



Investigation of the effect of vaccination on Covid 19

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Abstract— A mathematical model for the spread of coronavirus 2019 is proposed and studied. The effect of vaccination on the control of disease is also considered. The basic reproduction number R_0 was computed and the results showed that backward bifurcation occurred. The positivity and boundedness of the solutions, local stability of the disease-free equilibrium point of the model, was studied.

Keywords—Backward bifurcation, COVID-19, Mathematical modeling , Stability

I. Introduction

Coronavirus disease 2019 (COVID-19) began in December 2019 in Wuhan, China, and quickly spread to all parts of the world. This pandemic has had effects on many aspects of the human lives such as education, economic, health, religion, entertainment. To prevent the spread of the virus, countries started cutting off international trades, and they also shut down the borders and quarantined their individuals.

It is expected that vaccination will stop the pandemic. WHO is working tirelessly with partners to develop, manufacture and deploy safe and effective vaccines. In this article, the author considers two groups of susceptible individuals: 1) susceptible individuals who have not been vaccinated. 2) susceptible individuals who have been vaccinated. The aim of this paper is to investigate the effect of vaccination on the spread of the disease.

The author presents the model and proves the positivity and boundedness of the solutions. She computes the basic reproduction number. She proves that if the rate of loss of immunity exceeds a certain value, backward bifurcation occurs, that leads to bistability and makes it more difficult to control the disease.

II. The mathematical model

Our model has the following compartments: the class S for susceptible individuals; the class S_v for vaccinated susceptible individuals; I for infected individuals; and the class of recovered individuals R .

We consider the recruitment Λ and the natural death rate μ in the model because the period of the disease may be long. Furthermore, we assume that mortality rate m is due to Covid 19. The fraction θR of the recovered individuals lose their immunity and become susceptible again, θ is called the rate of loss of immunity.

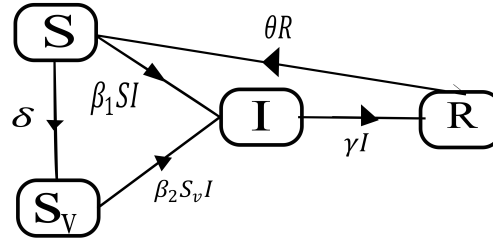


Fig. 1. Diagram the model for Covid-19

β_1 is the probability of getting infected for susceptible individuals and β_2 is the probability of getting infected for vaccinated susceptible individuals. δ is called the rate of vaccinated.

Based on the flow diagram of the model depicted in Figures 1, the author defines the following system of ordinary differential equations:

$$(1) \quad \begin{cases} S' = \Lambda - \beta_1 S I + \theta R - (\delta + \mu)S, \\ S_v' = \delta S - \beta_2 S_v I - \mu S_v, \\ I' = \beta_2 S_v I + \beta_1 S I - (\gamma + \mu + m) I, \\ R' = \gamma I - (\theta + \mu) R. \end{cases}$$

In Lemma 1, the author proves that the solutions are nonnegative.

Lemma 1. If the initial conditions are nonnegative, i.e., $S(0) \geq 0$, $S_v(0) \geq 0$, $I(0) \geq 0$, and $R(0) \geq 0$, then all components of the solution $(S(t), S_v(t), I(t), R(t))$ in the system are nonnegative for all $t \geq 0$.

PROOF. Let the function $F : \text{int}(\mathbb{R}_+^4) \rightarrow \mathbb{R}_+^4$ as follows:

$$(2) \quad F(W) = (f_1(W), f_2(W), f_3(W), f_4(W)),$$

where functions f_1, f_2, f_3 and f_4 are the right side of model (1) with following initial conditions $S(0) \geq 0$,

$S_v(0) \geq 0$, $I(0) \geq 0$, and $R(0) \geq 0$. It is clearly $\text{int}(\mathbb{R}_+^4)$ is open subset of \mathbb{R}_+^4 and the functions f_1, f_2, f_3 and f_4 satisfy in Lipschitz condition locally. Regarding the Picards theorem, one is able to see any arbitrary solution of model (1) satisfying initial conditions $y_1(0) > 0, y_2(0) > 0$ is positive for all $t \geq 0$. \square

In the following lemma, the author proves the boundedness of the solutions:

Lemma 2. For any nonnegative initial values, the total population $N(t) = S(t) + S_v(t) + I(t) + R(t)$ is bounded.

