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RESEARCH ARTICLE

A mathematical model to assess COVID-19 vaccination in Thailand

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Abstract

In this article, a COVID-19 transmission mathematical model incorporating vaccination and non-pharmaceutical interventions was formulated and theoretically analysed. Here, the COVID-19 free and endemic equilibrium points, vaccine reproduction number were computed. The derived vaccination reproduction number largely depends on vaccine efficacy for disease eradication to occur. Infection risk is significantly reduced whenever the vaccine intake is greater than one dosage. The simulation results indicate that the administered COVID-19 vaccines and non-pharmaceutical interventions have been effective for the current variants, additional efforts such as a third vaccine booster shot should be considered and implemented to greatly mitigate the risk of the emerging variants of the COVID-19 pandemic.

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 1.9 trillion-baht (US$60 billion) stimulus package [1]. After more than a year of ongoing cycles of imposing different travelling 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 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) is fully vaccinated, and 8.9% (6,226,249) has received a booster shot. COVID-19 vaccinations have tapered off from the government's peak rollout push in late September and early October. Booster shots were relatively rare in September when they were primarily given to medical and frontline workers and those requiring them to travel abroad. However, with the recent Omicron variant becoming a concern worldwide [5], booster shots have become a heavy focus of 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 for most brands has been found to increase the protection against Omicron [6] significantly.

As COVID-19 vaccines are still being administered in different regions of the world, formulating and analysing 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 of a five-dimensional compartment system for the COVID-19 pandemic to assess epidemic course if all restrictions are gradually eased and if variants of concern are introduced. The model included vaccination campaign. They also assessed the impact of different levels of vaccine coverage, duration for vaccine scale-up, and different schedules for easing social distancing restrictions on COVID-19 incidence. Angeli et al.[9] modelled the effect of the vaccination campaign on the COVID-19 pandemic by formulating a mathematical model that describes 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 study, we proposed a model incorporating some key epidemiological and biological features of COVID-19 to identify the effect of vaccination and non-pharmaceutical interventions on COVID-19 in Thailand. To the best of our knowledge, this study is the first in-depth study that combines vaccination with non-pharmaceutical interventions in Thailand using non-linear ordinary differential equations. The remainder of this article is organised as follows. The formulated model is described in Section 2. The analysis of the model is presented in Section 3. The details of numerical simulations are performed in Section 4 and the conclusion made from this study is provided in Section 5.

2 | MODEL FORMULATION

Recently, Riyapan et al.[13] formulated a mathematical model of COVID-19 pandemic in Bangkok, 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 seven compartments given in Table 1 . The assumptions governing the model

TABLE 1 Variables and their meaning used in the model.

Variables in the model	Meaning
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

formulation are given as follows:

- The entire population considered in this study is non-constant. Thus, there is inflow, outflow, and death in all compartments.
- Individual infected with COVID-19 are considered to be both symptomatic.
- The recovered compartment consists of individuals who have recovered from COVID-19 infection either through quarantine or hospitalisation.
- Susceptible individuals can be vaccinated.
- The doses of vaccine intake reduce the risk of COVID-19 infection.

TABLE 2 Parameters used in the model and their meaning.

Model parameters	Meaning
λ	the rate at which individuals move into the susceptible compartment
β	the transmission rate
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 COVID-19 mortality rate for individuals in the infected compartment
λ_q	the rate at which individuals in the quarantine compartment recover
δ_q	the COVID-19 mortality rate 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 natural death rate of all individuals

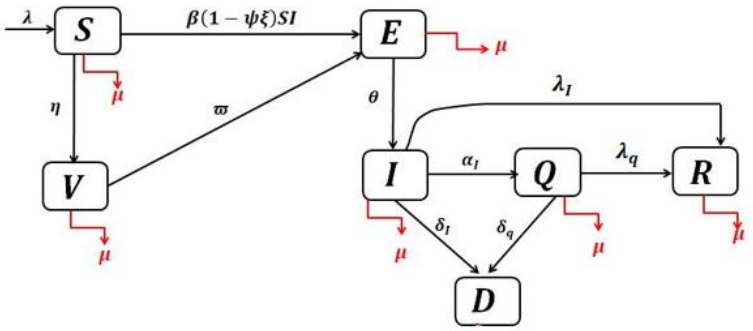

FIGURE 1 A flowchart for describing the model formulation.

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

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

Let $P(t)$ be the total population of the system. We have $P(t) = S(t)+V(t)+E(t)+I(t)+Q(t)+R(t)+D(t)$, 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 $P(t) \to \frac{\lambda}{\mu}$ as $t \to \infty$. So the model (1) is biologically and epidemiologically meaningful. It can be considered in the invariant region given by

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

3 | MODEL ANALYSIS

3.1 | Non-negativity of the model

Theorem 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 the solutions of the system of equations denoting model (1) remain non-negative for all $t > 0$.

