

A Compartmental Model for Assessing Effects of COVID-19 Vaccination in Thailand

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Abstract A dynamical model for COVID-19 spread relating to non-pharmaceutical interventions and vaccination is mathematically generated by adding a gradual vaccination compartment for the susceptible population and considering only a symptomatic infectious stage. In our model, there are seven compartments dividing a given population into susceptible (S), vaccinated (V), exposed (E), infected (I), quarantined (Q), recovered (R) and death (D) groups, respectively. Then, theoretical analysis is given by investigating the COVID-19 free and endemic equilibrium points, and computing the vaccination reproduction number of this model denoted as R_{vac} using the next generation matrix. If $R_{vac} > 1$, then the COVID-19 transmission increases exponentially and depends on vaccine efficacy. On the other hand, if $R_{vac} < 1$, then there occurs the COVID-19 disease eradication. The risk from infection can be importantly reduced whenever the intake of COVID-19 vaccines exceeds one dose. The numerical results reveal that the nonpharmaceutical ways and the administered COVID-19 vaccines can be effective against the current variants of COVID-19, and the additional efforts such as a third vaccine booster shot should be considered and implemented to greatly mitigate the risks of emerging variants of the COVID-19 virus. Moreover, combining different types of COVID-19 vaccines can be appeared as a possible way to give better protection against COVID-19 as well.

Keywords COVID-19 Vaccination, Disease-free Equilibrium, Endemic Equilibrium, Mathematical Model, Vaccination Reproduction Number

1 Introduction

Thailand documented its first COVID-19 case on the 13th of January 2020. To reduce the havoc caused by the pandemic on its people, the Thai government assisted its citizens in several ways including a stimulus package with 1.9 trillion-baht (US\$60 billion) [1]. After more than a year of ongoing cycles of imposing various travel restrictions (international and provincial) to suppress the pandemic, Thailand is yet to fully recover economically as the pandemic has heavily disrupted the tourism sector that contributes the most to the country's economy. As of the 31st of December 2021, about 2,220,324 confirmed cases and 21,698 deaths had been documented [2], for a population of 69.8 million inhabitants [3].

On the 7th of June 2021, the Thai government commenced its mass vaccination campaign [4]. As of the 27th of December, at least 73.1% (51,032,649) of the total population has received at least one vaccine dose, 65.1% (45,423,045) were fully vaccinated, and 8.9% (6,226,249) has received a booster shot. COVID-19 vaccinations have declined from the highest government stimulus in late September and early October. Booster shots were quite rare in September when they are mainly given to medical and frontline workers and to those who have to travel abroad. However, with the recent Omicron variant becoming a concern worldwide [5], booster shots have been concentrated by different governments' vaccination efforts, especially as reporting shows

that two doses of most vaccines are not very effective against the new Omicron variant. However, a booster shot from the most brands has been noticed to spread the protection against Omicron [6] significantly.

As COVID-19 vaccines are still being administered in different regions of the world, formulating and analyzing a COVID-19 mathematical model remains the focus of many researchers. Alvarez et al. [7] investigated the importance of vaccination rates to contain COVID-19 in urban areas. The model formulated in their study includes social distancing demography, the efficacy of massive testing and quarantine, and coverage and rate of vaccination. Yavuz et al. [8] formulated a new mathematical model comprising a five-dimensional compartmental system for the COVID-19 pandemic to assess the epidemic course if all restrictions are gradually eased and if variants of concern are introduced. The model included a vaccination campaign. They also assessed the impacts on COVID-19 incidence of different levels of vaccine coverage, duration for vaccine scale-up, and different schedules for easing social distancing restrictions. Angeli et al. [9] gave a COVID-19 model associated with the effects of the vaccination campaign in order to show the evolution of the disease and how it is affected by the current vaccination effort. Some other recent studies of COVID-19 vaccinations can be found in the references [10, 11, 12].

Thus, in this article, we present a COVID-19 compartmental model associated with some important biological and epidemiological characteristics in order to identify the vaccination effects and non-pharmaceutical interventions in Thailand. According to our knowledge, the first in-depth study which combines vaccination with non-pharmaceutical interventions in Thailand by using nonlinear ordinary differential equations is given. For the rest of this paper, it provides the following details. We formulate a model in section 2. Section 3 presents the model analysis. In section 4, we report the details of simulation results. For the last section, we give the conclusion of this research.

