Journal of the Nigerian Association of Mathematical Physics
Volume 45 (March, *2018 Issue*), pp91 – 94

DERIVATION OF THE REPRODUCTION NUMBERS FOR CHOLERA MODEL

A.A. Ayoade[1], O.J. Peter[2], F.A. Oguntolu[3] and C. Y. Ishola[4]

Department of Mathematics, University of Ilorin, Ilorin, Nigeria[1&2]
Department of Mathematics/Statistics, Federal University of Technology, Minna, Nigeria[3]
Department of Mathematics, National Open University of Nigeria, Abuja, Nigeria[4]

Abstract

It is expected of the epidemiologists to predict whether a disease will spread in a community or not and at the same time, forecast the degree of severity of the disease if it spreads in the community. By that, a cholera model is formulated and the procedure for obtaining the effective reproduction number and the basic reproduction number of the model is presented following the Next Generational Matrix approach. The two reproduction numbers (the effective reproduction number and the basic reproduction number) are successfully derived. While the effective reproduction number can be used to predict the effectiveness of intervention strategies in inhibiting the spread of cholera disease, the basic reproduction number can be used to forecast the severity of cholera spread in a community where the intervention strategies are not on ground.

Keywords: Model, reproduction number, Next Generational Matrix

1.0 Introduction

Sir Ronald Ross, the 1902 Nobel Prize winner in Medicine and Physiology, was the pioneer of threshold dynamics in Mathematical Biology. Sir Ronald Ross was able to discover that mosquitoes were the vectors that transmit malaria and was honoured for his discovery in 1902. He introduced mathematical models to analyse mosquito/malaria dynamics and was able to establish how reducing the population of mosquitoes below certain threshold could help reducing or removing malaria [1].

The basic reproduction number, conventionally denoted by R_0, is defined in [2] as the average number of secondary infections generated by a typical infectious individual during his or her entire period of infectiousness. The basic reproduction number is an important non-dimensional quantity in epidemiology as it sets the threshold in the study of a disease both for predicting its outbreak and for evaluating its control strategies. Thus, whether a disease becomes persistent or dies out in a community depends on the size of the basic reproduction number.

If $R_0 < 1$, it means that every infectious individual produces on average less than one secondary infection and the outbreak will not take off in the population for the chain of transmission cannot be maintained but if $R_0 > 1$, it means that every infectious individual produces on average more than one secondary infection and the outbreak will take off in the population because the chain of transmission is maintained. A large value for R_0 may indicate the possibility of a major epidemic [3].

The basic idea of the reproduction number as introduced by Sir Ronald Ross is that the value of the reproduction number below unity, 0.8, say indicates that if an infectious individual emerges in the population of susceptible individuals, he will not infect a single individual in the population and the outbreak will not take off. On the other hand, the value of the reproduction number above unity, 2, say implies that if an infectious individual enters the population of susceptible individuals, he will infect, on average, two individuals and the outbreak will take off in the population.

Furthermore, all control measures of a disease are effective if the value of R_e, the effective reproduction number, is less than one.

Corresponding Author: Ayoade A.A., Email: ayoadeabbayomi@gmail.com, Tel: +2347033702969

The effective reproduction number, R_e measures the average number of new infections generated by a typical infectious individual in a community where intervention strategies are on ground [4]. Hence, the computation of the basic reproduction number is central to the analysis of any epidemic model in order to be able to predict whether an epidemic will take off or not in a population. In this work, the Next Generational Matrix approach shall be adopted to compute the reproduction numbers of a cholera model.

2.0 The Model

The cholera model is formulated as follows:

$$\frac{dS}{dt} = \pi - (1-\theta)\frac{\beta_1}{(B+\chi)}BS - (1-\theta)\beta_2 IS - (\mu+\nu)S + \sigma R \quad (1)$$

$$\frac{dI}{dt} = (1-\theta)\frac{\beta_1}{(B+\chi)}BS + (1-\theta)\beta_2 IS - (\mu+\mu_c)I \quad (2)$$

$$\frac{dR}{dt} = \nu S - \mu R - \sigma R \quad (3)$$

$$\frac{dB}{dt} = (1-\theta)\varepsilon I - \delta B \quad (4)$$

where S, I and R are the human compartments denoting the population of susceptible, infectious and recovered individuals at time t respectively; B is the compartment for the population of vibrios. Also, in the model, π, θ, β_1, β_2, μ, ν, σ, χ, μ_c, ε and δ are parameters representing recruitment rate into susceptibility, rate of cholera awareness, contact rate between susceptible individuals and contaminated water, contact rate between susceptible and infectious individuals, death rate unrelated to cholera, vaccination rate of susceptible individuals, rate of losing immunity, concentration of vibrios that makes 50% of susceptible population ill, death rate due to cholera, rate at which infectious individuals contributes to the growth of vibrios and death rate of vibrios unrelated to water treatment respectively.

