

# An SIR Model Assumption for The Spread of COVID-19 With The Effects of Vaccination

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**Abstract:** Vaccination becomes one of the crucial roles in lessening the impact of this virus on society. Since not much research proposed the model that considers vaccination for the newer infectious disease, COVID-19, this study is to propose a Susceptible-Infected-Recovered (SIR) model to describe the spread of the COVID-19 pandemic with the effects of vaccination. To investigate this impact, it is worth making a comparison between the models without and with vaccination effort in studying the models. In this study, the analytical solutions are derived with the aid of stability analysis. The solutions consist of both numerical and graphical approaches using Maple and MATLAB software. The steady-states, associated eigenvalues, and reproduction number of  $R_0$  and  $R_v$  are calculated, and it showed that disease-free equilibrium and the endemic equilibrium could not exist together. The infection rate and the reproductions numbers are vital factors in the emergence of an epidemic, and this epidemic can be controlled with vaccination. These results concluded that the effect of vaccination is significant in mitigating this virus from spreading unboundedly.

**Keywords:** SIR Model, Stability Analysis, Vaccination, Reproduction Number

## 1. Introduction

Vaccination is one of the important ways to avoid any disease and help maintain our body in good health. According to Understanding How Vaccines Work [1], the vaccine helps create immunity to protect our bodies from infection without causing harmful side effects. It contains antigens that are obtained from part or all of a certain virus or bacterial structure turned off or weakened. Antigens in vaccines act to stimulate the immune system of the body to form immunity against infection of specific diseases. The technology makes vaccine administration more practical and less painful.

According to Asita [2], the current pandemic, COVID-19, is a coronavirus known as SARS-CoV-2. Starting in Wuhan, China, in December 2019, then spread globally, COVID-19 is a contagious infection that can spread when an infected person coughs or sneezes then infect others through droplets of saliva or nasal discharge. This infection is similar to other influenza infections, and complications

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are worse for people who have a weak immune system. Standard Operating Procedure (SOP), such as social distancing and wearing a face mask, has been introduced in the Transmission of SARS-COV-2: Implications for infection prevention precautions (2020) [3], and Movement Control Order (MCO) is also implemented in every country to reduce the COVID-19 infection [4]. However, not all countries' success following the SOP and implementation of MCO has caused other waves of COVID-19 cases. Vaccination seems like the country's best way to curb the spread of COVID-19 [5]. The prime minister is the first to take the vaccination in Malaysia since the vaccination program started in February 2021, aimed to achieve herd immunity against COVID-19 among its citizens and non-citizens residing in the country, targeting over 26 million residents [6]. Herd immunity is protection from infectious disease, and the higher population gets vaccinated, the tougher the virus can infect each other [7].

Mathematical modelling is an important alternative to an abstract model that describes the behavior of a system using mathematical language. Mathematical modelling could be used to study infectious diseases to predict the future of an outbreak and measure the level of uncertainty in these forecasts [8]. In mathematical modelling, an epidemic model such as the SIR model has been widely used for studying and investigating a spread of disease with a compartment of susceptible (S), infected (I) and recovered (R). The model can be modified to study any infectious disease by adding suitable compartments and parameters.

This research studies the assumption of the SIR model to describe the spread of COVID-19, mainly discussed in Chauhan *et al.* [9], where the model considered vaccination effects. The disease-free equilibrium point and endemic equilibrium point of the model are discussed. The local stability analysis of the model is determined by the associated eigenvalues and the basic reproduction number, where the reproduction number is explicitly linked to the vaccination effort.

## 2. Methodology

We investigate the effects of vaccinations on a population using the SIR model approach. The work has also been discussed in Chauhan *et al.* [9]. However, we work out a more detailed analysis of the eigenvalues and the corresponding threshold conditions for the model without vaccination and with vaccination.