Proof. The first equation in model (1) can be expressed 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

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

Hence $S(t)$ remains 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 $D(t) \geq 0$. □

3.2 | The boundedness of model (1)

Theorem 2. All solutions of the proposed model with non-negative initial conditions are bounded and $P(t) \leq \frac{\lambda}{\mu}$ for all $t > 0$.

Proof. By adding all the equations in model (1), the population growth of the total population can be written as

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

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

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

Integrating both sides of the above equation yields the solution for $P(t)$ in equation (7)

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

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

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

From Theorem 1 and equation (9), we can obtain $0 \leq P(t) \leq \frac{\lambda}{\mu}$. Hence $S(t), V(t), E(t), I(t), Q(t), R(t)$ and $D(t)$ are bounded and the proof of Theorem 2 is established. □

3.3 | Disease-free equilibrium and basic reproduction number of model (1)

The disease-free equilibrium $\chi^* = (S^*, V^*, E^*, I^*, Q^*, R^*, D^*)$ of model (1) is obtained by setting all the derivatives to be zero with $I = 0$, that yields to equation (10):

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

The basic reproduction number of model (1) is computed using the next-generation matrix method[14]. Let $X = (E, I)^T$ then model (1) can be expressed as:

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

where $G(x) = (\beta(1-\psi\xi)SI + \varpi\beta VI, 0)^T$ and $H(x) = ((\theta+\mu)E, -\theta E + (\alpha_I + \delta_I + \lambda_I + \mu)I)^T$. The corresponding jacobian matrices of $G(X)$ and $H(X)$ at the disease-free equilibrium 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], the basic reproduction number $\mathcal{R}_{vac}$ is defined as 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 equation (12) is the basic reproduction number of model (1). Equation (12) represents the number of secondary cases that can likely arise from a single infectious individual in a completely susceptible population[15]. It will be used to measure the transmission potential of the COVID-19 disease. An epidemic will likely increase exponentially if $\mathcal{R}_{vac} > 1$, and reduce if $\mathcal{R}_{vac} < 1$. It will be used to measure the transmission potential of the COVID-19 disease.

From (12), we can obtain $\mathcal{R}_0$, which is the secondary cases that can likely arise from a single infectious 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, the existence of the endemic equilibrium point when $\mathcal{R}_0 > 1$ is investigated. Let $\chi^{**} = (S^{**}, V^{**}, E^{**}, I^{**}, Q^{**}, R^{**}, D^{**})$ be the endemic equilibrium point of model (1), then χ^{**} can be obtained by setting all derivatives of the equations in model (1) to be zero as given below:

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

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

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

4 | NUMERICAL SIMULATIONS

This section presents the numerical simulations carried out in this study. Firstly, numerical simulations were carried out to explore the short term dynamics of the COVID-19 pandemic (Disease Free and Endemic Equilibrium Point). Next, we compare the hypothetical scenario where COVID-19 begins to spread within a community that has some of its individuals vaccinated and another community without vaccination. Lastly, we explore the vaccine effect 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	[19]
λ_q	0.13978	[17,18]
δ_q	0.015	[17]
η	0.02202643	[20]
θ	0.5	[21,22]
ϖ	0.30–0.88	[20]
μ	9.9259×10^{-3}	[23]

4.1 | Short-term dynamics of the disease

Here, we consider the short term dynamics of the disease by simulating the disease-free equilibrium (DFE) and endemic equilibrium points (EE), respectively. Using parameter values in Table 3, we explore the dynamics when no single individual is infected in a population (DFE) and when a single individual in an entirely safe population is infected with COVID-19 (EE). The simulation results are presented in Figures 2 and 3, respectively. 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. However, the reverse is shown in Figure 3 , where a single infected individual can lead to more infections.

4.2 | Community vaccination

Here, we consider the hypothetical scenario where COVID-19 begins to spread within a community that has most of its individuals vaccinated and another community without vaccination. The plot obtained from this simulation is presented in Figure 3 . The plot shows that lack of vaccination of susceptible and exposed individuals could lead to a more significant prevalence of COVID-19 within a country. 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.