3.0 Existence of the Disease Free Equilibrium

Disease free equilibrium is obtained when all the infection agents are reduced to zero. It exists when the population is free from infection so that each of the compartments B, I and R in the model is equal to zero. Hence, the disease free equilibrium for the model is obtained as

$$E_0 = \left(\frac{\pi}{\mu+\nu}, 0, 0, 0\right). \quad (5)$$

4.0 The Next Generation Matrix

The size of the basic reproduction number R_0 can be evaluated by using the technique knowing as the Next Generation Matrix. This technique, which was originally formulated in [2] and subsequently developed in [5], construct $n \times n$ matrix from the system of equations of the model by considering only the infective classes. The Next Generation Matrix procedure outlined in [6] is described as follows:

Define X_s to be the set of all Disease Free State, i.e. $X_s = \{x \geq 0 | x_i = 0, i = 1, 2, 3, \mathrm{K}\}$. In order to compute R_0; it is important to distinguish new infections from all other changes in the population.

Let $F_i(x)$ be the rate of appearance of new infections in compartment i;

V_i^+ be the rate of transfer of individuals into compartment i by all other means;

V_i^- be the rate of transfer of individuals out of compartment i.

It is assumed that each function $(F_i(x), V_i^+, V_i^-)$ is continuously differentiable at least twice with respect to each variable.

The transmission model consists of the non-negative initial conditions together with the following system of equations

$$\dot{x}_i = f_i(x) = F_i(x) - V_i(x), i = 1, 2, 3, \mathrm{K}, n. \quad (6)$$

where $V_i(x) = V_i^- - V_i^+$ and the function satisfies the following conditions:

(a) If $x \geq 0$, then $F_i(x), V_i^-(x), V_i^+(x) \geq 0$ for $i = 1, 2, 3, \mathrm{K}, n$. That is, if the compartment is empty, there will be no transfer of individuals out of the compartment by death, infections nor other means.

(b) If $x_i = 0$, then $V_i^-(x) = 0$. That is, nobody leaves the compartment. In particular if $x \in X_s$, then $V_i^- = 0$ for $i = 1, 2, 3, \cdots, m$.

(c) $F_i = 0$, for $i > m$ (m is the number of infective classes)

(d) $x \in X_s$, then $F_i = 0$ and $V_i^- = 0$ for all $i = 1, 2, 3, \cdots, m$.

(e) If $F_i(x)$ is set to zero, then all the eigenvalues of $D f(x_0)$ have negative real parts.

Following [2], if x_0 is the disease-free point of the system of the model and $f_i(x)$ satisfies conditions (a) – (e), then the derivatives of $DF(x_0)$ and $DV(x_0)$ are partitioned as :

$$DF(x_0) = \begin{pmatrix} F & 0 \\ 0 & 0 \end{pmatrix}, \qquad V(x_0) = \begin{pmatrix} V & 0 \\ K_3 & K_4 \end{pmatrix}. \tag{7}$$

where F and V are the $m \times m$ matrices defined by

$$F = \left[\frac{\partial F(x_0)}{\partial x_j}\right] \quad \text{and} \quad V = \left[\frac{\partial V(x_0)}{\partial x_j}\right] \tag{8}$$

with $1 \leq i \leq m$. F is non-negative and V is non-singular matrix.

Based on the result in [2], the product FV^{-1} is called the Next Generation Matrix for the model and the reproduction number R_0 is the largest eigenvalue (spectral radius) of the matrix.

4.1 Application of the Next Generation Matrix

In what follows, the procedure described above shall be followed to obtain the reproduction number of the cholera model given by the system of equations (1) – (4). Only the infective compartments I and B [i.e. eqn. (2) and eqn. (4)] are needed in the computation of the reproduction number hence, $m = 2$ and, according to [2], F_i and V_i are obtained as

$$F_i = \begin{pmatrix} (1-\theta)\beta_2 IS & \frac{(1-\theta)\beta_1 BS}{B+\kappa} \\ 0 & 0 \end{pmatrix}, \qquad V_i = \begin{pmatrix} (\mu+\mu_c)I & 0 \\ -(1-\theta)\varepsilon I & \delta B \end{pmatrix} \tag{9}$$

F and V are obtained by finding the partial derivatives of the above matrices as defined in eqn. (8) with respect to the infective compartments.

$$\therefore F = \begin{pmatrix} (1-\theta)\beta_2 S & (1-\theta)\left[\frac{\beta_1 S}{B+\kappa} - \frac{\beta_1 BS}{(B+\kappa)^2}\right] \\ 0 & 0 \end{pmatrix}, \qquad V = \begin{pmatrix} (\mu+\mu_c) & 0 \\ -(1-\theta)\varepsilon & \delta \end{pmatrix} \tag{10}$$