### 2.1 SIR Model without Vaccination

This model is considering a model without vaccination and the total population density is assumed as  $R(t) + S(t) + I(t) = 1$  [9]. The mathematical modelling is written as

$$\begin{aligned}\frac{dS}{dt} &= \mu - \beta IS - \mu S, \\ \frac{dI}{dt} &= \beta IS - \gamma I - \mu I, \\ \frac{dR}{dt} &= \gamma I - \mu R,\end{aligned}\tag{Eq. 1}$$

where  $\mu$  is the natural birth and death rate,  $\beta$  is the effective contact rate between susceptible and infected individuals, and  $\gamma$  is the recovery rate of infected individuals. Consider the reduced model

$$\begin{aligned}\frac{dS}{dt} &= \mu - \beta IS - \mu S, \\ \frac{dI}{dt} &= \beta IS - \gamma I - \mu I,\end{aligned}\tag{Eq. 2}$$

where  $R(t)$  is not considered since the value can be derived from the total population density that is  $R(t) = 1 - S(t) - I(t)$ .

### 2.1.1 Stability Analysis of SIR Model without Vaccination

For stability analysis of the model, Maple software is used to find the solutions. Firstly, we need to find the equilibrium point by letting Eq. 2 equal to zero and it is resulting in two equilibrium points that stand for disease-free equilibrium and endemic equilibrium. The following are the solutions obtained for each equilibrium

- i. Disease-free equilibrium:  $(S, I) = (1, 0)$ ,
- ii. Endemic equilibrium:  $(S, I) = (\gamma + \mu\beta, \mu(\beta - \gamma - \mu)\beta(\gamma + \mu))$ .

These solutions will become the steady-state for the system of equations in stability analysis. The Jacobian of the system for Eq. 2 is

$$J = \begin{bmatrix} -\beta I & -\mu & -\beta S \\ \beta I & \beta S & -\gamma - \mu \end{bmatrix}. \tag{Eq. 3}$$

#### i. Disease-free equilibrium

By substituting the steady-state of disease-free equilibrium into Eq. 3, we get the yields of the Jacobian for the disease-free equilibrium is

$$J = \begin{bmatrix} -\mu & -\beta & 0 \\ 0 & \beta & -\gamma - \mu \end{bmatrix}. \tag{Eq. 4}$$

From Eq. 4, the determinant is  $-\mu(\beta - \gamma - \mu)$  and the trace is  $\beta - \gamma - 2\mu$ . To determine the stability of the equilibrium point, the eigenvalues solved from  $-(\mu + \lambda)(\beta - \gamma - \mu - \lambda)$  are

$$\lambda_1 = -\mu, \quad \lambda_2 = \beta - \gamma - \mu. \tag{Eq. 5}$$

All eigenvalues with negative real parts and  $\beta < \gamma + \mu$  are said to be stable. From the determination and trace, we have  $\beta - \gamma - \mu$  same as the result of eigenvalues,  $\lambda_2$  and it can be assumed as reproduction number,  $R_0$ . This endemic equilibrium exists if

$$\beta - \gamma - \mu > 0 \rightarrow R_0 > 1. \tag{Eq. 6}$$

Assume that  $R_0 = \frac{\beta}{\gamma + \mu}$  where  $R_0$  is the reproduction number of the disease-free equilibrium for the SIR model without vaccination.

#### ii. Endemic equilibrium

By substituting the steady-state point of endemic equilibrium into Eq. 3, we obtain the Jacobian matrix as

$$J = \begin{bmatrix} -\frac{\mu(\beta - \gamma - \mu)}{\gamma + \mu} & -\mu & -\gamma - \mu & \frac{\mu(\beta - \gamma - \mu)}{\gamma + \mu} & 0 \end{bmatrix}. \tag{Eq. 7}$$

From Eq. 7, the determinant is  $\mu(\beta - \gamma - \mu)$  and the trace is  $-\frac{\mu(\beta - \gamma - \mu)}{\gamma + \mu} - \mu$  which resulting eigenvalues

$$\lambda_{3,4} = \frac{1}{2} \left[ -\frac{\mu\beta}{\gamma + \mu} \pm \sqrt{\frac{\beta^2\mu^2}{(\mu + \gamma)^2} - 4\mu(\beta - \gamma - \mu)} \right]. \tag{Eq. 8}$$

By substituting  $R_0$  into  $\lambda_{3,4}$ , the eigenvalues become

$$\lambda_{3,4} = \frac{1}{2} \left[ -\mu R_0 \pm \sqrt{\mu R_0 - 4\mu(\beta - \gamma - \mu)} \right] \tag{Eq. 9}$$

The endemic equilibrium point exists only when the reproduction number is  $R_0 > 1$ .

