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Backward Bifurcation and Hysteresis in a Mathematical Model of COVID19 with Imperfect Vaccine

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Abstract Vaccination has been used as strategy to eradicate the spread of COVID-19. But imperfect vaccine has been reported to induce backward bifurcation and hysteresis in mathematical models of disease transmission. Backward bifurcation is a phenomenon whereby a stable endemic equilibrium exists contemporaneously with a stable disease-free equilibrium when the basic reproduction number is less than 1. This situation can cause difficulty in controlling an epidemic because the basic reproduction is no longer the only means of eradicating the disease. In this paper, we propose a mathematical model for the transmission of disease which includes imperfect vaccination. We show that our model is capable of capturing backward bifurcation under certain conditions. By using parameters that are relevant to COVID-19 transmission in Malaysia, our numerical analysis shows that low vaccine efficacy can trigger backward bifurcation.

Keywords Hysteresis; Backward Bifurcation; Forward Bifurcation; COVID-19; Pandemic.

Mathematics Subject Classification 93A30

1 Introduction

The basic reproduction number ($\mathcal{R}_0$) has long been used as the key indicator to determine whether a disease will persist (i.e., becomes endemic) or not. In bifurcation theory, this typical role of the basic reproduction number is depicted via the so-called forward bifurcation phenomena. It is a type of local bifurcation in which the system transits from a single stable fixed point to double non-negative fixed points, in which one is stable and the other is not stable. In mathematical epidemiology, the bifurcation parameter is considered to the value of $\mathcal{R}_0$. In this setting, a single, stable disease-free equilibrium (DFE) persists when $\mathcal{R}_0 < 1$. When $\mathcal{R}_0 > 1$, the DFE becomes unstable, while a stable branch of endemic equilibrium emerges. Another type of bifurcation phenomena that has been observed in mathematical models of epidemic is the backward bifurcation. While in a forward bifurcation there is no likelihood of an endemic state when $\mathcal{R}_0 < 1$, endemic equilibrium can exist for a system which exhibits a backward bifurcation when $\mathcal{R}_0 < 1$. In such systems, there is a large jump in the force

of infection when $\mathcal{R}_0$ reaches slightly above one that making $\mathcal{R}_0$ less than one alone would not be sufficient to eradicate the disease. To eradicate the disease, there is need to reduce $\mathcal{R}_0$ to a value where endemic equilibrium does not exist and the DFE is globally asymptotically stable. Imperfect vaccine is known to be one of the causes of backward bifurcation as stated in standard Kermack–McKendrick type of models of disease transmission as given by Fred [1], Christopher [2], Abba [3] and Elamin [4].

Covid-19 vaccines are the most important strategy towards ending the COVID-19 pandemic and to date, 66.9% of the world population have received at least one dose of a COVID-19 vaccine as stated in Hannah et al. [5]. Nevertheless, the administered vaccines have different efficacy's levels. COVID-19 vaccines authorised by WHO are mostly effective at reducing the risk of developing serious illness and death but does not provide 100% full protection WHO [6]. This means that depending on vaccination alone for the controlling or eradicating the disease can't give a full protection for the population against the disease. Several mathematical models have been proposed to quantitatively explore and predict the trends in the transmission of COVID-19 under various vaccination scenarios. See Enahoro et al[7], Sheliei et al.[8] and Lahbib et al [9]. These studies suggest that, even with a large-scale vaccination program, non-pharmaceutical interventions are still needed to effectively curb the spread of the disease.

As pointed out by Abba [3], imperfection in the vaccine is one of the leading causes of backward bifurcation in vaccination models. Low efficacy of the vaccine means that the vaccine does not give full protection (100% protection) against infection in vaccinated individuals. We proposed, in this paper, a COVID-19 model with imperfect vaccination which exhibits a phenomenon of backward bifurcation when the vaccine efficacy goes below a certain threshold value. We use parameter values that have been reported to agree with the transmission of the disease in Malaysia to examine the tendency of backward bifurcation phenomenon [10,11,12,13]. The paper is arranged as follows: Section 2 provides the description of the model and how it is formed, followed by its mathematical analysis. The numerical analysis we use to validate the theoretical results are later described.

2 The Mathematical Model

We formulate a deterministic model for COVID-19 dynamic with five ordinary differential equation in this paper. The total population is divided into five compartments representing a sub-population: susceptible(S), vaccinated (V), exposed (E), infected (I) and recovered(R). In this study, the total population is assumed to be constant (N), is the natural death rate. The recruitment rate is π and force of infection is $g_2 = \beta I$ where β the effective contact rate. The rate at which infected individuals develop clinical symptoms is α, γ is the rate of recovery and death rate caused by COVID-19 is d. It is possible that recovered individuals acquire certain level of immunological memory for a certain duration Shakhany [12] and we assume that recovered individuals are losing immunological memory at a rate of $(1 - \Psi)\beta$ where $0 < \Psi < 1$. The vaccine coverage rate is Ω and vaccinated individuals can die naturally with rate μ or get infected with force of infection $(1 - \tau)\beta I$ where τ is the vaccine efficacy. The value of τ is between 0 and 1 with $\tau = 1$ means perfect vaccine and $\tau = 0$ means that the vaccine is not effective. Here we assume that the vaccine is imperfect, that is a vaccinated individual is not completely protected and can still become infected when they come in contact with an infected person. We also assume that the vaccination can fail, i.e., vaccinated individual goes back to become susceptible at the rate ξ. The flowchart of this SVEIRE model is shown in Figure 1.

