Modified Maternally-Derived-Immunity Susceptible Infectious Recovered (MSIR) Model of Infectious Disease: Existence of Equilibrium and Basic Reproduction Number

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Abstract

In this paper we modified the MSIR Model by adding the vaccination rate and death rate due to the disease to the existing MSIR model. We verified the positivity of the solution and obtained the Disease Free Equilibrium (DFE) of the model. We also determined the basic reproduction number using next generation Matrix and Jacobian matrix methods.

Key words: Modified, Model, Equilibrium and Basic Reproduction Number

1. Introduction

MSIR model is a mathematical model of infectious disease. For many infections, including measles, babies are not born into the susceptible compartment but are immune to the disease for the first few months of life due to protection from maternal antibodies (passed across the placenta and additionally through colostrum). This added detail can be shown by including an M class (for maternally derived immunity) at the beginning of the model.

In 1927, W. O. Kermack and A. G. McKendrick proposed the $S-I-R$ model in which they considered a fixed population with only three compartments: susceptible, $S(t)$; infected, $I(t)$; and removed, $R(t)$. Later an additional compartment is added, M(t), $M-S-I-R.$

In epidemiology, the next-generation matrix is a method used to derive the basic reproduction number, for a compartmental model of the spread of infectious diseases. This method is given by Diekmann *et al.* (1990)[3] and was further analyzed by Driessche and Watmough (2002).[8] To calculate the basic reproduction number by using a next-generation matrix, the whole population is divided into n compartments in which there are $m<n$ infected compartments. Let x_i, $i=1,2,3,...,m$ be the numbers of infected individuals in the i^{th} infected compartment at time *t*.

The next-generation matrix (NGM) is the natural basis for the definition and calculation of R_0 where finitely many different categories of individuals are recognized. According to Diekmann et al., (2000) and Murray (2002), the basic reproduction number denoted by R_0, is the expected number of secondary cases produced, in a completely susceptible population, by a typical infective individual. It is one of the most useful threshold parameters, which characterize mathematical problems concerning infectious diseases. If $R_0 < 1$, this implies that, on average an infected individual produces less than one new infected individual during the infectious period and the infection can be wiped out. Conversely, if $R_0 > 1$, then , each infected individual produces, on average, more than one new infection, and the disease is spread in the population. For a single infected compartment, R_0 is simply the product of the infection rate and the mean duration of the infection. The estimation of reproductive numbers is typically an indirect process because some of the parameters on which these numbers depend are difficult, if not impossible, to quantify directly. A commonly used indirect approach involves fitting a model to some epidemiological data, providing estimates of the required parameters.[1]

In this paper we verified the invariant region of the model, the positivity of solution of the model. We also calculated the disease free equilibrium DFE, and the basic reproduction number using next generation matrix and Jacobian matrix methods.

2. Modified Model

$$\frac{dM}{dt} = \Lambda - \theta M - \mu M \tag{1}$$

$$\frac{dS}{dt} = \theta M - \alpha SI - (\mu + v)S \tag{2}$$

$$\frac{dI}{dt} = \alpha SI - (\gamma + \mu + \delta)I \tag{3}$$

$$\frac{dR}{dt} = \gamma I - \mu R + vS \tag{4}$$

Where,

M = Maternally-derived-immunity

S = Susceptible class

I = Infected class

R = Recovered class

N = Total Population; $N = M + S + I + R$.

α = Contact rate

Λ = recruitment rate

μ = natural death rate

δ = death rate due to disease

θ = loss of temporal immunity period

γ = recovery rate

v = vaccination rate

Model Assumption

We added vaccination rate and death rate due to disease in the existing MSIR model. The infants are born into M class and after some time, the immunity period, θ expires and the infants move to S class. The S, class is vaccinated at the rate v, and R class where they remain recovered for life i.e. no loss of immunity after recovery from infection or immunization.

Invariant Region

The total population size N can be determined by

$$N = M + S + I + R$$

$$\frac{dN}{dt} = \frac{dM}{dt} + \frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt}$$

$$\frac{dN}{dt} = \Lambda - \mu N - \delta I \qquad (5)$$

Theorem 1: $Let\ \Omega = (M, S, I, R) \in \mathbb{R}^4{}_+$ be any solution of the system (1) to (4) with non-negative initial conditions.

The solution of the system (1) to (4) are feasible for all $t > 0$ if they enter the invariant region Ω .

Proof:

From equation (5) in absence of the disease $\delta = 0$ and (5) becomes

$$\frac{dN}{dt} \leq \Lambda - \mu N \qquad (6)$$

$$\frac{dN}{dt} + \mu N \leq \Lambda$$

By theorem on differential inequality, Birkhoff and Rota (1982), we have

$0 \leq N \leq \frac{\Lambda}{\mu}$, hence

$\Lambda - \mu N \geq ke^{-\mu t}$, where *k* is a constant.

Therefore, the feasible solutions set of the model (1) to (4) enters the region

$$\Omega = \left\{ (M, S, I, R) \in \mathbb{R}^4 : M, S, I, R \geq 0, N \leq \frac{\Lambda}{\mu} \right\} \qquad (7)$$

which is a positively invariant (i.e. solutions remain positive for all times, *t*) and the model is well posed and biologically meaningful.