### 2.2 SIR Model with Vaccination

This model is considering a model with vaccination and the total population density is assumed as  $R(t) + S(t) + I(t) + V(t) = 1$  [9]. The mathematical modelling is as follows

$$\begin{aligned} \frac{dS}{dt} &= (1 - p)\mu - \beta IS - \mu S, \\ \frac{dI}{dt} &= \beta IS - \gamma I - \mu I, \\ \frac{dR}{dt} &= \gamma I - \mu R, \\ \frac{dV}{dt} &= p\mu - \mu V, \end{aligned} \tag{Eq. 10}$$

and the reduced model is

$$\begin{aligned} \frac{dS}{dt} &= \mu - \beta IS - \mu S, \\ \frac{dI}{dt} &= \beta IS - \gamma I - \mu I, \\ \frac{dV}{dt} &= p\mu - \mu V. \end{aligned} \tag{Eq. 11}$$

$R(t)$  was assumed as the total population density,  $R(t) = 1 - S(t) - I(t) - V(t)$ .

#### 2.2.1 Stability Analysis of SIR Model with Vaccination

Maple software was used to conduct the stability analysis of the model. Firstly, let Eq. 11 equal to zero to find the equilibrium point. There are two equilibriums for this model, which are disease-free equilibrium and endemic equilibrium. The solutions obtained for each equilibrium that used as steady-states for the system of equations are as follows

- i. Disease free equilibrium:  $(S, I, V) = (1, 0, p)$
- ii. Endemic equilibrium:  $(S, I, V) = (\gamma + \mu\beta, \mu(\beta - \gamma - \mu)\beta(\gamma + \mu), p)$

Therefore, the Jacobian of the system for Eq. 11 is

$$J = \begin{bmatrix} -\beta i - \mu & -\beta s & 0 & \beta i & \beta s & -\gamma & -\mu & 0 & 0 & 0 & -\mu \end{bmatrix} \tag{Eq. 12}$$

##### i. Disease free equilibrium

By substituting the steady-state point of disease-free equilibrium into Eq. 12, we get the Jacobian matrix for the disease-free equilibrium is

$$J = [-\mu - \beta(1 - p) \ 0 \ 0 \ \beta(1 - p) - \gamma - \mu \ 0 \ 0 \ 0 \ -\mu]. \tag{Eq. 13}$$

From Eq. 13, the determinant is  $\mu(\beta - \gamma - \mu)$  and the trace is  $-\mu(\beta - \gamma - \mu)\gamma + \mu - \mu$ . To determine the stability of the equilibrium point, the eigenvalues from solving  $-(\mu + \lambda)^2(\beta p - \beta + \gamma + \lambda + \mu)$  is

$$\lambda_1 = -\mu, \quad \lambda_2 = -\mu, \quad \lambda_3 = \beta(1 - p) - \gamma - \mu. \tag{Eq. 14}$$

To reach stability, the eigenvalues of  $\lambda_1$  and  $\lambda_2$  should have negative real parts where  $\beta(1 - p) < \gamma + \mu$ . By looking at the determination and trace, we have  $\beta(1 - p) - \gamma - \mu$  same as the result of eigenvalues,  $\lambda_3$  where it can be assumed as  $R_v$ .  $R_v$  is defined as new reproduction in the model as vaccination is introduced.