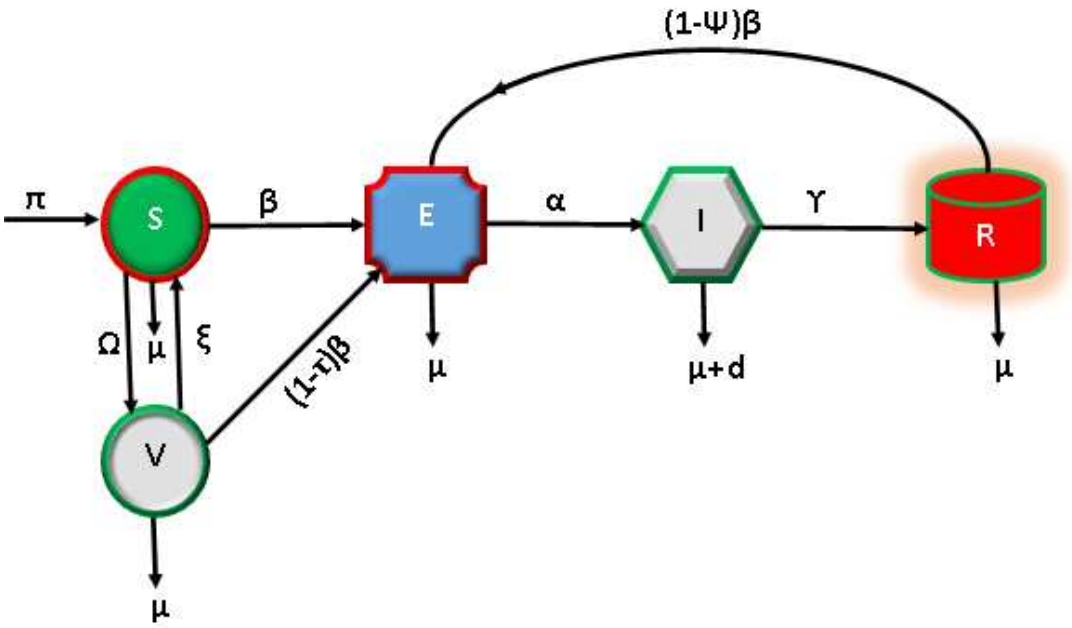


Figure 1: The Schematic Flowchart of the SVEIRE Model for COVID-19

From the flowchart above, the following system of ordinary differential equations are derived:

$$\begin{aligned}
\frac{dS}{dt} &= \pi + \xi V - \beta IS - (+\Omega) S, \\
\frac{dV}{dt} &= \Omega S - (1-\tau)\beta VI - (+\xi) V, \\
\frac{dE}{dt} &= \beta IS + (1-\Psi)\beta IR + (1-\tau)\beta VI - (\alpha+\mu) E, \\
\frac{dI}{dt} &= \alpha E - (\gamma+\mu+d) I, \\
\frac{dR}{dt} &= \gamma I - (\mu + (1-\Psi)\beta I) R,
\end{aligned} \tag{1}$$

with the initial conditions $S(0) = S_0 \geq 0$, $V(0) = V_0 \geq 0$, $E(0) = E_0 \geq 0$, $I(0) = I_0 \geq 0$, $R(0) = R_0 \geq 0$. We assumed that all the parameters of system (1) are positive when time $t > 0$. In the following subsections, we discussed the properties of the proposed model.

2.1 Basic Properties

The following theorem guarantees the non-negativity of the solutions to system (1).

Theorem 1 *Given the initial conditions* $S(0) = S_0 \geq 0$, $V(0) = V_0 \geq 0$, $E(0) = E_0 \geq 0$, $I(0) = I_0 \geq 0$, $R(0) = R_0 \geq 0$, *the solution of system* (1), *namely* $S(t), V(t), E(t)$, $I(t)$, *and* $R(t)$ *remains in the non-negative region for all* $t > 0$.

Proof A non-negative initial condition implies the followings:

$$\left.\frac{dS}{dt}\right|_{S=0,\ V\geq 0,E\geq 0,I\geq 0,R\geq 0} = \pi+\xi V > 0,$$
$$\left.\frac{dV}{dt}\right|_{S>0,\ V=0,E\geq 0,I\geq 0,R\geq 0} = \Omega S > 0,$$
$$\left.\frac{dE}{dt}\right|_{S>0,\ V\geq 0,E=0,I\geq 0,R\geq 0} = \beta IS + (1-\Psi)\,\beta IR + (1-\tau)\,\beta VI \geq 0,$$
$$\left.\frac{dI}{dt}\right|_{S>0,\ V\geq 0,E\geq 0,I=0,R\geq 0} = \alpha E \geq 0,$$
$$\left.\frac{dR}{dt}\right|_{S>0,\ V\geq 0,E\geq 0,,I\geq 0,R=0} = \gamma I \geq 0.$$

The conditions above guarantees the non-negativity of the rate of change of the state variables. S(*t*), *V*(*t*), *E*(*t*), *I*(*t*), and *R*(*t*) at the boundary of $\mathbb{R}^5_+$. Thus, the vector fields are pointing inward from the boundary planes. Therefore, the solution of system (1) will always be non-negative for all time $t > 0$ ■

Next, we establish the boundness the solutions of system (1) via the following theorem.