2 Mathematical formulation of the model

Recently, Riyapan et al. [13] generated a COVID-19 mathematical model by considering a case study of Bangkok in Thailand. Here, we adapt the model of Riyapan et al. [13] by adding a vaccination compartment and considering only symptomatic infectious stage. The total population of the model is divided into the seven compartments given in Table 1. The assumptions for

Table 1. Descriptions of all variables which appear in the formulated model.

Variable	Description
S	the susceptible compartment
V	the vaccinated compartment
E	the exposed compartment
I	the infected compartment
Q	the quarantine compartment
R	the recovered compartment
D	the death compartment

generating the model are presented by these details:

- The entire population considered in this study is non-constant. Therefore, all compartments consist of inflow, outflow, and death.
- Individuals infected with COVID-19 are considered to be also symptomatic.
- For the recovered compartment, we consider that the individuals recovered from COVID-19 infection either through quarantine or hospitalization.
- Susceptible individuals can be vaccinated.
- The doses of vaccine intake reduce the risk of COVID-19 infection.

Table 2. Symbols and definitions of parameters.

symbol	explanation
λ	the rate at which individuals move into the susceptible compartment
β	the rate of transmission
ψ	the proportion of individuals who wear a face mask
ξ	the face mask efficacy
α_I	the rate at which infected individuals are isolated
λ_I	the rate at which infected individuals recover
δ_I	the rate of COVID-19 mortality for individuals in the infected compartment
λ_q	the rate at which individuals in the quarantine compartment recover
δ_q	the rate of COVID-19 mortality for individuals in the quarantined compartment
η	the vaccination rate
θ	incubation period
ϖ	the reduction infection risk as a result of vaccination
μ	the rate of natural death for all individuals

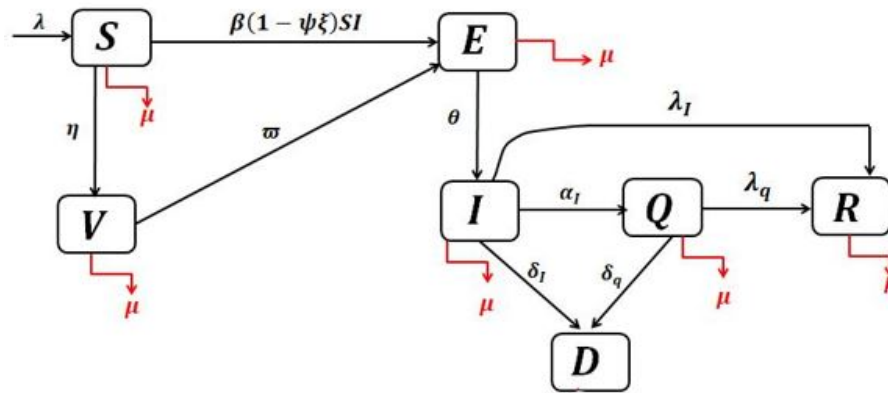


Figure 1. A flowchart for describing the model formulation.

Combining the assumptions and parameter variables, the model described by a flowchart in Figure 1 can be generated as follows.

$$\begin{aligned}
 \frac{dS}{dt} &= \lambda - \beta(1 - \psi\xi)SI - \eta S - \mu S, \\
 \frac{dV}{dt} &= \eta S - \varpi\beta VI - \mu V, \\
 \frac{dE}{dt} &= \varpi\beta VI + \beta(1 - \psi\xi)SI - (\theta + \mu)E, \\
 \frac{dI}{dt} &= \theta E - (\alpha_I + \delta_I + \lambda_I + \mu)I, \\
 \frac{dQ}{dt} &= \alpha_I I - (\lambda_q + \delta_q + \mu)Q, \\
 \frac{dR}{dt} &= \lambda_I I + \lambda_q Q - \mu R, \\
 \frac{dD}{dt} &= \delta_I I + \delta_q Q.
 \end{aligned}
 \tag{1}$$

Let $P(t)$ be the total population of this system. So $P(t) = S(t) + V(t) + E(t) + I(t) + Q(t) + R(t) + D(t)$, for all $t \geq 0$. Then

$$\frac{dP}{dt} = \frac{dS}{dt} + \frac{dV}{dt} + \frac{dE}{dt} + \frac{dI}{dt} + \frac{dQ}{dt} + \frac{dR}{dt} + \frac{dD}{dt} = \lambda - \mu P.
 \tag{2}$$

From (2), this gives that $P(t) \rightarrow \frac{\lambda}{\mu}$ as $t \rightarrow \infty$. So the model (1) is biologically and epidemiologically meaningful. It has been considered in the invariant region:

$$\Omega_v = \{(S, V, E, I, Q, R, D) \in \mathfrak{R}_+^7 : 0 \leq S + V + E + I + Q + R + D \leq \frac{\lambda}{\mu}\}.
 \tag{3}$$

3 Model analysis

Here, we would like to give the properties of the dynamical model (1) as the following details.