The inverse of the matrix V is obtained as:

$$V^{-1} = \begin{pmatrix} \frac{1}{(\mu+\mu_c)} & 0 \\ \frac{(1-\theta)\varepsilon}{(\mu+\mu_c)\delta} & \frac{1}{\delta} \end{pmatrix} \tag{11}$$

The product of matrices F and V^{-1} is :

$$FV^{-1} = \begin{pmatrix} (1-\theta)\beta_2 S & (1-\theta)\left[\frac{\beta_1 S}{B+\kappa} - \frac{\beta_1 BS}{(B+\kappa)^2}\right] \\ 0 & 0 \end{pmatrix} \begin{pmatrix} \frac{1}{(\mu+\mu_c)} & 0 \\ \frac{(1-\theta)\varepsilon}{(\mu+\mu_c)\delta} & \frac{1}{\delta} \end{pmatrix} \tag{12}$$

Since R_0 is evaluated at the DFE therefore, the values of S and B in eqn. (5) into eqn. (12) and, FV^{-1} becomes

$$FV^{-1} = \begin{pmatrix} \frac{(1-\theta)\pi\beta_2}{\mu+\nu} & \frac{(1-\theta)\pi\beta_1}{\kappa(\mu+\nu)} \\ 0 & 0 \end{pmatrix} \begin{pmatrix} \frac{1}{(\mu+\mu_c)} & 0 \\ \frac{(1-\theta)\varepsilon}{(\mu+\mu_c)\delta} & \frac{1}{\delta} \end{pmatrix} \tag{13}$$

Eqn. (13) simplifies to

$$FV^{-1} = \begin{pmatrix} \frac{(1-\theta)\pi\beta_2}{(\mu+\nu)(\mu+\mu_c)} + \frac{(1-\theta)^2\pi\beta_1\varepsilon}{\kappa\delta(\mu+\nu)(\mu+\mu_c)} & \frac{(1-\theta)\pi\beta_1}{\kappa\delta(\mu+\nu)} \\ 0 & 0 \end{pmatrix} \tag{14}$$

The reproduction number is thus obtained as the spectral radius (larger eigenvalues) of the above matrix, which is :

$$R_e = \frac{\pi(1-\theta)[(1-\theta)\beta_1\varepsilon + \kappa\beta_2\delta]}{\kappa\delta(\mu+\nu)(\mu+\mu_c)} \tag{15}$$

Eqn. (15) is the effective reproduction number that is, the average number of secondary infection generated whe education and vaccination are on ground as intervention strategies. In the absence of the two intervention strategies i. $\theta = \nu = 0$ and neglecting disease transmission from person-to-person i.e. β_2 then, eqn. (15) reduces to

$$R_0 = \frac{\pi[\beta_1\varepsilon + \kappa\delta]}{\kappa\mu\delta(\mu+\mu_c)} \tag{16}$$

Eqn. (16) is the basic reproduction number that is, the average number of secondary infection generated when intervention strategy is on ground.

5.0 Conclusion

The Next Generation Matrix approach was successfully applied to obtain the effective reproduction number (eqn. 15) and the basic reproduction number (eqn. 16) of the presented cholera model. On that ground, if reliable data are obtained for each parameter to determine the numerical values of the two results (eqns 15 and 16), the results can be used by the epidemiologists for two purposes. They can use the result for the effective reproduction number to predict the effectiveness of the two intervention strategies in inhibiting cholera outbreak in the community where they are on ground. Besides, they can also use the result for the basic reproduction number to predict the severity of the cholera outbreak in the community where interventions are not on ground.

6.0 References

[1] Johnson, L. R. (2006). *Mathematical modeling of cholera: from bacteria life histories to human epidemics* (Unpublished Ph.D. Dissertation). University of California, Santa Cruz.

[2] Diekmann, O., Heesterbeek, J. A. P., & Metz, J. A. J. (1990). On the definition and computation of the basic reproduction ratio R_0 in models for infectious diseases in heterogeneous population. *Journal of Mathematical Biology*, *28*, 365-382.

[3] Edward, S., Kuznetsov, D., & Mirau, S. (2014). Modelling the impact of immunization on epidemiology of varicella zoster virus. *Mathematical Theory and Modelling*, *4*(8), 16 – 25.

[4] Kadaleka, S. (2011). *Assessing the effects of nutrition and treatment in cholera dynamics: The case of Malawi*. M. Sc. Dissertation, University of Der es Salaam.

[5] van den Driessche, P., & Watmough, J. (2002). Reproduction number and sub – threshold endemic equilibria for compartmental models of disease transmission. *Mathematical Biosciences*, *180*, 29 – 48.

[6] Lungu, E. M., Kgosimore, M., & Nyabadza, F. (2007). Lecture notes: mathematical epidemiology pp. 45-50 (Available online).