Theorem 2 *The solution of system (1) is strictly contained in the bounded region*

$$\mathrm{D} = \left\{ (\, S, V, E, I, R) \in \Re^5 \colon S + \mathrm{V} + \mathrm{E} + I + \ R \leq \frac{\pi}{\mu} \right\}.$$

Proof Summing both sides of system (1) give

$$\frac{d\,(S + V + E + I + R)}{dt} = \frac{dN}{dt} \leq \ \pi - N - dI.$$

If there is no death from COVID-19, then the equation above becomes $\frac{dN}{dt} \leq \quad \pi - \mu N$, which solves as

$$0 \leq N \ \leq \frac{\pi}{\mu} + N(0)e^{-\mu t},$$

where $N\,(0)$ is the initial value of the total population, assumed to be non-negative. Therefore, if S(0), *V*(0), *E*(*0*), *I*(*0*), and *R*(0) are inside of *D*, then S(*t*), *V*(*t*), *E*(*t*), *I*(*t*), and *R*(*t*) will stay within *D* as $t \to \infty$. Likewise, if the initial condition starts outside of *D*, then the solution will approach *D* as $t \to \infty$. That completes the prove of the theorem ■

3 Equilibrium Points and Their Dynamics

In this section, we look at types of equilibrium points of system (1), which are the disease-free equilibrium, abbreviated as (DFE) and the endemic equilibrium, abbreviated as (EE). To analyze the dynamics of the equilibrium points, we start by computing the effective reproduction number, using the next generation matrix method described in Driessche and Watmough [15] on system (1). The matrix form by the new infection terms, *F*, and that of the matrix of the transition terms, $\hat{V}$ are given by

$$F=\left(\begin{array}{cc}\frac{\partial \mathrm{f}_1}{\partial \mathrm{E}} & \frac{\partial \mathrm{f}_1}{\partial \mathrm{I}} \\ \frac{\partial \mathrm{f}_2}{\partial \mathrm{E}} & \frac{\partial \mathrm{f}_2}{\partial \mathrm{I}}\end{array}\right)\Bigg|_{E_0}, \ \hat{V}=\left(\begin{array}{cc}\frac{\partial \mathrm{v}_1}{\partial \mathrm{E}} & \frac{\partial \mathrm{v}_1}{\partial \mathrm{I}} \\ \frac{\partial \mathrm{v}_2}{\partial \mathrm{E}} & \frac{\partial \mathrm{v}_2}{\partial \mathrm{I}}\end{array}\right)\Bigg|_{E_0}.$$

where $f_1=\beta IS \ + (1-\Psi)\beta IR + (1-\tau)\beta VI$, $f_2=0$ are the vector for new infection rate and $v_1=(\alpha+\mu)E$, $v_2=-\alpha E+(\gamma+\mu+d)I$ are the vector for new transition rate

Differentiating f_1 with respect to E and with respect to I and substitute the values of S and V at the disease free equilibrium, we get

$$\frac{\partial f_1}{\partial E}=0,$$
$$\frac{\partial f_1}{\partial I}=\beta S \ +(1-\tau)\beta V.$$

At E_0,

$$\frac{\partial f_1}{\partial I}=\beta S_0+(1-\tau)\beta V_0=\beta\frac{\pi(\mu+\xi)}{\mu(\mu+\xi+\Omega)}+(1-\tau)\beta\frac{\pi\Omega}{\mu(\mu+\xi+\Omega)}=\beta\pi\left(\frac{(\mu+\xi)}{\mu(\mu+\xi+\Omega)}+\frac{(1-\tau)\Omega}{\mu(\mu+\xi+\Omega)}\right)$$

$$\frac{\partial f_1}{\partial I}=\frac{\beta\mathrm{up}(\mu+\xi+\Omega-\tau\Omega)}{\mu(\mu+\xi+\omega)}$$

Differentiating f_2 with respect to E and with respect to I we get

$$\frac{\partial f_2}{\partial E}=0, \frac{\partial f_2}{\partial I}=0$$

$$F=\left(\begin{array}{cc}0 & \frac{\beta\pi(\mu+\xi+\Omega-\tau\Omega)}{\mu(\mu+\xi+\Omega)} \\ 0 & 0\end{array}\right), \hat{V}=\left(\begin{array}{cc}\alpha+\mu & 0 \\ -\alpha & \gamma+\mu+d\end{array}\right).$$

The next generation matrix is $G=F\hat{V}^{-1}$. Thus, the basic reproduction number $\mathcal{R}_{\mathrm{vac}}=\rho(F\hat{V}^{-1})$ ($\rho(\cdot)$ denotes the spectral radius), is given by

$$\mathcal{R}_{\mathrm{vac}}=\frac{\beta\alpha\pi(\mu+\xi+\Omega-\tau\Omega)}{\mu(\alpha+\mu)(\gamma+\mu+d)(\mu+\xi+\Omega)}. \tag{2}$$

3.1 The Disease-Free Equilibrium Point

We obtained the disease-free equilibrium (*DFE*) point, E_0, of system (**??**) by setting the right-hand side of the equation to zero and let $E=I=R=0$. Then, solving for S and V at this state gives:

$$E_0=\left(\frac{\pi(\mu+\xi)}{\mu(\mu+\xi+\Omega)}, \frac{\pi\Omega}{\mu(\mu+\xi+\Omega)}, 0, 0, 0\right).$$

Using Routh-Hurwitz criteria Altahir [14], we proposed the following theorem:

Theorem 3 *The DFE point is locally asymptotically stable if* $\Re_{vac}<1$ *and unstable if* $\Re_{vac}>1$.