$$\beta(1 - p) - \gamma - \mu < 0 \rightarrow R_v < 1. \tag{Eq. 15}$$

By substituting  $R_0$  into  $R_v$ , the new reproduction number is  $R_v = R_0(1 - p)$ . The endemic equilibrium point exists only when  $R_v < 1$ .

ii. Endemic equilibrium

By substituting the steady-state point of endemic equilibrium into Eq. 12, we get the yields of the Jacobian for the disease-free equilibrium is

$$J = [-\beta i - \mu - \beta s \ 0 \ \beta i \ \beta s - \gamma - \mu \ 0 \ 0 \ 0 \ -\mu]. \tag{Eq. 16}$$

From the Eq. 16, the determinant is  $\mu(\beta p - \beta + \gamma + \mu)$  and the trace is  $-\frac{\mu(\beta p - \beta + \gamma + \mu)}{\gamma + \mu} - 2\mu$  which resulting eigenvalues

$$\lambda_4 = -\mu, \quad \lambda_{5,6} = -\frac{\mu\beta(1 - p)}{\gamma + \mu} \pm \sqrt{\frac{\mu^2\beta^2(1 - p)^2}{(\gamma + \mu)^2} - 4\mu[\beta(1 - p) - \gamma - \mu]}. \tag{Eq. 17}$$

By substituting  $R_v$  into  $\lambda_{5,6}$ , the eigenvalues become

$$\lambda_{5,6} = -\mu R_v \pm \sqrt{\mu^2 R_v^2 - 4\mu(\gamma + \mu)(R_v - 1)}. \tag{Eq. 18}$$

The endemic equilibrium exists if  $\lambda_4$  is the negative real part and the reproduction number,  $R_v$  satisfy the condition  $R_v < 1$ .

**3. Results and Discussion**

We derive the eigenvalues and reproduction number for the equilibrium of both models based on the results from the stability analysis. MATLAB software is used to simulate the time series plot of both models. Next, the value of vaccination rate in the SIR model with vaccination is observed to see how the vaccination affects the populations.

3.1 SIR Model without Vaccination

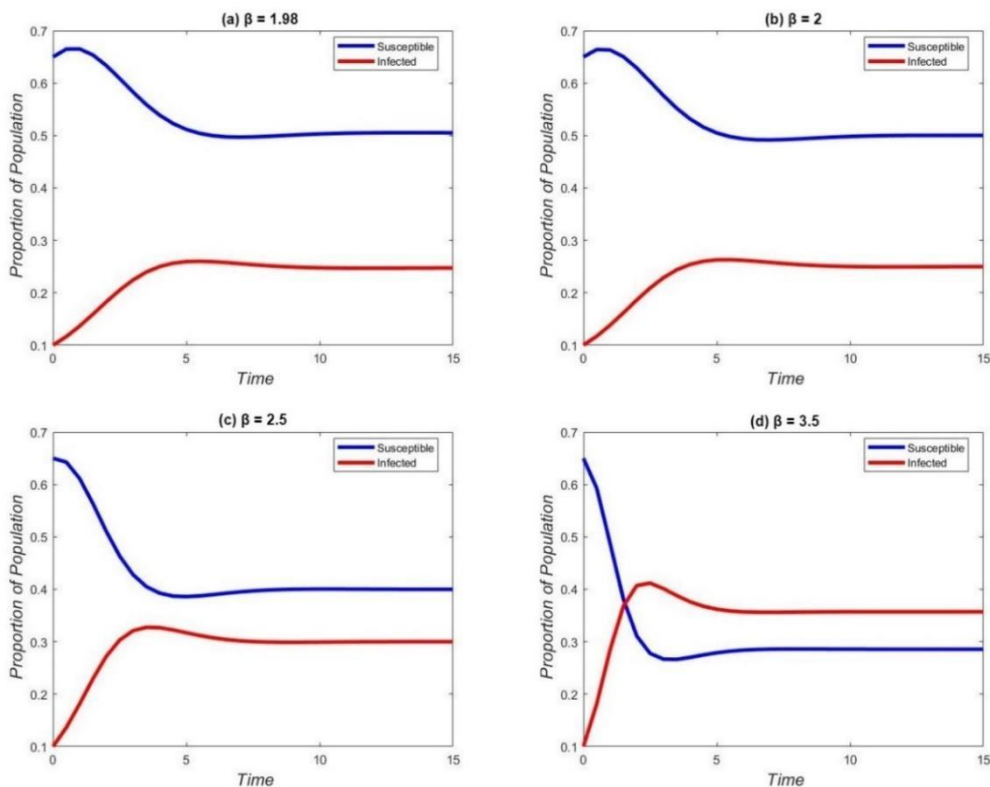
For the model without vaccination (Eq.2), the parameters are  $\beta = 1.98$  and  $\mu = \gamma = 0.5$  [9]. To find stability, the values of  $\beta$  by considering the cases  $\beta > \gamma + \mu$  and  $\beta < \gamma + \mu$ , we have suggested to use  $\beta = 0.9, 1.98$ . Meanwhile,  $\beta = 0.9$  represent the case  $\beta < \gamma + \mu$  and  $\beta = 1.98, 2, 2.5, 3.5$  represent the case  $\beta > \gamma + \mu$  are used to produce the time series plot for the susceptible and infected populations in Figure 3.1. The initial conditions for each population are  $S(0) = 0.65$  and  $I(0) = 0.1$  [9].