Positivity of Solutions

Lemma 1

Let the initial data be $\Omega = \left\{M(0), S(0), I(0), R(0) \geq 0, N \leq \frac{\Lambda}{\mu}\right\} \in \mathbb{R}^4$. then the solution set $\{M(t), S(t), I(t), R(t)\}$ of the system (1) to (4) is positive for all $t > 0$.

Proof

From (1)

$$M' = \Lambda - \theta M - \mu M$$
$$M' = \Lambda - (\theta + \mu)M \geq -(\theta + \mu)M$$
$$M' \geq -(\theta + \mu)M$$

$$\frac{M'}{M} \geq -(\theta + \mu) \tag{8}$$

Integrating (8) we have

$$M(t) \geq M(0)e^{-(\theta+\mu)t} \geq 0 \qquad \text{since } (\theta + \mu) \geq 0 \tag{9}$$

Using (2)

$$S' = \theta M - \alpha SI - (\mu + v)S \geq -(\mu + v)S$$

$$\frac{S'}{S} \geq -(\mu + v) \tag{10}$$

Integrating (10) we have

$$S(t) \geq S(0)e^{-(\mu+v)t} \geq 0 \text{ since } (\mu + v) \geq 0 \tag{11}$$

Using (3)

$$I' = \alpha SI - (\gamma + \mu + \delta)I \geq -(\gamma + \mu + \delta)I$$

$$\frac{I'}{I} \geq -(\gamma + \mu + \delta) \tag{12}$$

Integrating (12) we have

$$I(t) \geq I(0)e^{-(\gamma+\mu+\delta)t} \geq 0 \text{ since } (\gamma + \mu + \delta) \geq 0 \tag{13}$$

Using (4)

$$R' = \gamma I - \mu R + vS \geq \mu R$$

$$\frac{R'}{R} \geq \mu \tag{14}$$

Integrating (14) we have

$$R(t) \geq R(0)e^{\mu t} \geq 0 \text{ since } \mu \geq 0 \tag{15}$$

Therefore, all the solutions of equations of system (1) to (4) are positive for all $t > 0$.

3 Existence of Equilibrium Points

At equilibrium $\frac{dM}{dt} = \frac{dS}{dt} = \frac{dI}{dt} = \frac{dR}{dt} = 0$

Let $E(M^*, S^*, I^*, R^*)$ be the equilibrium points of the model system

$$\Lambda - \theta M - \mu M = 0 \tag{16}$$

$$\theta M - \alpha SI - (\mu + v)S = 0 \tag{17}$$

$$\alpha SI - (\gamma + \mu + \delta)I = 0 \tag{18}$$

$$\gamma I - \mu R + vS = 0 \tag{19}$$

Existence of Disease Free Equilibrium (DFE), E_0

In the absence of the disease, this implies that $(I^* = 0)$, therefore the above system (16) to (19) reduces to

$$\Lambda - \theta M - \mu M = 0 \tag{20}$$

$$\theta M - (\mu + v)S = 0 \tag{21}$$

$$vS - \mu R = 0 \tag{22}$$

Let $a=(\theta+\mu),\ b=(\mu+\nu),\ c=(\gamma+\mu+\delta)$

From (20)

$$M^{*}=\frac{\Lambda}{a} \tag{23}$$

From (21)

$$S^{*}=\frac{\Lambda\theta}{ab} \tag{24}$$

From (22)

$$R^{*}=\frac{\Lambda\nu\theta}{ab\mu} \tag{25}$$

Hence, the DFE is:

$$E_0=E\left(M^{*},S^{*},I^{*},R^{*}\right)=\left(\frac{\Lambda}{a},\ \frac{\Lambda\theta}{ab},\ 0,\ \frac{\Lambda\theta}{ab\mu}\right)$$

i.e.

$$E_0=E\left(M^{*},S^{*},I^{*},R^{*}\right)=\left(\frac{\Lambda}{(\theta+\mu)},\ \frac{\Lambda\theta}{(\theta+\mu)(\mu+\nu)},\ 0,\ \frac{\Lambda\theta}{(\theta+\mu)(\mu+\nu)\mu}\right) \tag{26}$$

4. The Basic Reproduction Number R_0, using Next Generation Matrix.

We therefore compute the basic reproduction number R_0, using the next generation operator approach by Driesshe and Watmough, (2002). This method is described as follows:

Assume that there are n compartments so that the first m compartments correspond to infected individuals. Let $F_i(x)$ be the rate of appearance of new infections in compartment i. $V_i^{+}(x)$ be the rate of transfer of individuals into compartment i by all other means, other than the epidemic

and $V_i^-(x)$ represents the rate of transfer of individuals out of compartment i. The disease transmission model consists of the system of equations

$$\frac{dx_i}{dt} = F_i(x) - V_i(x) \tag{27}$$

Where

$$V_i(x) = \left[V_i^-(x) - V_i^+(x)\right] \tag{28}$$

We then compute matrices F and V which are $m \times m$ matrices, where m represents the infected classes, defined by

$$F = \frac{\partial F_i}{\partial x_j}(x_0) \text{ and } V = \frac{\partial V_i}{\partial x_j}(x_0) \tag{29}$$