3.1 Non-negativity property of the solutions

Theorem 3.1. *If $S_0 \geq 0, V_0 \geq 0, E_0 \geq 0, I_0 \geq 0, Q_0 \geq 0, R_0 \geq 0$ and $D_0 \geq 0$, then all solutions of the system of the model (1) are non-negative for all $t > 0$.*

Proof. The first equation in (1) can be described below as

$$\frac{dS}{dt} = \lambda - \beta(1 - \psi\xi)SI - \eta S - \mu S \geq -\beta(1 - \psi\xi)SI - \eta S - \mu S \geq -\mu S. \tag{4}$$

Integrating equation (4), we obtain

$$S(t) \geq S_0 e^{-\mu t} \geq 0. \tag{5}$$

Therefore, $S(t)$ is non-negative for all $t \geq 0$. The other equations in model (1) can be similarly expressed as the first equation. Thus, we can obtain $V(t) \geq 0, E(t) \geq 0, I(t) \geq 0, Q(t) \geq 0, R(t) \geq 0$ and $D(t) \geq 0$. \square

3.2 The boundedness of the solutions

Theorem 3.2. *All bounded solutions with non-negative initial conditions in the formulated model are shown and $P(t) \leq \frac{\lambda}{\mu}$ for all $t > 0$.*

Proof. To do this by combing all equations in model (1), we can write the population growth rate as follows:

$$\frac{dP}{dt} = \frac{dS}{dt} + \frac{dV}{dt} + \frac{dE}{dt} + \frac{dI}{dt} + \frac{dQ}{dt} + \frac{dR}{dt} + \frac{dD}{dt}. \tag{6}$$

From equation (6), the following equation can be obtained:

$$\frac{dP}{dt} = \lambda - \mu P. \tag{7}$$

Next, we consider the equation (7) by integrating both sides of it, this provides the solution for $P(t)$ with the following details.

$$\frac{dP}{dt} = \frac{\lambda}{\mu} - \left(P_0 - \frac{\lambda}{\mu}\right) e^{-\mu t}. \tag{8}$$

Therefore, when $t \rightarrow \infty$, we obtain

$$P(t) \leq \frac{\lambda}{\mu}. \tag{9}$$

From Theorem 3.1 and equation (9), we can obtain $0 \leq P(t) \leq \frac{\lambda}{\mu}$. Therefore, the boundedness of all solutions and the proof of Theorem 3.2 are established. \square

3.3 Disease-free equilibrium point and vaccination reproduction number of model (1)

The disease-free equilibrium point $\chi^* = (S^*, V^*, E^*, I^*, Q^*, R^*, D^*)$ of model (1) can be generated by taking all derivatives to zero with $I = 0$, which gives equation (10):

$$\chi^* = \left(\frac{\lambda}{\eta + \mu}, \frac{\lambda}{\mu(\eta + \mu)}, 0, 0, 0, 0, 0 \right) \tag{10}$$

Next, we calculate the vaccination reproduction number of the formulated model via applying the next generation matrix idea [14]. Suppose that $Y = (E, I)^T$ then, the model is expressed by the following steps:

$$Y = G(Y) - H(Y), \tag{11}$$

where $G(Y) = (\beta(1 - \psi\xi)SI + \varpi\beta VI, 0)^T$ and $H(Y) = ((\theta + \mu)E, -\theta E + (\alpha_I + \delta_I + \lambda_I + \mu)I)^T$. The corresponding Jacobian matrices of $G(Y)$ and $H(Y)$ at the disease-free equilibrium point are

$$F = \begin{pmatrix} 0 & \beta(1 - \psi\xi)S^* + \varpi\beta V^* \\ 0 & 0 \end{pmatrix} \quad \text{and} \quad W = \begin{pmatrix} \theta + \mu & 0 \\ -\theta & \alpha_I + \delta_I + \lambda_I + \mu \end{pmatrix}.$$

According to Nishiura in 2010 [14], we calculate the vaccination reproduction number \mathcal{R}_{vac} using the spectral radius of the next generation matrix FW^{-1} which yields

$$\mathcal{R}_{vac} = \frac{\theta\beta(1 - \psi\xi)}{(\theta + \mu)(\alpha_I + \delta_I + \lambda_I + \mu)}(S^* + \varpi V^*), \tag{12}$$

where $S^* = \frac{\lambda}{\eta + \mu}$ and $V^* = \frac{\lambda}{\mu(\eta + \mu)}$.