Proof The prove of the local stability of disease-free equilibrium is obtained by first computing the Jacobian matrix of the system (1) at the DFEP $\boldsymbol{E_0}$**.** The first three eigenvalues of the Jacobian matrix at the DFEP are $\lambda_1 = -(\mu+\Omega)$, $\lambda_2 = -\mu$, $\lambda_3 = -(\mu+\xi+\Omega)$ while the other two eigenvalues λ_4 and λ_5 are the solutions of the quadratic equation $\mathfrak{F}_0\lambda^2 + \mathfrak{F}_1\lambda + \mathfrak{F}_2 = 0$, where $\mathfrak{F}_0 = 1, \mathfrak{F}_1 = 2\mu+\alpha+\gamma+d$ and $\mathfrak{F}_2 = (\alpha+\mu)(\gamma+\mu+d)(1-\mathcal{R}_{\text{vac}})$. Applying Routh-Hurwitz criteria [16,17,18,19] on this quadratic equation shows that λ_4 and λ_5 have negative real parts. Since all the eigenvalues are either negative or they have negative real parts, it shows that the DFE point is locally asymptotically stable when $\Re_{vac} < 1$ and unstable when $\Re_{vac} > 1$ ■

Theorem 3 reveals a threshold that decides whether COVID-19 may be removed from the population if the bifurcation at $\Re_{vac} = 1$ is a global forward bifurcation. In this scenario, there will always be free disease condition when $\Re_{vac} < 1$. Due to the significance of $\Re_{vac}$ in determining epidemic condition, it will be good to know how $\Re_{vac}$ behave with respect to change in each parameter in (2). In particular

- $\dfrac{d\mathcal{R}_{\text{vac}}}{d\beta} = \dfrac{\mathcal{R}_{\text{vac}}}{\beta} > 0$ shows that if the contact rate is reduced, there will reduction in $\mathcal{R}_{\text{vac}}$ linearly.
- $\dfrac{d\mathcal{R}_{\text{vac}}}{d\alpha} = \dfrac{\mu\mathcal{R}_{\text{vac}}}{\alpha(\alpha+\mu)} > 0$ shows that increasing the treatment rate for exposed individual will reduce $\mathcal{R}_{\text{vac}}$ linearly.
- $\dfrac{d\mathcal{R}_{\text{vac}}}{d\gamma} = -\dfrac{\mathcal{R}_{\text{vac}}}{(\gamma+\mu+d)} < 0$ shows that stepping up the treatment rate of infected individual will course an increase in the chance of eradicating COVID-19 in the population.
- $\dfrac{d\mathcal{R}_{\text{vac}}}{d\tau} = -\dfrac{\Omega\mathcal{R}_{\text{vac}}}{(\mu+\xi+\Omega-\tau\Omega)} < 0$ shows that increasing the vaccine efficacy will reduce $\mathcal{R}_{\text{vac}}$ and therefore increase the chance of eradicating COVID-19 in the population.
- $\dfrac{d\mathcal{R}_{\text{vac}}}{d\Omega} = -\dfrac{\tau(\mu+\xi)\mathcal{R}_{\text{vac}}}{(\mu+\xi+\Omega)(\mu+\xi+\Omega-\tau\Omega)} < 0$ shows that increasing the vaccine coverage rate will reduce $\mathcal{R}_{\text{vac}}$ and therefore increase the chance of eradicating COVID-19 in the population.

However, in previous mathematical models of infectious disease with imperfect vaccine, backward bifurcation and hysteresis have been reported to occur. Under these situations, for certain initial conditions it is possible that disease will persist even when $\Re_{vac} < 1$. To investigate this situation further requires a careful study of the endemic equilibrium points.

3.2 Endemic Equilibrium Point

The endemic equilibrium point (EEP) is given as

$$E_* = \left(S^* = \frac{\pi\left[(1-\tau)\beta I^* + (\mu+\xi)\right]}{A_1 I^{*2} + A_2 I^* + A_3},\ V^* = \frac{\Omega\pi}{A_1 I^{*2} + A_2 I^* + A_3},\right.$$

$$\left. \mathrm{I}^* = \mathrm{I}^*,\ E^* = \frac{(\gamma+\mu+d)I^*}{\alpha},\ R^* = \frac{\gamma I^*}{\mu + (1-\psi)\beta I^*} \right),$$

where

$$A_1 = (1-\tau)\beta^2, A_2 = (\beta(\mu+\xi) + (\mu+\Omega)(1-\tau)\beta), A_3 = \mu(\mu+\xi+\Omega).$$

If we substitute the values of S^*, V^*, E^* and R^* into Eqs. (1), insert the values of A_1, A_2 and A_3 and simplify, then I^* is gotten from the positive roots of the cubic polynomial:

$$f(I) = m_1 I^3 + m_2 I^2 + m_3 I + m_4,$$

where

$$\begin{aligned}
m_1 &= (1-\tau)\beta^3(1-\psi)((\alpha+\mu)(\gamma+\mu+d) - \alpha\gamma),\\
m_2 &= -\alpha\beta^3\pi(1-\psi)(1-\tau) - \gamma(1-\psi)\alpha\beta^2((\mu+\xi) - (\mu+\Omega)(1-\tau))\\
&\quad + (\alpha+\mu)(\gamma+\mu+d)\left(\mu(1-\tau)\beta^2 + (1-\psi)\beta^2(\mu+\Omega)(1-\tau) + (1-\psi)\beta^2(\mu+\xi)\right),\\
m_3 &= -\alpha\beta^2\pi(1-\tau)\mu - (1-\psi)\alpha\beta^2\pi(\mu+\xi) - \gamma(1-\psi)\alpha\beta\mu(\mu+\xi+\Omega) - (1-\tau)\alpha\beta^2\Omega\pi(1-\psi)\\
&\quad + (\beta\mu(\mu+\xi) + \mu(1-\tau)\beta(\mu+\Omega))(\alpha+\mu)(\gamma+\mu+d)\\
&\quad + (1-\psi)\beta\mu(\alpha+\mu)(\gamma+\mu+d)(\mu+\xi+\Omega),\\
m_4 &= \mu^2(\mu+\xi+\Omega)(\alpha+\mu)(\gamma+\mu+d)(1-\mathcal{R}_{vac}).
\end{aligned}$$

The Theorem below proves that there exists at least one endemic equilibrium.