Where x_0 is the DFE

Now, the matrix FV^{-1} is known as the next-generation matrix. The largest eigenvalue or spectral radius of FV^{-1} is the basic reproduction number of the model.

$$R_0 = \rho\left(FV^{-1}\right) \tag{30}$$

Where $\rho(A)$ is the largest eigenvalue or spectral radius of matrix A

We will only consider the infected class of the model (3)

$$\frac{dI}{dt} = \alpha SI - (\gamma + \mu + \delta)I$$

$$F_i(x) = F_1 = [\alpha SI] \tag{31}$$

$$V_i(x) = V_1 = [(\gamma + \mu + \delta)I] \tag{32}$$

$$F = \frac{\partial F}{\partial I}(x_0) = \left[\frac{\Lambda \alpha \theta}{(\theta + \mu)(\mu + \nu)}\right] \tag{33}$$

$$V = \frac{\partial V}{\partial I}(x_0) = [(\gamma + \mu + \delta)] \tag{34}$$

$$V^{-1} = \frac{1}{(\gamma + \mu + \delta)} \tag{35}$$

$$FV^{-1} = \frac{\Lambda\alpha\theta}{(\theta + \mu)(\mu + \nu)(\gamma + \mu + \delta)} \tag{36}$$

We now calculate the eigenvalue to determine the basic reproduction number, R_0, by taking the largest eigenvalue. Our work is easy since the matrix is 1×1 matrix.

Therefore,

$$R_0 = \frac{\Lambda\alpha\theta}{(\theta + \mu)(\mu + \nu)(\gamma + \mu + \delta)} \tag{37}$$

5. The Basic Reproduction Number R_0, using Jacobian matrix.

In this method we are going to use our model equations (1) to (4). This is to verify whether the next generation matrix will give us the same result with Jacobian method.

$$J = \begin{bmatrix} -a & 0 & 0 & 0 \\ \theta & -(\alpha I + b) & \alpha S & 0 \\ 0 & \alpha I & \alpha S - c & 0 \\ 0 & \nu & \gamma & -\mu \end{bmatrix} \tag{38}$$

At DFE

$$J = \begin{bmatrix} -a & 0 & 0 & 0 \\ \theta & -b & d & 0 \\ 0 & 0 & d - c & 0 \\ 0 & \nu & \gamma & -\mu \end{bmatrix} \tag{39}$$

Where

$$d = \frac{\Lambda\alpha\theta}{ab}$$

$$|J - \lambda I| = 0$$

$$\begin{bmatrix} -(a+\lambda) & 0 & 0 & 0 \\ \theta & -(b+\lambda) & d & 0 \\ 0 & 0 & d-c-\lambda & 0 \\ 0 & v & \gamma & -(\mu+\lambda) \end{bmatrix} = 0 \tag{40}$$

$$(-a-\lambda)(-b-\lambda)(-\mu-\lambda)(d-c-\lambda) = 0 \tag{41}$$

Equation (41) is the characteristics equation

From (41) we have

$\lambda_1 = -a,\ \lambda_2 = -b,\ \lambda_3 = -\mu$ and $\lambda_4 = d - c$

therefore,

$$\lambda_1 = -(\theta+\mu),\ \lambda_2 = -(v+\mu),\ \lambda_3 = -\mu \text{ and } \lambda_4 = \frac{\Lambda\alpha\theta - (\theta+\mu)(\mu+v)(\gamma+\mu+\delta)}{(\theta+\mu)(\mu+v)(\gamma+\mu+\delta)}$$

Hence, the Basic reproduction number is the largest eigenvalue (i.e. λ_4)

At Disease Free $I = 0$ i.e. $R_0 < 0$

$$\Lambda\alpha\theta - (\theta+\mu)(\mu+v)(\gamma+\mu+\delta) < 0$$

$$\Lambda\alpha\theta < (\theta+\mu)(\mu+v)(\gamma+\mu+\delta) \tag{42}$$

$$\frac{\Lambda\alpha\theta}{(\theta+\mu)(\mu+v)(\gamma+\mu+\delta)} < 1 \tag{43}$$

$$R_0 = \frac{\Lambda\alpha\theta}{(\theta+\mu)(\mu+v)(\gamma+\mu+\delta)} \tag{44}$$

We observe that (37) and (44) are the same.

6. Results

The basic reproduction number, R_0 of next generation matrix and Jacobian matrix are the same, this is an indication that any of the two methods can be used to calculate the R_0. $R_0 < 1$, implies that the disease will die out from the population with time while $R_0 > 1$ implies that the disease will persist in the population with time if the necessary measures are not taken. From (37) or (44) $R_0 < 1$ if the numerator is less than the denominator and vice versa.

7. Conclusion

The feasible solutions set of the model (1) to (4) enters the region Ω which is positively invariant and the model is well posed and biologically meaningful. The equilibrium points exist for the Disease Free that was calculated, we also discovered that the basic reproduction number, R_0 for the next generation matrix and that of Jacobian matrix are the same.

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