Hence, the vaccination reproduction number of model (1) can be shown in equation (12). Equation (12) provides the number of secondary cases which can likely arise from the only infected individual in a completely susceptible population [15]. It will be applied to measure the transmission potential of COVID-19. An epidemic will likely increase exponentially if $\mathcal{R}_{vac} > 1$, and reduce if $\mathcal{R}_{vac} < 1$.

From equation (12), we can obtain \mathcal{R}_0 , which is the secondary cases that can likely arise from the only infected individual in a completely susceptible population without vaccination:

$$\mathcal{R}_0 = \frac{\lambda\theta\beta(1 - \psi\xi)}{\mu(\theta + \mu)(\alpha_I + \delta_I + \lambda_I + \mu)}. \tag{13}$$

3.4 Endemic equilibrium point

In this part, we focus on the existence of the endemic equilibrium point when $\mathcal{R}_0 > 1$. Suppose that $\chi^{**} = (S^{**}, V^{**}, E^{**}, I^{**}, Q^{**}, R^{**}, D^{**})$ is the endemic equilibrium point of the model (1), then χ^{**} can be computed by taking all derivatives of the equations in model (1) to zero as described below:

$$\begin{aligned} \lambda - \beta(1 - \psi\xi)S^{**}I^{**} - \eta S^{**} - \mu S^{**} &= 0, \\ \eta S^{**} - \varpi\beta V^{**}I^{**} - \mu V^{**} &= 0, \\ \beta(1 - \psi\xi)S^{**}I^{**} + \varpi\beta V^{**}I^{**} - (\theta + \mu)E^{**} &= 0, \\ \theta E^{**} - (\alpha_I + \delta_I + \lambda_I + \mu)I^{**} &= 0, \\ \alpha_I I^{**} - (\lambda_q + \delta_q + \mu)Q^{**} &= 0, \\ \lambda_I I^{**} + \lambda_q Q^{**} - \mu R^{**} &= 0, \\ \delta_I I^{**} + \delta_q Q^{**} &= 0. \end{aligned} \tag{14}$$

Thus from equations (14), we can get χ^{**} :

$$\begin{aligned} S^{**} &= \frac{\lambda}{\beta(1 - \psi\xi)I^{**} + \eta + \mu}, \\ V^{**} &= \frac{\eta S^{**}}{\varpi\beta I^{**} + \mu}, \\ E^{**} &= \frac{\beta(1 - \psi\xi)S^{**}I^{**} + \varpi\beta V^{**}I^{**}}{\theta + \mu}, \\ I^{**} &= \frac{\theta E^{**}}{\alpha_I + \delta_I + \lambda_I + \mu}, \\ Q^{**} &= \frac{\alpha_I I^{**}}{\lambda_q + \delta_q + \mu}, \\ R^{**} &= \frac{\lambda_I I^{**} + \lambda_q Q^{**}}{\mu}, \\ D^{**} &= 0. \end{aligned} \tag{15}$$

4 Numerical simulations

In this section, we show the numerical simulations carried out in this study. Firstly, numerical simulations were presented in order to explore the short term dynamics of the COVID-19 spread (disease-free and endemic equilibrium points). Next, we compare a hypothetical scenario which COVID-19 starts to overspread within a community that has some of its individuals vaccinated and another community without vaccination. Lastly, we explore the vaccine effects used in Thailand to determine how many secondary infections will arise from a single individual if different dosage intakes are considered. The model parameter values used for the numerical simulation, their description and references are provided in Table 3. In a situation where a parameter value is not available from literature, realistic values are assumed for the purpose of illustration.

Table 3. Parameter values and their sources.