Theorem 4 *When $\Re_{vac} > 1$, there exists at least one endemic equilibrium point in System (1).*

Proof It is clear from the expression m_1 that $m_1 > 0$. Meanwhile from the expression of m_4, if $\Re_{vac} > 1$, $m_4 < 0$. Because $m_1 > 0$, as $I \to \infty$, $f(I) \to \infty$ and as $I \to -\infty$, $f(I) \to -\infty$. When $\Re_{vac}$= 1, $m_4 = 0$ and zero is a root. Therefore, when $\Re_{vac} > 1$ and $m_4 < 0$, the polynomial will be shifted downward to give at least one positive root ■

To show the possibility of backward bifurcation or hysteresis occurring, we need to show that there is a possibility of the existence of another positive equilibrium point when $\Re_{vac} < 1$. Using Descarte's rule of sign [19, 20] the number of possible positive roots of f is summarized in Table 1.

Table 1: Number of Possible Positive Roots According to Descarte's Rule

Cases	m_1	m_2	m_3	m_4	$\mathcal{R}_{vac}$	Sign Changes	Total Possibility of Positive Roots
1	+	−	−	−	$\mathcal{R}_{vac} > 1$	1	1
2	+	+	−	−	$\mathcal{R}_{vac} > 1$	1	1
3	+	+	+	−	$\mathcal{R}_{vac} > 1$	1	1
4	+	−	+	−	$\mathcal{R}_{vac} > 1$	3	3,1
5	+	−	−	+	$\mathcal{R}_{vac} < 1$	2	2,0
6	+	+	−	+	$\mathcal{R}_{vac} < 1$	2	2,0
7	+	−	+	+	$\mathcal{R}_{vac} < 1$	2	2,0
8	+	+	+	+	$\mathcal{R}_{vac} < 1$	0	0

From Table 1, we can deduce the following:

1. A unique endemic equilibrium when $\mathcal{R}_{vac}$ >1 which satisfies case 1–3.
2. One or three endemics equilibrium when $\mathcal{R}_{vac} > 1$ and case 4 is satisfied.
3. Two endemic equilibria when $\mathcal{R}_{vac}< 1$ and this satisfies cases 5–7.
4. There is no endemic equilibrium when $\mathcal{R}_{vac}$ <1 which satisfies case 8.

Hence, the results above suggest the possibility of backward bifurcation or hysteresis when either m_2 or m_3 is negative.

4 Direction of Bifurcation at $\mathcal{R}_{vac} = 1$

From the results in Table 1, we hypothesize three possible scenarios depending on the signs of m_2, m_3 and m_4:

1. Global forward bifurcation (m_2 and m_3 are both positive):
   This phenomenon is the most common bifurcation phenomenon found in many standard mathematical models of disease transmission. It is characterized by a transcritical bifurcation where the locally asymptotically stable DFE changes its stability from stable to unstable at $\Re_{vac} = 1$, and a unique positive locally stable endemic equilibrium which only exists when $\Re_{vac} > 1$ (see Figure 2(a)). From epidemiological perspective, a small endemic state will result when $\Re_{vac}$ increases slightly above 1, in other words, the endemic level at equilibrium is a continuous function of $\Re_{vac}$. Thus, the requirement that $\Re_{vac} < 1$ is not only necessary but also sufficient for the disease elimination.

2. Backward bifurcation at $\Re_{vac} = 1$ (when either $m_2 > 0$ and $m_3 < 0$ or $m_2, m_3 < 0$):
   In this situation, endemic equilibrium can exist when $\Re_{vac} < 1$. More specifically, a bi-stability region exists for $0 < \Re_{vac}^{(c)} < \Re_{vac} < 1$. This happen when a stable endemic equilibrium exists simultaneously with a stable DFE (see Figure 2(b)). As $\Re_{vac}$ increases slightly above 1, a big jump in the number of infectives is observed, creating a hysteresis loop. From epidemiological perspective, once $\Re_{vac}$ crosses unity, it is no longer sufficient to reduce $\Re_{vac}$ to below unity to eradicate the disease. A disease-free state can only be achieved if the value of $\Re_{vac}$ is reduced further to below some critical value $\Re_{vac}^{(c)}$.

3. Forward bifurcation with hysteresis (when $m_2 < 0$ and $m_3 > 0$):
   This situation occurs when a forward bifurcation at $\Re_{vac} = 1$ is combined with a hysteresis loop. As $\Re_{vac}$ increases above 1, a bi-stability region is observed for $1 < \Re_{vac} < \Re_{vac}^{(c2)}$, for some critical value $\Re_{vac}^{(c2)}$. When $\Re_{vac}$ increases slightly above $\Re_{vac}^{(c2)}$, a big jump in the number of infectives is observed, creating a hysteresis loop. In this case, there are two bi-stability regions; the first extends from a critical value $\Re_{vac}^{(c1)}$ $(0 < \Re_{vac}^{(c1)} < 1)$ to $\Re_{vac} = 1$ while the second extends from $\Re_{vac} = 1$ to $\Re_{vac} = \Re_{vac}^{(c2)}$. In the first bi-stability region, a stable endemic equilibrium co-exists with a stable DFE while in the second bi-stability region, a stable endemic equilibrium co-exists with another stable endemic equilibrium (see Figure 2(c)).