Table 3.1 shows when  $\beta = 1.98$ , the disease-free equilibrium is unstable node because there is a mixture of negative and positive real numbers of eigenvalues. We get  $R_0 = 1.98$  and endemic equilibrium is considered stable since it satisfies the condition  $R_0 > 1$  and the eigenvalues are stable

spiral. When  $\beta = 0.9$ , the disease-free equilibrium is stable but endemic equilibrium is not stable since the  $R_0 = 0.9$  is lower than 1.

**Table 3.1: The stability of SIR model (Eq. 2) without vaccination**

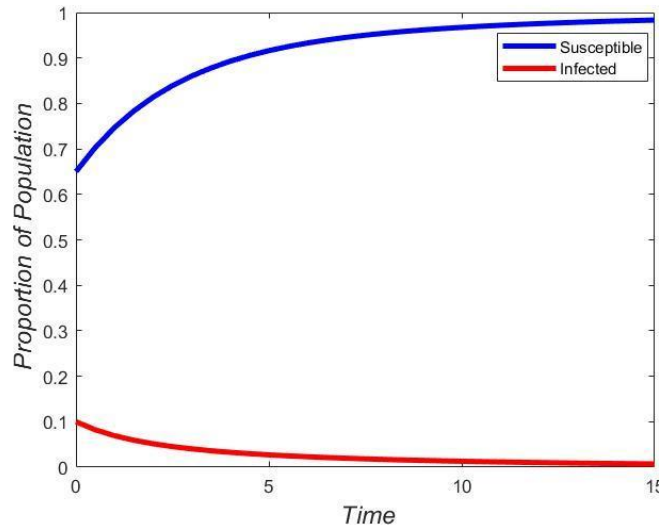
Effective Contact Rate, $\beta$	Equilibrium	Eigenvalues	Stability
1.98	Disease-free	$\lambda_1 = -0.5$ $\lambda_2 = 0.98$	Unstable node for case $\beta > \gamma + \mu$
	Endemic	$\lambda_{3,4} = -0.495 \pm 0.4949i$	Stable spiral for case $\beta > \gamma + \mu$
0.9	Disease-free	$\lambda_1 = -0.5$ $\lambda_2 = -0.1$	Stable node for case $\beta < \gamma + \mu$
	Endemic	$\lambda_3 = 0.0922$ $\lambda_4 = -0.5422$	Unstable node for case $\beta < \gamma + \mu$



**Figure 3.1: SIR model (Eq. 2) without vaccination using different values of effective contact rate,  $\beta > 1$**

From Figure 3.1, the susceptible population,  $S$ , decreases and the infected population,  $I$ , increases as the infection rate increases. Referring to Figure 3.1(d) when  $\beta = 3.5$ , the susceptible population becomes lower than the infected population compared to Figures 3.1(a), (b) and (c) where the infected population gradually increases, and the susceptible population decreases but still higher than the infected population. Figure 3.2 shows that the susceptible population is increasing over time. The

infected population is decreasing to zero where it describes there is no more infected population when disease-free equilibrium is stable.