Model parameters	Parameter values	Source
λ	20	-
β	assumed	-
ψ	0.1	[16]
ξ	0.5	[16]
α_I	0.20	[17]
λ_I	0.10	[17, 18]
δ_I	0.25	[18]
λ_q	0.13978	[17, 18]
δ_q	0.015	[17]
η	0.02202643	[19]
θ	0.5	[20, 21]
ϖ	0.30–0.88	[19]
μ	9.9259×10^{-3}	[22]

4.1 The COVID-19 short-term dynamics

Here, we consider the COVID-19 short term dynamics by simulating the disease free equilibrium (DFE) and endemic equilibrium points (EE), respectively. From Table 3, we use parameter values to explore the dynamics when no single individual is infected in a population (DFE), this can be presented in the first subfigure in Figure 2 and when a single individual in an entirely safe population is infected with COVID-19 (EE), this can be described in the second subfigure in Figure 2. In Figure 2, the first case shows that an increasing number of the susceptible and vaccinated compartments without COVID-19 infection while other compartments remain steady since the beginning of time. The second case of this figure presents that the number of people who got vaccination slightly decline compared with other compartments.

The basic reproduction number \mathcal{R}_0 , indicating both scenarios mentioned above (DFE and EE), are $\mathcal{R}_0 = 0.678 < 1$ and $\mathcal{R}_0 = 1.457 > 1$, respectively. In Figure 2, if there is no infection, then there is no one to be infected even if an individual within the population is not vaccinated (the first subfigure). However, the reverse is shown in Figure 2 (the second subfigure), where a single infected individual can lead to more infections.

4.2 Community vaccination

In this part, we focus on the hypothetical scenario which COVID-19 starts to spread within a community that has most of its individuals vaccinated and another community without vaccination. The plots obtained from this simulation are presented in Figure 3.

In Figure 3, the plots show that lack of vaccination of susceptible and exposed individuals could lead to a more significant prevalence of COVID-19 within a country (the first subfigure). This further confirms that adequate vaccination campaigns in all communities (both rural and urban) are an excellent way to reduce the risk posed by the COVID-19 pandemic. This can be described by the second subfigure in Figure 3.

4.3 Exploring different vaccination dosages using vaccination reproduction number

In order to understand the extent to which vaccination is effective, we explore the different vaccination doses. Though Thailand has administered different vaccines (Sinovac, AstraZeneca, Pfizer, Moderna) to its population, the highest number of vaccines administered is for AstraZeneca [23]. Thus, in this study, the vaccine efficacy considered for the simulation is set for AstraZeneca. Three vaccination scenarios (no dosage, one dosage and two dosage intakes) together with the parameter values in Table 1 were used for simulation. For the computation, two parameters are considered: η (vaccination rate) and ϖ (expected decrease in the risk of infection due to vaccination). For no vaccine dosage intake, it means that the vaccination rate and the expected decrease in the risk of infection as a result of vaccination are zero. No dosage, one dosage and two dosage intakes, respectively, are represented by $\varpi = 0\%$, $\varpi = 31 - 51\%$ and $\varpi = 59.8 - 87.9\%$ effective [19]. The results presented in Table 4 indicate that taking two dosages will greatly reduce the number of infections that can occur within the population.

5 Conclusion

This study used a modified SEIR model to simulate the conditions with and without the vaccination program and at various vaccine efficacy levels for the COVID-19 pandemic. The model applies minimal modification to the model proposed in the

