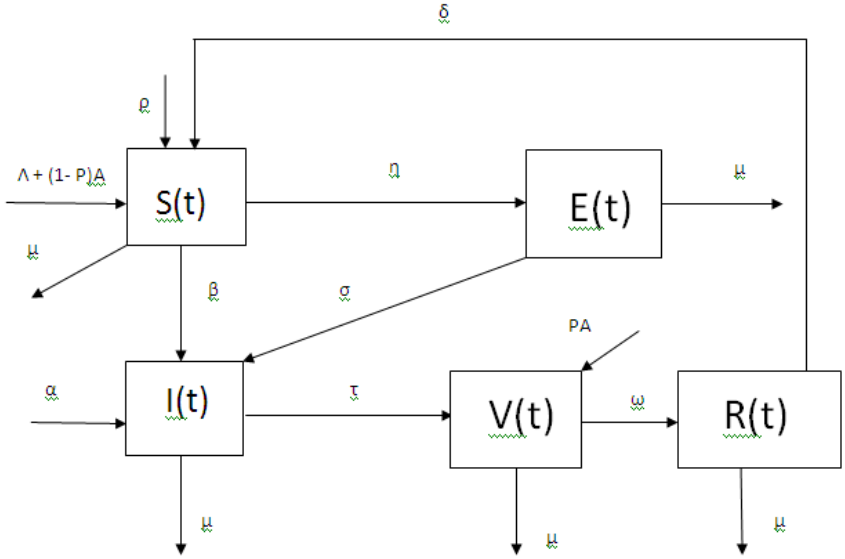

Figure 1. Diagrammatic representation of an SEIVR mathematical model

Mathematical Model

Keeping in view of above description, our population dynamics susceptible – exposed infants at latent period – infected – vaccinated – recovered is governed by the following set of ordinary differential equations given below. The SEIVR model is expressed as the system of nonlinear initial value problem given in the form;

$$\frac{dS}{dt} = \Lambda + (1-P)A + \rho\mu I + \delta R - \beta SI(1+\alpha I) - (\mu+\eta)S \quad (1)$$

$$\frac{dE}{dt} = \beta SI(1+\alpha I) + \eta S - (\mu+\sigma)E \quad (2)$$

$$\frac{dI}{dt} = \sigma E - \rho\mu I - (\mu+\tau)I \quad (3)$$

$$\frac{dV}{dt} = PA + \tau I - (\mu+\omega)V \quad (4)$$

$$\frac{dR}{dt} = \omega V - (\mu+\delta)R \quad (5)$$

in which S = S(t), E = E(t), I = I(t), V = V(t) and R = R(t) represent the population of susceptible infant class, the exposed infant class but not yet infected, the infected infant class, the vaccinated infant class and the temporary immune recovered infant class respectively with time t. the parameters in the mathematical model are positive and the Table 1 below provides the definitions for the model parameters. The model assumes a varying population of N(t) so that N(t) = S(t) + E(t) + I(t) + V(t) + R(t) and it is given in the form $N(t) = K + Ce^{-\mu t}$ for $K = \Lambda + A/\mu$.

Table 1. The interpretation of the parameters and variables used.

Parameters	Definitions
Λ	Birth rate of the infants into the susceptible class
a	Fraction of infants with the infectious diseases
A	Number of infants with the infectious diseases
P	Fraction of the recruited infants who are vaccinated
μ	Mortality rate of the infants
τ	Rate at which infected infants are treated with vaccines
β	Transmission coefficient
ω	Rate at which the vaccine wanes
σ	Rate at which the exposed infants become infectious
α	Past information about the fraction of infected infants
δ	Rate at which re-infection occurs among the infants
η	Rate at which the susceptible infants are exposed to the infectious diseases
ρ	Fraction of the parents for which their infants are susceptible
S_0	Number of the susceptible infant population at time t = 0
E_0	Number of the exposed infant population at time t = 0
I_0	Number of the infected infant population at time t = 0
V_0	Number of the vaccinated infant population at time t = 0
R_0	Number of the temporary recovered infant population at time t = 0

The Next Generation Matrix

In epidemiology, the next generation matrix is a method used to derive the basic reproductive number for a compartmental model of the spread of infectious diseases [6]. This method was derived by Diekmann et al (2000) and improved by Driessche and Watmough (2002) [3]. To calculate the basic reproductive number of a compartmental model by using the next generation matrix method, the whole population is divided into n compartments such that m x n infected compartments. Let X_i (i = 1, 2, 3, - - -, m) be the numbers of infected infants in the ith infected compartment at time t [2]. Then the epidemic model is given in the form:

$$\frac{dX_i}{dt} = JX_i \quad (6)$$

where X_i represents the vector disease states, $J = F_i(X) - V_i(X)$ represents the Jacobian matrix and $V_i(X) = V_i^-(X) - V_i^+(X)$. In equation 6, $F_i(X)$ represents the rate of appearance of new infection in compartment i by all other means and $V_i^-(X)$ represents the rate of transfer of individuals out of the compartment i. Equation 6 can also be written in the form;

