



A deterministic model for the transmission dynamics of infectious diseases among infants

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ABSTRACT

In this paper, a deterministic mathematical model for the transmission dynamics of infectious diseases among infants in a vaccinated and temporary recovered population is proposed. Although the equilibria of the model could not be expressed in closed forms, the existence and threshold conditions for their stabilities are theoretically investigated. The standard dynamical modelling methods are used for analyzing the behaviours of the solutions both at the disease free equilibrium and the endemic equilibrium. In addition, the conditions of the parameters for the disease free and endemic states are obtained through the basic reproductive number. The results of this study guide the way to reduce the disease outbreak among the infants.

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Introduction

The diseases which are most often modelled are the so-called infectious diseases; that is, diseases that are contagious and can be transferred from one individual to another through contact or other means [1]. Examples of such diseases among the infants include measles, rubella, chicken pox, mumps, polio, and so on. The prevalence and effects of many diseases in less developed countries are probably less well-known but may be of even more importance. Every year millions of people especially infants die of measles, respiratory infections, diarrhea, and other diseases that are easily treated and not considered dangerous in the Western World. Diseases such as malaria, typhus, cholera, schistosomiasis, meningitis, and sleeping sickness are endemic in many parts of the World. The effects of high disease mortality on mean life span and of disease debilitation and mortality on the economy in afflicted countries are considerable [9].

When infections are present in a population, a disease outbreak may progress in qualitatively different ways: the disease may die out or it may reach an endemic stage in which the disease is always present in the population. The latter will be the case if the number of secondary infections from each infected individual exceeds one [11]. This concept, formalized by the basic reproductive number R_0 , is the key concept in the literature behind modelling threshold conditions. Since the value of R_0 for a given model is a function of the parameters, R_0 provides a threshold condition for the parameters [6, 13]. As some parameters can be changed by vaccination or behavior, knowledge of threshold conditions can be very important for public health policy makers [2].

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
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	Number of the susceptible infant population
E	Number of the exposed infant population
I	Number of the infected infant population
V	Number of the vaccinated infant population
R	Number of the temporary recovered infant population

A deterministic model which consists of a set of differential equations has a long tradition in the study of infectious diseases. In 2003, Moghadas et al, considered a deterministic model and made a mathematical study for childhood diseases with non-permanent immunity [12]. In 2011, Dan Long et al, constructed a mathematical model for the transmission dynamics of infectious diseases [4].

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In this paper, transmission dynamics of infectious diseases among infants through a mathematical model is considered. Dan Long et al established and analyzed a deterministic mathematical model in their paper [4]. However, the temporary recovered infant class was not incorporated into their mathematical model. In this study, the temporary recovered infant class is incorporated into this model and the stability analyses of both the disease free and the endemic states were determined including the basic reproductive number of the new proposed mathematical model. The basic reproductive number R_0 is a threshold quantity that determines when an infection invades a population or not. This number is obtained using the next generation approach as described by Diekmann and Heesterbeek [5, 6].

Mathematical Model

The mathematical model is formulated by considering the dynamical equations for the infant population. The infants are classified into five groups as Susceptibles (S), Infectives (I), Exposed (E), Vaccinated (V) and Recovered (R). for the dynamical equations, the definition of variables and parameters used in the model are given as follows using the Table 1 below;

The transmission diagram for the infant population is represented in the Figure I below.