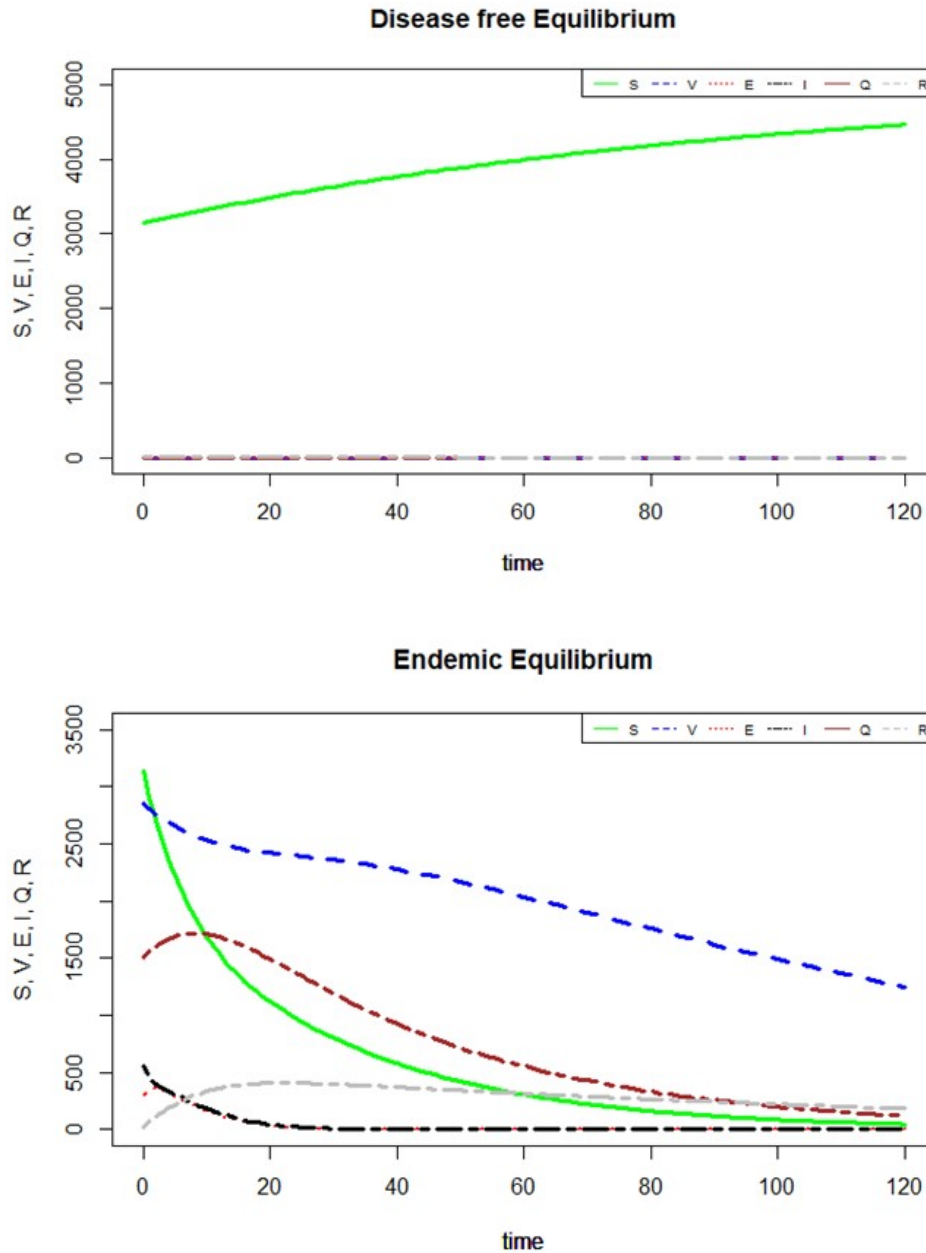


Figure 2. The results for the short-term dynamics of the COVID-19 spread when there is no single infection (the first subfigure) and when there is an infection (the second subfigure).

Table 4. Different vaccination scenarios explored in this study using the basic reproduction number obtained from our model.

Number of vaccine dosage	Expected decrease in COVID-19 cases due to vaccination	Vaccine reproduction number
No dosage intake	0%	$\mathcal{R}_{vac} = 3.368 > 1$
One dosage intake	31 – 51%	$\mathcal{R}_{vac} = 1.069 > 1$
Two dosages intake	59.8 – 87.9%	$\mathcal{R}_{vac} = 0.537 < 1$

study of Riyapan et al. [13] by considering only a single infectious stage and adding a gradual vaccination for the susceptible population. The results have shown that vaccination makes a significant difference in combating the pandemic. With the ongoing global vaccination campaign, there is a need for every individual to be vaccinated, most especially with the recent Omicron variant becoming a concern worldwide [5]. With the obtained results in Table 4, it is evident that taking booster shots will further reduce the risk of being infected.