$$\frac{dX_i}{dt} = F(X) - V(X) \quad (7)$$

where $F(X) = (f_1(X), f_2(X), - - -, f_n(X))^T$ and $V(x) = (v_1(X), v_2(X), - - -, v_n(X))^T$. Let X_0 be the disease free equilibrium point, the values of the Jacobian matrix F(X) and V(X) are given in the form $F(X) = \frac{\partial f(X_0)}{\partial X_j}$ and $V(X) = \frac{\partial v(X_0)}{\partial X_j}$ where F and V are m x m matrices with $1 \leq j \leq m$ and F and V are non – singular matrices. Following Diekmann et al [2], we call FV^{-1} the next generation matrix for the model usually written as R_0 and it is equal to the spectral radius $\rho(FV^{-1})$ in which the spectral radius command computes the maximum of the absolute values of the eigenvalues of the matrix [4] i.e.

$$R_0 = \rho(FV^{-1}) \quad (8)$$

The Basic Reproductive Number of the Mathematical Model

Consider the system of equations 1 to 5. Let the vector disease states be represented by $X_i = (E, I, V)^T$ such that;

$$f_1 = \frac{dE}{dt} = \beta S(t)I(t)\big(1 + \alpha I(t)\big) + \eta S(t) - (\mu + \sigma)E(t) \quad (9)$$

$$f_2 = \frac{dI}{dt} = \sigma E(t) - \rho\mu I(t) - (\mu + \tau)I(t) \quad (10)$$

$$f_3 = \frac{dV}{dt} = PA + \tau I(t) - (\mu + \omega)V(t) \quad (11)$$

The Jacobian matrix for equations 9 to 11 is obtained as;

$$J = \begin{pmatrix} -(\mu+\sigma) & \beta S^* + 2\alpha\beta S^* I^* & 0 \\ \sigma & -\rho\mu - (\mu+\tau) & 0 \\ 0 & \tau & -(\mu+\omega) \end{pmatrix} \quad (12)$$

At the disease free equilibrium point $X_0 = (1, 0, 0, 0, 0)$, the Jacobian matrix (12) is given as;

$$J(X_0) = \begin{pmatrix} -(\mu+\sigma) & \beta & 0 \\ \sigma & -\rho\mu - (\mu+\tau) & 0 \\ 0 & \tau & -(\mu+\omega) \end{pmatrix} \quad (13)$$

with

$$F = \begin{pmatrix} 0 & \beta & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \quad (14)$$

and

$$V = \begin{pmatrix} (\mu+\sigma) & 0 & 0 \\ -\sigma & \rho\mu + (\mu+\tau) & 0 \\ 0 & -\tau & (\mu+\omega) \end{pmatrix} \quad (15)$$

such that,

$$V^{-1} = \begin{pmatrix} \frac{1}{(\mu+\sigma)} & 0 & 0 \\ \frac{\sigma}{(\mu+\sigma)(\rho\mu+\mu+\tau)} & \frac{1}{\rho\mu+(\mu+\tau)} & 0 \\ \frac{\sigma\tau}{(\mu+\sigma)(\rho\mu+\mu+\tau)(\mu+\omega)} & \frac{\tau}{(\rho\mu+\mu+\tau)(\mu+\omega)} & \frac{1}{(\mu+\omega)} \end{pmatrix} \quad (16)$$

and

$$FV^{-1} = \begin{pmatrix} \frac{\beta\sigma}{(\mu+\sigma)(\rho\mu+\mu+\tau)} & \frac{\beta}{(\rho\mu+\mu+\tau)} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \quad (17)$$

Hence,

$$R_0 = \rho(FV^{-1}) = \frac{\beta\sigma}{(\mu+\sigma)(\rho\mu+\mu+\tau)} \quad (18)$$

With equation 18, the basic reproductive number of the mathematical model (1) to (5) is obtained. This means that an exposed infant that survives $\frac{\sigma}{(\mu+\sigma)}$ becomes infectious and contacts β susceptible infants during the period of infectivity at $\frac{1}{(\rho\mu+\mu+\tau)}$ which results in a new exposure. If $R_0 > 1$, an epidemic is prevented when $R_0 S(0) < 1$ [4]. Thus if the initial susceptible fraction has been reduced to less

than $\frac{1}{R_0}$ for example by vaccination or through immunization procedure, then an epidemic can be reduced or even eventually eradicated from the community.

Conclusion

Epidemiologically, the basic reproductive number of an infectious disease tells us how many secondary cases will one infected infant produce in an entirely susceptible population [3]. This means that if $R_0 < 1$, then there exists only the disease free equilibrium. This is attractive so that every solution of the system of ordinary differential equation approaches this equilibrium and the disease disappears from the population with time. In addition, if the $R_0 > 1$, then there are two equilibria i.e. the disease free equilibrium and the endemic equilibrium. The endemic equilibrium is attractive so that every solution of the system of ordinary differential equation approaches its solution as time goes to infinity. Thus, in this case the disease remains endemic in the population.

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