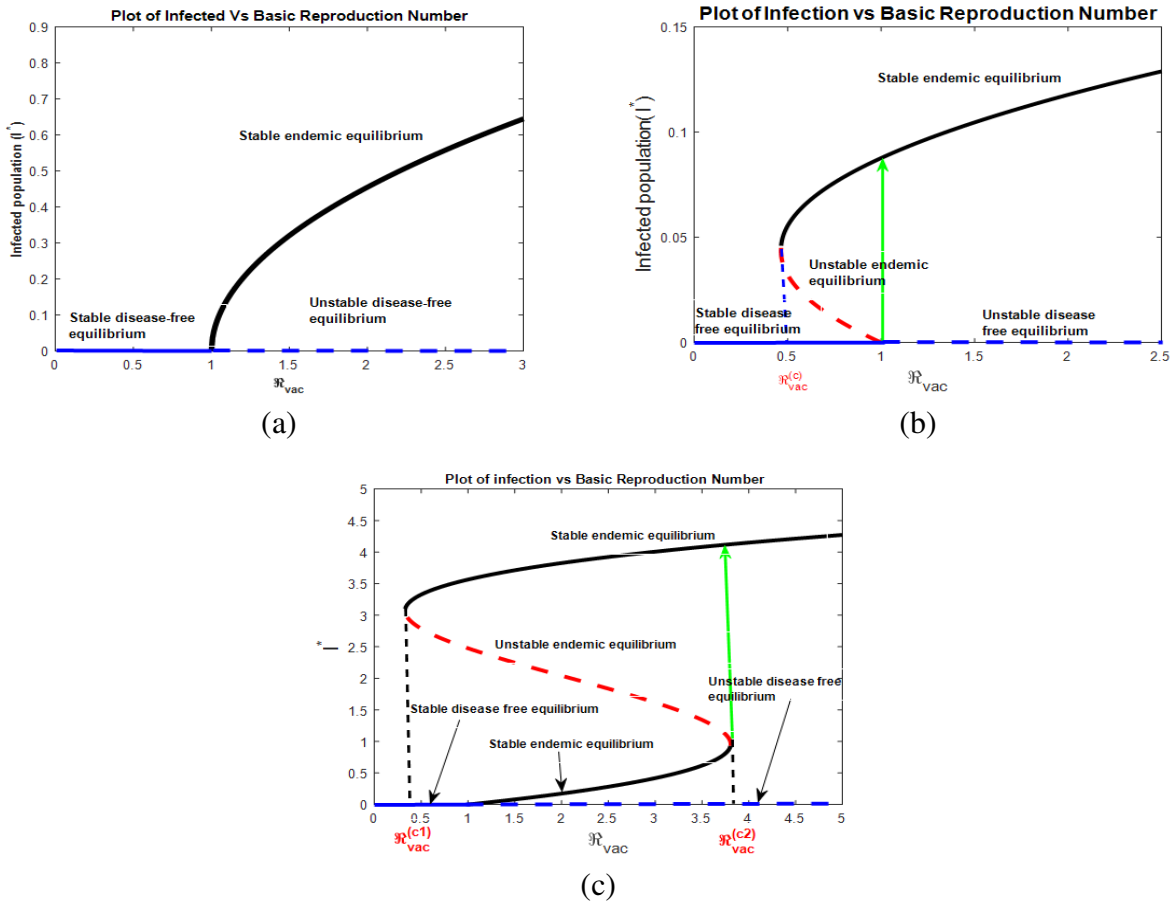


Figure 2:Three Types of Possible Bifurcation from the SVEIRE Model in (1): (a) Shows a Forward Bifurcation when m_2 and m_3 are both positive. (b) Shows a Backward Bifurcation when either $m_2 > 0$ and $m_3 < 0$ or $m_2, m_3 < 0$. (c) Shows a Forward Bifurcation with Hysteresis when $m_2 < 0$ and $m_3 > 0$

5 Numerical Results

To investigate the possible bifurcation phenomenon in the transmission of COVID-19 cases in Malaysia using numerical experiments, parameter values that have been reported to agree with the Malaysian data were used. A list of these values and their description are given in Table 2. In the following subsections, we present the numerical results based on the parameter values in Table 2.

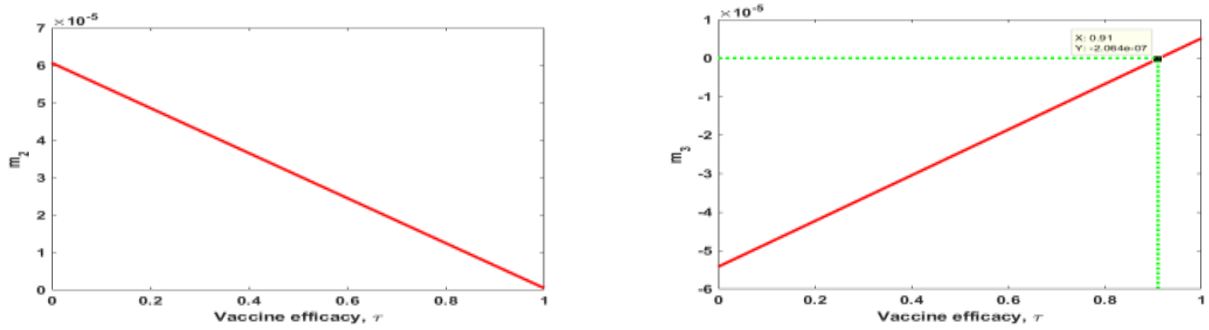
5.1 Signs of m_2 and m_3

From the previous section, we saw that the type of bifurcation is mostly determined by the signs of m_2 and m_3. To investigate the bifurcation phenomenon of the SVEIRE model that is triggered by imperfect vaccine, we use the values of the parameter in Table 2 to analyze the signs of m_2 and m_3 as a function of τ which is the vaccine efficacy.