PROOF. The four equations of system (1) are added together:

$$(3) \quad N'(t) = \Lambda - \mu N - m I \leq \Lambda - \mu N,$$

and integration yields

$$(4) \quad N(t) \leq N(0) e^{-\mu t} + \frac{\Lambda}{\mu} (1 - e^{-\mu t}) \leq \max\{N(0), \frac{\Lambda}{\mu}\}$$

for all $t \geq 0$. This proves the boundedness of the solutions of system. □

III. Disease-free equilibrium

This system has a unique disease-free equilibrium $E_0 = (S^*, S_v^*, 0, 0)$, where

$$S^* = \frac{\Lambda}{\delta + \mu}, \quad S_v^* = \frac{\Lambda}{\mu(\mu + \delta)}.$$

We rewrite the model (1) as $\frac{dX}{dt} = \mathcal{F}(X) - \mathcal{V}(X)$ where,

$$\mathcal{F}(X) = \begin{bmatrix} 0 \\ 0 \\ \beta_2 S_v I + \beta_1 S I \end{bmatrix}$$

$$\mathcal{V} = \begin{bmatrix} -\Lambda - \theta R + (\delta + \mu)S + \beta_1 S I \\ \beta_2 S_v I - \delta S + \mu S_v \\ (\gamma + \mu + m) I \end{bmatrix}$$

The following linearizations F and V can be obtained, at the infection-free equilibrium E_0 :

$$F = \begin{bmatrix} 0 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & \beta_1 S^* + \beta_2 S_v^* \end{bmatrix}, \quad V = \begin{bmatrix} \delta + \mu & 0 & \beta_1 S^* \\ -\delta & \mu & \beta_2 S_v^* \\ 0 & 0 & \gamma + \mu + m \end{bmatrix},$$

By using next-generation matrix, the basic reproduction number of the model obtains the following form:

$$R_0 = \frac{\beta_1 S^* + \beta_2 S_v^*}{\gamma + \mu + m}$$

Theorem 3. The disease-free steady state E_0 is locally asymptotically stable if $R_0 \leq 1$ and unstable if $R_0 \geq 1$.

PROOF. The Jacobian matrix of the system at the point E_0 has the following form:

$$J_0 = \begin{bmatrix} -\delta - \mu & 0 & -\beta_1 S & \theta \\ \delta & -\mu & -\beta_2 S_v & 0 \\ 0 & 0 & a_{33} & 0 \\ 0 & 0 & \gamma & -\mu - \theta \end{bmatrix}$$

where

$$a_{33} = \frac{\beta_2 \Lambda}{\mu(\mu + \delta)} + \frac{\beta_1 \Lambda}{\mu + \delta} - (\gamma + \mu + m)$$

that has the four eigenvalues:

$$\lambda_1 = -\mu, \quad \lambda_2 = -\mu - \delta, \quad \lambda_3 = -\mu - \theta, \quad \lambda_4 = a_{33}.$$

if $R_0 \leq 1$ then all eigenvalues have negative real parts. Therefore the point E_0 is locally asymptotically stable. □

IV. Backward bifurcation

In this section, we study the occurrence of backward bifurcation , by using the theorem of Castillo-Chavez and Song. If the initial size of all compartments of the model are in the basin of attraction of the disease-free equilibrium E_0 , then the spread of infection can be controlled by reducing R_0 to the region $R_0 < 1$. But in some models, reducing R_0 to $R_0 < 1$ is not enough for eliminating the disease because endemic equilibrium points may also exist. In such models, backward bifurcation occurs.

Theorem 4. Backward bifurcation occurs in the model at $R_0 = 1$, provided $\frac{\theta \gamma}{\mu + \theta} > \frac{\beta_2^2 \Lambda}{\mu (\beta_1^* \mu + \beta_2 \delta)} + \frac{\beta_1 \Lambda}{\delta + \mu}$.

PROOF. Corresponding right and left eigenvalues are $w = (w_1, w_2, w_3, w_4) = \left(\frac{-\beta_1 \Lambda}{(\delta + \mu)^2} + \frac{\theta w_4}{\mu + \delta}, \frac{\delta w_1}{\mu} - \frac{\beta_2 \Lambda}{\mu (\delta + \mu)}, 1, \frac{\gamma}{\mu + \theta} \right)$, $v = (0, 0, 1, 0)$. Now as it is proved in Castillo-Chavez and Song theorem [3], if the bifurcation quantities a and b are both positive, then backward bifurcation occurs in the system, and we have

$$\mathbf{a} = \sum_{k,i,j=1}^4 v_k w_i w_j \frac{\partial^2 f_k}{\partial x_i \partial x_j} (E_0, \beta_1^*) = \beta_1 w_1 + \beta_2 w_2 = \frac{\theta \gamma}{\mu + \theta} - \left(\frac{\beta_2^2 \Lambda}{\mu (\beta_1^* \mu + \beta_2 \delta)} + \frac{\beta_1 \Lambda}{\delta + \mu} \right) > 0,$$

$$\mathbf{b} = \sum_{k,i=1}^4 v_k w_i \frac{\partial^2 f_k}{\partial x_i \partial x_j} (E_0, \beta_1^*) = \frac{\gamma}{\delta + \mu} > 0$$

We observe that \mathbf{a} is negative provided $\frac{\theta \gamma}{\mu + \theta} > \frac{\beta_2^2 \Lambda}{\mu (\beta_1^* \mu + \beta_2 \delta)} + \frac{\beta_1 \Lambda}{\delta + \mu}$ and \mathbf{b} is positive. Therefore, backward bifurcation (subcritical) occurs. \square

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