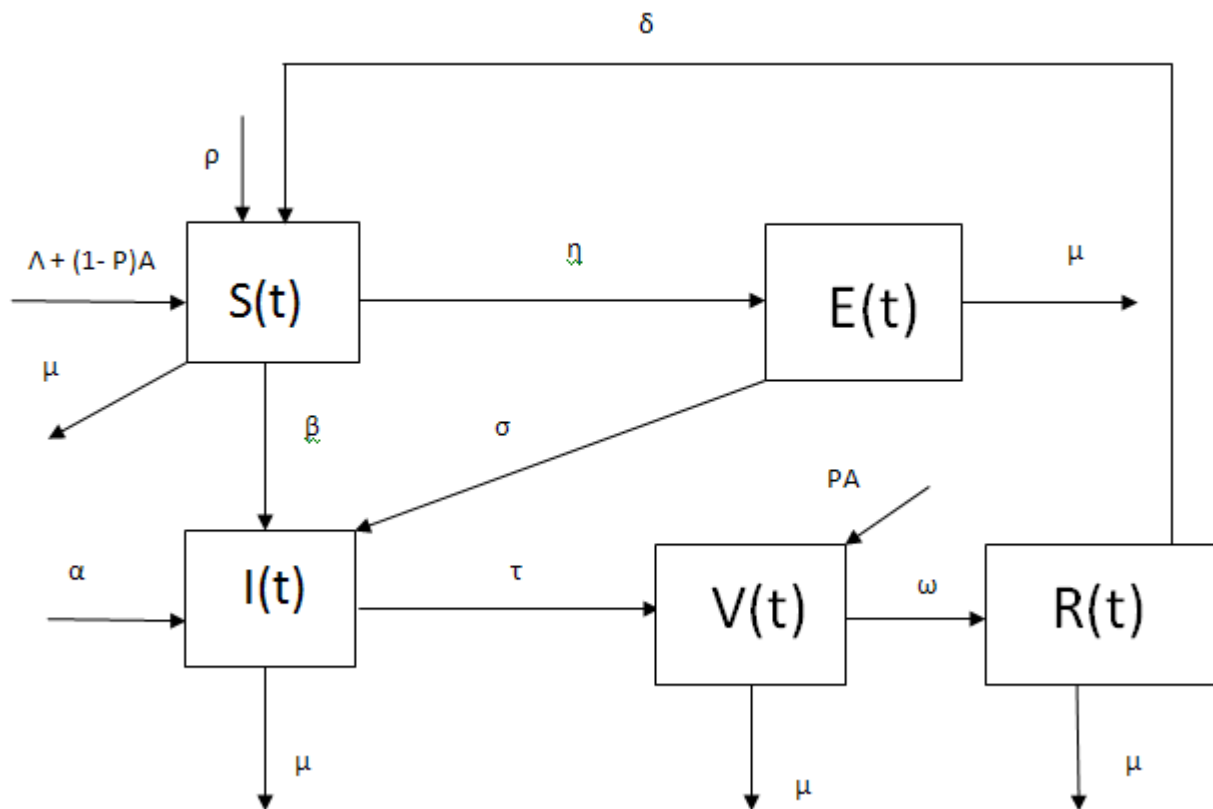


Figure 1: Diagrammatic representation of an SEIVR mathematical model.

The dynamical equations for the infant population are given as follows;

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

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

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

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

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

Such that $S = S(t)$, $E = E(t)$, $I = I(t)$, $V = V(t)$ and $R = R(t)$ represent the infant population of susceptible infant class, exposed infant class but not yet infected, the infected infant class, the vaccinated infant class and the temporary recovered infant class respectively. The parameters in the model are assumed positive and the Table 1 provides the definitions for the model parameters. The model assumes a varying population of $N(t)$ such that $N(t) = K + Ce^{-\mu t}$ for $K = \frac{\Lambda + a}{\mu}$ in which $\Lambda \neq \mu$. So, the dynamical change of each

class equals to zero. Normalizing the dynamical equations (1) to (5) by setting,

$s = S/N$, $e = E/N$, $i = I/N$, $v = V/N$ and $r = R/N$, then the reduced equation becomes

$$\frac{ds}{dt} = \Lambda + (1 - P)a + \rho\mu i + \delta r - \beta si(1 + \alpha i) - (\mu + \eta)s \tag{6}$$

$$\frac{de}{dt} = \beta si(1 + \alpha i) + \eta s - (\mu + \sigma)e \tag{7}$$

$$\frac{di}{dt} = \sigma e - \rho\mu i - (\mu + \tau)i \tag{8}$$

$$\frac{dv}{dt} = Pa + \tau i - (\mu + \omega)v \tag{9}$$

$$\frac{dr}{dt} = \omega v - (\mu + \delta)r \tag{10}$$

1. ANALYSIS OF THE MODEL

To find the equilibrium states, the right hand side of equations (6) to (10) are set equal to zero [8]. So, the equilibrium states are obtained as;

(i) Disease free state: $H_0 = (s^*, e^*, i^*, v^*, r^*) = (1, 0, 0, 0, 0)$ (11)

(ii) Endemic state: $H_1 = (s^*, e^*, i^*, v^*, r^*)$ where

$$s^* = \frac{(\mu + \sigma)(\rho\mu + \mu + \tau)i^*}{\sigma(\alpha\beta(i^*)^2 + \beta i^* + \eta)}, e^* = \left(\frac{\rho\mu + \mu + \tau}{\sigma}\right)i^*, v^* = \frac{Pa + \tau i^*}{\mu + \omega} \text{ and } r^* = \frac{\omega(Pa + \tau i^*)}{(\mu + \delta)(\mu + \omega)} \tag{12}$$

where i^* is the positive root of the equation $a(i^*)^3 + b(i^*)^2 + ci^* + d = 0$ for

$$a = \alpha\beta\rho\mu\sigma(\mu + \delta)(\mu + \omega) + \sigma\delta\omega\tau\alpha\beta - \alpha\beta(\mu + \delta)(\mu + \omega)(\mu + \sigma)(\rho\mu + \mu + \tau). \tag{13}$$

$$b = \alpha\beta\sigma(\Lambda + (1 - P)a)(\mu + \delta)(\mu + \omega) + \alpha\beta\sigma\delta\omega Pa + \rho\beta\mu\sigma(\mu + \delta)(\mu + \omega) + \sigma\delta\omega\tau\beta - \beta(\mu + \delta)(\mu + \omega)(\mu + \sigma)(\rho\mu + \mu + \tau). \tag{14}$$

$$c = \sigma\beta(\Lambda + (1 - P)a)(\mu + \delta)(\mu + \omega) + \sigma\beta\delta\omega Pa + \eta\rho\mu\sigma(\mu + \delta)(\mu + \omega) + \sigma\delta\omega\tau\eta - (\mu + \delta)(\mu + \omega)(\mu^2 + \mu\sigma)(\rho\mu + \mu + \tau) - \eta(\mu + \delta)(\mu + \omega)(\mu + \sigma)(\rho\mu + \mu + \tau) \tag{15}$$