Table 2: The Parameters and Baseline Values of the Covid-19 Model with Imperfect Vaccine

Parameter	Description	Value	Source
π	Recruitment rate of the susceptible human	0.158	Estimated to be 5 times the percentage of daily tests positive (3.16% on 28 June 2022 [5])
ξ	Rate of vaccine failure	0.01	Assumed
μ	Natural death rate	5.3 per 1000	[10]
Ω	The vaccine coverage rate	0.83	[5]
ψ	Rate of immunological memory loss	0.011	[7]
β	Effective contact rate of susceptible	0.0578	Estimated based on $R_0 = 1.04$ (28 June 2022) [7]
α	The rate of development of clinical symptoms	1/6.5	[14]
γ	Recovery rate of infected individuals	1/18	[15]
d	COVID-19 induced death rate	0.14	[5]

We observe from Figure 3(a) that the values of m_2, computed using the values of the parameters in Table 2 and for $0 < \tau < 1$ are strictly positive. Therefore, we can rule out the possibility of forward bifurcation with hysteresis. Based on Figure 3(b), it shows that m_3 changes sign when $\tau \approx 0.9$, which suggests a transition from global forward bifurcation ($m_3 > 0$) to a backward bifurcation ($m_3 < 0$) as vaccine efficacy reduces to below 90%. Hence, these results provide evidence of the possibility of backward bifurcation (and hysteresis) as vaccine efficacy decreases.



(a) (b)

Figure 3: (a) The Values of m_2, (b) The Values of m_3, as Functions of τ ($0 < \tau < 1$).

5.2 Bifurcation Diagrams for Different Values of τ

Here we plot the bifurcation diagrams for the values of τ as it crosses the critical value of 0.9. We see from Figure 4 that as the vaccine efficacy τ reduces from 0.95 to 0.9, the bifurcation scenario switches

from a forward bifurcation to a backward bifurcation as expected in the previous analysis. Reducing τ further has the effect of reducing the critical value $\Re_{vac}^{(c)}$. In other words, as vaccine efficacy reduces, elimination of COVID-19 will become harder and harder. The situation becomes much worse when τ decreases to 0.821 and less (i.e. less than 82% efficacy) because as can be seen in Figure 4 (e) and (f), a return to disease-free state is longer possible.