**Figure 3.2: SIR model (Eq. 2) without vaccination when the effective contact rate,  $\beta = 0.9$**

3.2 SIR Model with Vaccination

The cases of  $\beta > \frac{\gamma + \mu}{1 - p}$  and  $\beta < \frac{\gamma + \mu}{1 - p}$  are considered for this model (Eq. 11). The parameters suggested are  $\beta = 3.5$  and  $\mu = \gamma = 0.5$  [9]. Based on the cases, we used  $\beta = 2, 3.5$  to find the stability. The time series plot for the susceptible, infected, and vaccinated population are stimulated in Figure 3.3 by using the values of  $\beta = 1.5, 2$  represent the case  $\beta < \frac{\gamma + \mu}{1 - p}$  and  $\beta = 3.5, 5$  represent the case  $\beta > \frac{\gamma + \mu}{1 - p}$ . The initial conditions for each population are  $S(0) = 0.65, I(0) = 0.1$  and  $V(0) = 0.2$  [9].

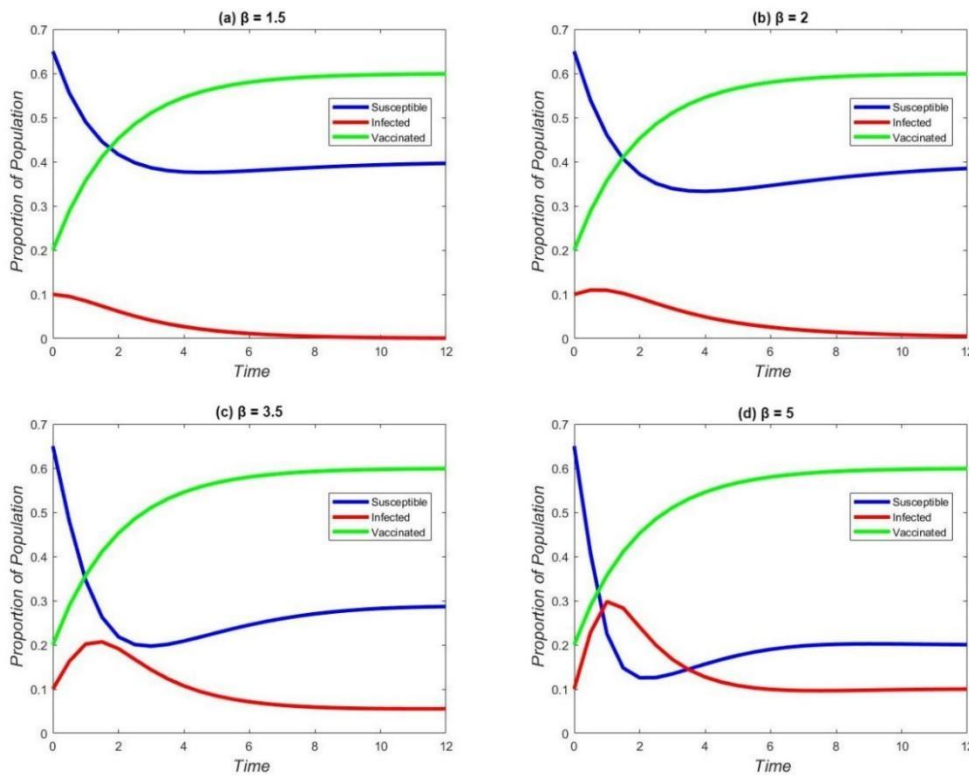
**Table 3.2: The stability of SIR model (Eq. 11) with vaccination**