Based on vaccination rollout so far in Thailand, we can conclude that it has been very beneficial and has lessened the risk

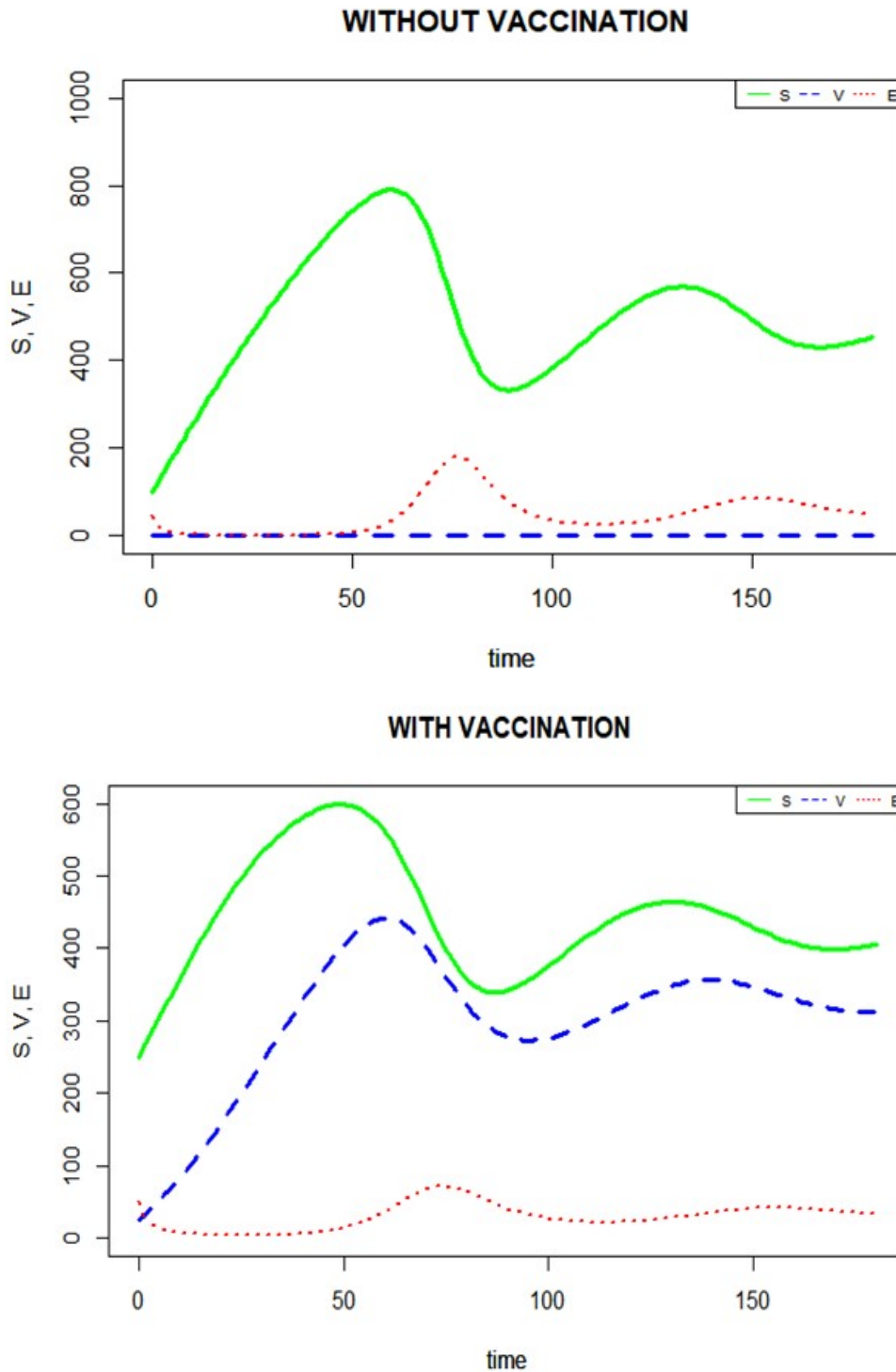


Figure 3. The results of susceptible, vaccinated and exposed compartments in two different communities (community 1 has individuals vaccinated and community 2 has unvaccinated individual).

posed by COVID-19. Nevertheless, since Thailand is a tourist destination spot, challenges may arise from outside its borders, especially from tourists who are yet to vaccinate or with one dose of vaccination. Thus, for the tourist economy in Thailand to return to normal situation, the global population must be vaccinated against the virus. Though some countries are far ahead in administering vaccine to its citizens, a number of obstacles are preventing other countries from achieving the same feat. Combining different types of COVID-19 vaccines has been considered as a potential way to solve the problem mentioned above. Not only combining vaccine doses gives global vaccine rollouts a faster push, but the studies of Liu et al. and Schmidt et al. [24, 25] have also suggested that it could offer better protection against COVID-19, as well. In conclusion, a similar model

can be formulated for other countries to estimate the efficacy of vaccination based on their individual data.

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