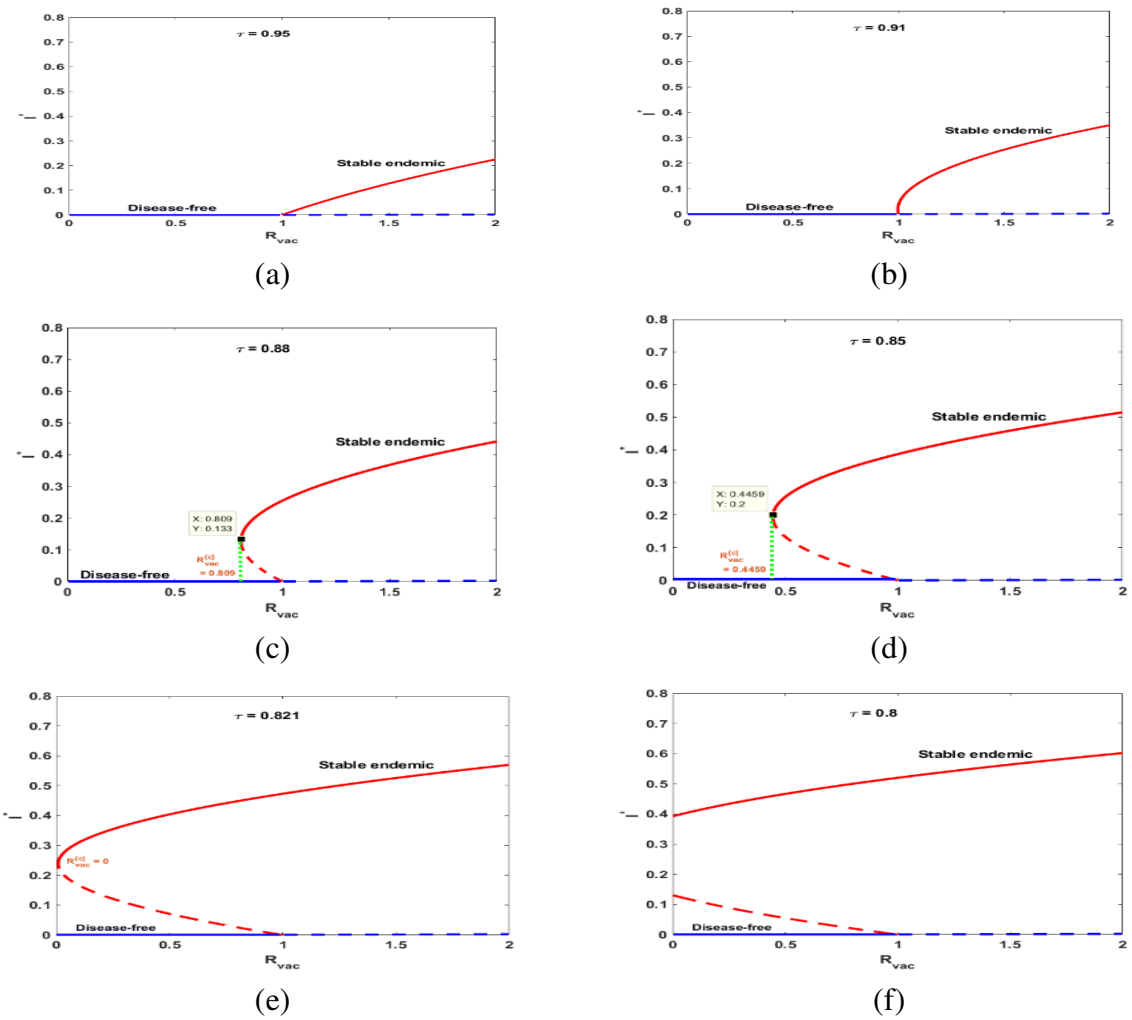


Figure 4: Bifurcation Diagrams for Six Different Efficacy Levels: (a) $\tau = 0.95$. (b) $\tau = 0.91$. (c) $\tau = 0.88$(d) $\tau = 0.85$. (e) $\tau = 0.821$. (f) $\tau = 0.8$

6 Conclusion

We presented, in this paper, a mathematical model of COVID-19 transmission with imperfect vaccination using deterministic approach. The mathematical analysis of the model suggests three different types of bifurcation phenomenon; (1) global forward (2) backward and (**??**) forward with hysteresis. Using parameter values associated with the Malaysian COVID-19 situation, we showed how vaccine efficacy can trigger backward bifurcation in the Malaysian situation. A backward bifurcation will make it a lot harder to control COVID-19 because a critical value of the $\Re_0$ which is much less than 1 is needed to achieve disease-free state.

The basic reproduction number R_0 (R-Naught) (often defined as the ratio β/γ), is one of the main indicators used by the Ministry of Health Malaysia to measure transmissibility of the disease in Malaysia. This is due to the typical believe that the $\Re_0$ is necessary and sufficient to determine the fate of an epidemic. However, imperfect vaccination creates the possibility of a backward bifurcation as shown in this paper. Therefore, controlling R_0 (i.e. controlling contact rate and recovery rate) alone is no longer sufficient to control the transmission of COVID-19.

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References

[1] Fred, B. Backward bifurcations in simple vaccination models. *Journal of Mathematical Analysis and Application*.2004. 298(2): 418–431.

[2] Christopher, M. K., Jorge, X. V. A simple vaccination model with multiple endemic states. *Mathematical Biosciences*. 2000.164(2):183-201.

[3] Abba, B. G. Causes of backward bifurcations in some epidemiological models. *Journal of Mathematical Analysis and Application*.2012. 395(1): 355-365.

[4] Elamin, H. E., Chandrani.N. P., Abba, B. G. Analyzing the dynamics of an SIRS vaccination model with waning natural and vaccine-induced immunity. *Nonlinear Analysis: Real World Application.* 2011. 12(5):2692–2705.

[5] https://ourworldindata.org/covid-vaccinations

[6] https://www.who.int/covid-19/vaccines

[7] Enahoro, A. I., Calistus, N. N., Abba, B. G. Will an imperfect vaccine curtail the COVID-19 pandemic in the U.S.? *Infectious Disease Modelling.* 2020. 5:510-524.

[8] Sheliei, Z. S., Tong, S., Chung, W.Yongbiao, X, Hua, C. Will the large-scale vaccination succeed in containing the covid-19 pandemic and how soon? *Quantitative Biology*. 2021. 9(3):304-316.

[9] Lahbib, B., Mustapha, L., Abdessamad, T., Omar, Z., Mostafa, R. Modeling the Impact of the Imperfect Vaccination of the COVID-19 with Optimal Containment Strategy. *Axioms*. 2022. 11(3): 124.

[10] https://www.macrotrends.net/countries/MYS/malaysia/death-rate

[11] Shakhany,M. Q., Salimifard,K. Predicting the dynamical behavior of COVID-19 epidemic and the effect of control strategies. *Chaos, Soliton and Fractals*. 2021. 146. 110823 .

[12] https://covid-19.moh.gov.my/kajian-dan-penyelidikan/nilai-r-malaysia

[13] Backer, J.A., Klinkenberg,D. Wallinga, J. The incubation period of 2019-nCoV infections among travellers from Wuhan, China. *EuroSurveill*. **25**, 2000062 (2020).

[14] Altahir, A. A., Nirbhay, M., Loshini, T. Ghulam, E.M.A., Radzi, S.S M., Dass,S. C., Gill, B. S., Sebastian, P., Zulkifli,S.A., Asirvadam, V. S. Modeling the Impact of Lock-down on COVID-19 Spread in Malaysia. bioRxiv 2020.07.17.208371; doi: https://doi.org/10.1101/2020.07.17.208371.

[15] Driessche, P. and Watmough, J. Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission. Mathematical Biosciences. 2002 Nov-Dec;180:29-48. doi: 10.1016/s0025-5564(02)00108-6.

[16] Emam, F. 2022. Routh-Hurwitz stability criterion. http://www.aast.edu/cv.php?disp_unit=346 &ser=68525

[17] Tim, D. Introduction to Linear Control Systems.Stability and Routh-Hurwitz Condition. 2020. https://www.ece.mcmaster.ca/~davidson/EE3CL4/slides/Routh_Hur... ·

[18] Jongeun, C. C. Control Systems, Routh-Hurwitz stability criterion https://www.javatpoint.com/ control-system-routh-hurwitz-stability-criterion 2021.

[19] Descartes Rule of Signs. https://www.cuemath.com/algebra/descartes-rule-of-signs.

[20] Descarte's rule of sign. Wikimedia. https://en.wikipedia.org/wiki/Descartes'_rule_of_signs. 2022.