and

$$d = \sigma\delta\omega\eta Pa + \sigma\eta(\Lambda + (1 - P)a)(\mu + \delta)(\mu + \omega). \tag{16}$$

with these values for s^*, e^*, i^*, v^* and r^* , the positivity and uniqueness of H_1 are guaranteed if and only if $R_0 > 1$ where R_0 is the basic reproductive number given in the form

$$R_0 = \frac{\sigma\beta}{(\rho\mu + \mu + \tau)(\mu + \sigma)}. \tag{17}$$

In the endemic disease state, the number of infected infants is strictly positive and constant. So, if some of the solutions of the system of equations $i(t)$ approach as time goes to infinity, the number of infectives will remain strictly positive for a long time and approximately equal to $i(t)$. Thus, the disease remains in the population and becomes endemic except adequate measures are done to control or prevent the rapid spread of the disease among the infant population [10].

The locally asymptotical stability of each equilibrium state is determined by the sign of eigenvalues for each equilibrium state. If all eigenvalues have negative real parts, then that equilibrium state is local stability [14].

The eigenvalues are obtained by solving the following characteristic equation of the form;

$$\det(J_{H_i} - \lambda I_5) = 0 \tag{18}$$

where I_5 is the identity matrix dimension 5×5 and J is the Jacobian matrix of the steady state H_i , ($i = 0, 1$). For the disease free state $H_0 = (1, 0, 0, 0, 0)$, the Jacobian matrix is given by

$$J_{H_0} = \begin{pmatrix} -(\mu + \eta) & 0 & \rho\mu - \beta & 0 & \delta \\ \eta & -(\mu + \sigma) & \beta & 0 & 0 \\ 0 & \sigma & -\rho\mu - (\mu + \tau) & 0 & 0 \\ 0 & 0 & \tau & -(\mu + \omega) & 0 \\ 0 & 0 & 0 & \omega & -(\mu + \delta) \end{pmatrix} \tag{19}$$

The characteristic equation is obtained from the Jacobian matrix with the eigenvalues λ_i ($i = 1, 2, 3, 4, 5$). The eigenvalues are;

$$\lambda_1 = -\rho\mu - (\mu + \tau), \lambda_2 = -(\mu + \eta), \lambda_3 = -(\mu + \omega), \lambda_4 = -(\mu + \delta) \text{ and } \lambda_5 = -(\mu + \omega) \tag{20}$$

Since all the model parameter values are assumed positive, it follows that the eigenvalues are all negative. Obviously, if $R_0 < 1$, then H_0 is locally asymptotically stable but if $R_0 > 1$, then, H_1 is unstable [7]. Therefore, in the event of an epidemic, the theoretical determination of condition that can make R_0 less than unity is of great public health interest such that the disease can be greatly reduced or eventually eradicated among the infant population [2].

In the same manner, for the endemic disease state, $H_1 = (s^*, e^*, i^*, v^*, r^*)$, the Jacobian matrix is given by;

$$J_{H_1} = \begin{pmatrix} -\beta i^*(1 + \alpha i^*) - (\mu + \eta) & 0 & \rho\mu - \beta s^* - 2\alpha\beta s^* i^* & 0 & \delta \\ \beta i^* - \alpha\beta(i^*)^2 + \eta & -(\mu + \sigma) & \beta s^* + 2\alpha\beta s^* i^* & 0 & 0 \\ 0 & \sigma & -\rho\mu - (\mu + \tau) & 0 & 0 \\ 0 & 0 & \tau & -(\mu + \omega) & 0 \\ 0 & 0 & 0 & \omega & -(\mu + \delta) \end{pmatrix} \tag{21}$$

The eigenvalues for the matrix (21) are given as follows;

$$\lambda_1 = -\rho\mu - (\mu + \tau), \lambda_2 = -i^*\beta - (i^*)^2\alpha\beta - (\mu + \eta), \lambda_3 = -2\beta i^* - 2\eta - \mu, \lambda_4 = -2(i^*)^2\alpha\beta - \mu \text{ and } \lambda_5 = -(\mu + \delta) \tag{22}$$

The above eigen values have negative real parts for $R_0 > 1$. Therefore, the disease free state is locally asymptotically stable for $R_0 < 1$ and the endemic disease state is locally asymptotically stable for $R_0 > 1$. The basic reproductive number (R_0) of the disease is evaluated from the averaging of the number of secondary case that one case can produce if a single infant is introduced into a susceptible infant population [3].

Conclusion

In this study, the stability analyses of the deterministic mathematical model have been analyzed using the linearization technique via the Jacobian matrix approach. The basic reproductive number of the model was obtained to be the alternative way for identifying how the spread or the outbreak of the infectious diseases among the infants can be greatly reduced. It was observed that the mathematical model produced an asymptotically stable population such that the infectious diseases among the infants die out from the infant population as time increases when adequate measures are used such as administering vaccines to the infants.

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