Effective Contact Rate, $\beta$	Equilibrium	Eigenvalues	Stability
3.5	Disease-free	$\lambda_1 = -0.5$ $\lambda_2 = -0.5$ $\lambda_3 = 0.4$	Unstable node for case $\beta > \frac{\gamma + \mu}{1 - p}$
	Endemic	$\lambda_4 = -0.5$ $\lambda_{5,6} = -0.35 - 0.2784i$	Stable for case $\beta > \frac{\gamma + \mu}{1 - p}$
2	Disease-free	$\lambda_1 = -0.5$ $\lambda_2 = -0.5$ $\lambda_3 = -0.2$	Stable node for case $\beta < \frac{\gamma + \mu}{1 - p}$
	Endemic	$\lambda_4 = -0.5$ $\lambda_5 = -0.5742$	Unstable node for case: $\beta < \frac{\gamma + \mu}{1 - p}$

$$\lambda_6 = 0.1742$$

From Table 3.2 when  $\beta = 3.5$ , the eigenvalues of disease-free equilibrium resulting a mixture of positive and negative real numbers. This means the disease-free equilibrium is an unstable node. The calculation new reproduction number,  $R_v$  when  $R_0 = 1.98$  resulting  $R_v = 0.792$ . Since  $R_v < 1$  and eigenvalues resulting a stable node and stable spiral, the endemic equilibrium is stable. When  $\beta = 2$ , we get all eigenvalues are negative real numbers and allow the disease-free equilibrium to exist. Calculating the  $R_v$  when  $R_0 = 0.9$  will be resulting  $R_v = 0.36$  and satisfy the condition  $R_v < 1$  but the endemic equilibrium cannot exist since the eigenvalues have a mixture of negative and positive real numbers to become unstable node.

Figures 3.3(a) and (b) represent the graph when  $\beta < \frac{\gamma + \mu}{1 - p}$  while Figure 3.3(c) and (d) represent the graph when  $\beta > \frac{\gamma + \mu}{1 - p}$ . The figure showed that the infected population keeps increasing as values of  $\beta$  become higher even when the vaccination rate was introduced. The susceptible population declines to more than half of its level and the infected population decreases.



**Figure 3.3: SIR model (Eq. 11) with vaccination using different values of effective contact rate,  $\beta$**

### 3.2.1 Vaccination Effects to the Population

The value of vaccination rate,  $p$  are then assumed to other values to see how the vaccination can affect the population when endemic equilibrium exists. The new values are assumed based on the total population where then we are suggesting the values is  $p < 1$ . By using parameters of  $\beta = 3.5$  and  $p = 0, 0.2, 0.4, 0.6$ , the time series plot is produced in Figure 3.4.

Referring to Figure 3.4, the susceptible population keeps decreasing even though the vaccination rate has changed. Figures 3.4(a), (b) and (c) show that the infected population increases but in Figure 3.4(a), the susceptible and infected population moves to half of its level since there is no vaccination



effort. Meanwhile, Figures 3.4(d) show that the infected population declines lower than the initial values.

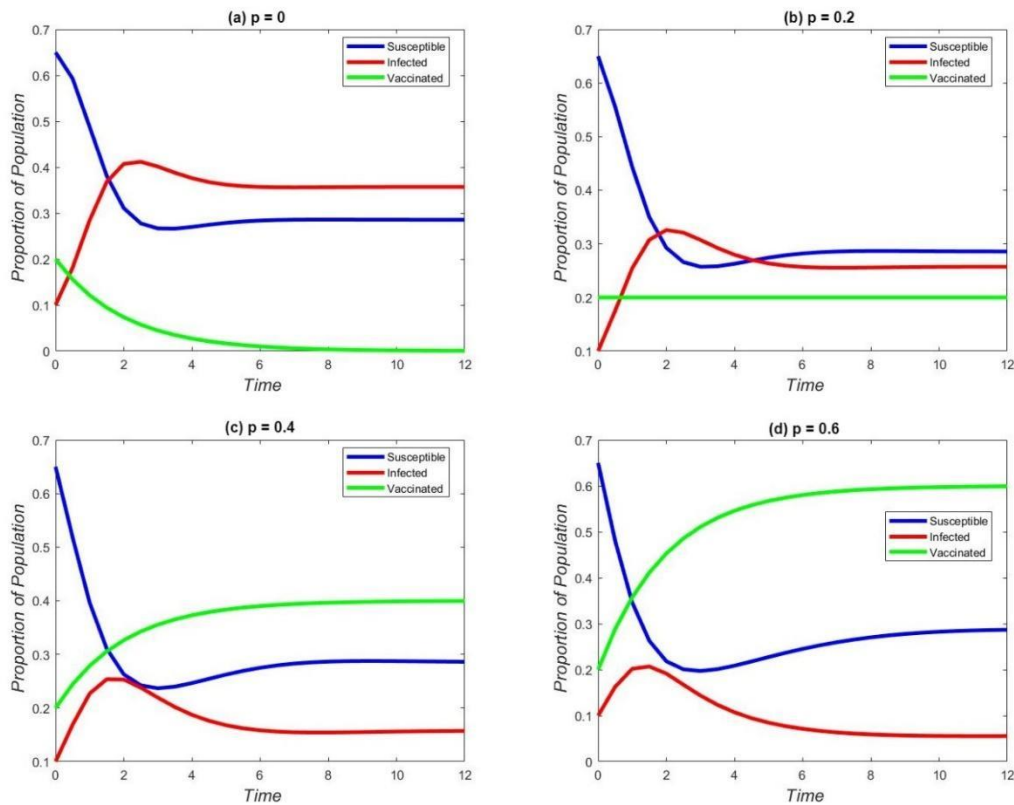


Figure 3.4: SIR model (Eq. 11) with vaccination using different values of vaccination rate,  $p$

#### 4. Conclusion

Both with and without vaccination models to describe the spread of COVID-19 by considering vaccination have been discussed in this study. For the SIR model without vaccination, the stability for disease-free equilibrium is unstable saddle point when  $\beta > \gamma + \mu$ . Meanwhile,  $R_0 > 1$  and all stable node eigenvalues allow endemic equilibrium to exist. Next, for the SIR model with vaccination, there is one eigenvalue that is an unstable node for diseases-free equilibrium when  $\beta > \frac{\gamma + \mu}{1 - p}$  while endemic equilibrium is considered stable since  $R_v < 1$ . But when the case changed to  $\beta < \gamma + \mu$ , all eigenvalues of disease-free equilibrium in the SIR model without vaccination resulting stable node. The endemic equilibrium in the SIR model without vaccination is not stable since the  $R_0 < 1$ . For SIR model with vaccination, when  $R_v > 1$ , the endemic equilibrium is unstable. However, the disease-free equilibrium is stable since the  $\beta < \frac{\gamma + \mu}{1 - p}$ . It can be concluded that the disease-free equilibrium and endemic equilibrium cannot be exist together when the case  $\beta > \gamma + \mu$  or  $\beta < \gamma + \mu$  and case  $\beta > \frac{\gamma + \mu}{1 - p}$  or  $\beta < \frac{\gamma + \mu}{1 - p}$ .

In the comparison of simulation, the SIR model without vaccination showed that a higher effective contact rate between susceptible and infected individuals could make the susceptible population decline until lower than the infected population as the infection is introduced. For the SIR model with vaccination, the induce of vaccination and higher effective contact rate causes the susceptible population to decrease and the infected population to increase. Based on the observations on vaccination rate for endemic equilibrium, the higher the vaccination rate, the higher the possibility to overcome infectious diseases.

As a conclusion, we may conclude that the infection rate and reproduction number are extremely crucial factors in the occurrence of an epidemic and that this epidemic can be prevented through vaccination. Furthermore, the SIR model with vaccination can be extended by introducing new parameters such as targeted individuals to be vaccinated to see if it can affect the reproduction number and the possibility of the disease-free equilibrium and endemic equilibrium can exist together.

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