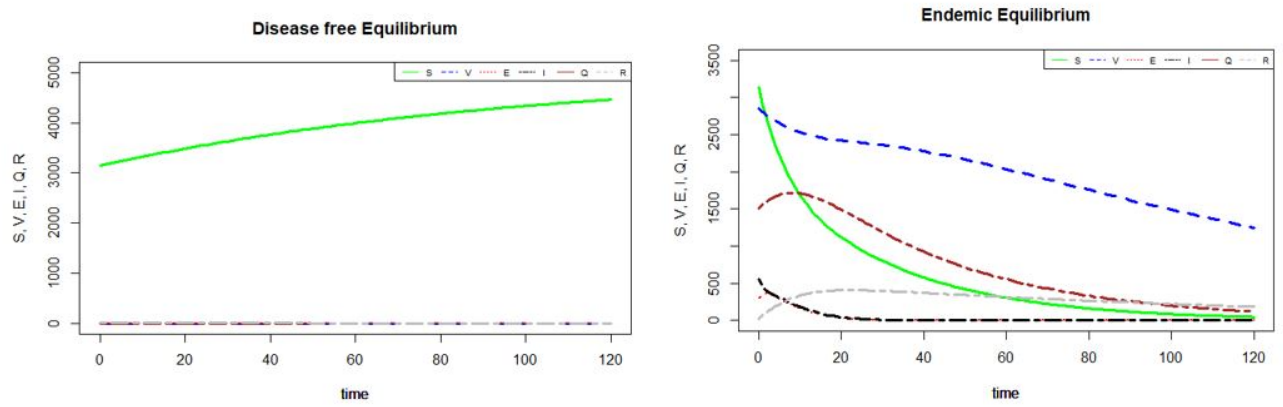

FIGURE 2 Simulation results of the short-term dynamics of the COVID-19 pandemic when there is no single infection and when there is an infection.

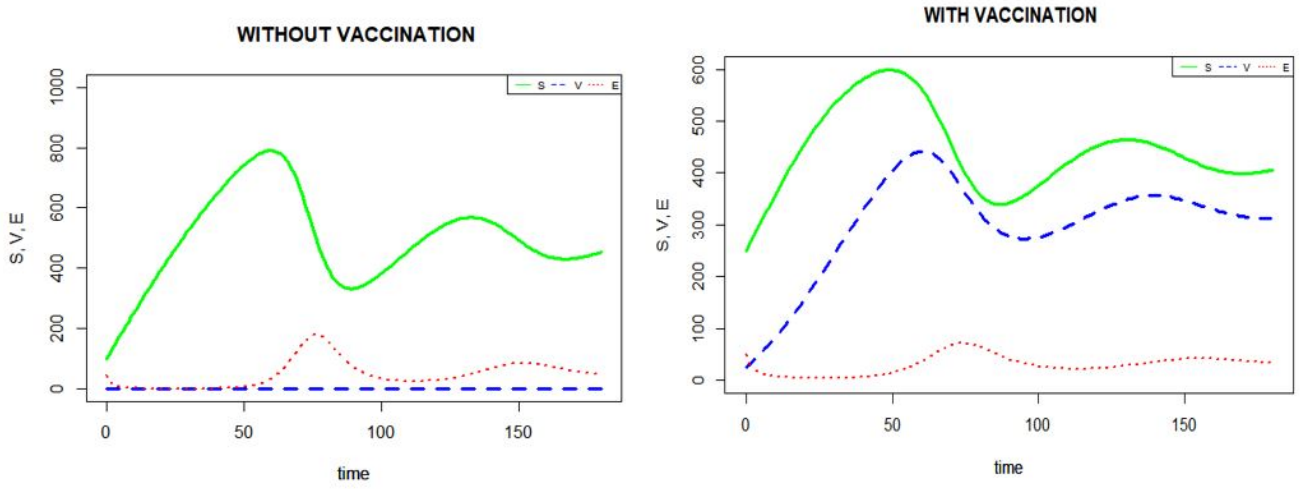

FIGURE 3 Simulation results of susceptible, vaccinated and exposed compartments in two (community 1 has individuals vaccinated and community 2 has unvaccinated individual) different communities.

4.3 | Exploring different vaccination dosages using vaccine 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 AstraZeneca[24]. Thus, in this study, the vaccine efficacy considered for the simulation is AstraZeneca. Three vaccination scenarios (no dosage, one dosage and two dosage intakes) together with the parameter values in Table 1 was 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 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[20]. The results presented in Table 4 indicates that taking two dosages will greatly reduce the number of infections that can be occur within the population.

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	$59.8 - 87.9\%$	$\mathcal{R}_{vac} = 0.537 < 1$

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 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 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 COVID-19 vaccines has emerged as a potential solution to the problem mentioned above. Not only combining vaccine doses give global vaccine rollouts a faster push, but the studies of Liu et al. and Schmidt et al.[25,26] 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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References

1. Theparat C. Cabinet gives green light to B1.9tn stimulus. 2020. https://www.bangkokpost.com/business/1894985/cabinet-gives-green-light-to-b1-9tn-stimulus. Accessed November 8, 2021.
2. Department of Disease control Thailand. 2021. https://ddc.moph.go.th/viralpneumonia/eng/index.php.
3. The world bank. 2021. https://datatopics.worldbank.org/world-development-indicators/.
4. Thailand starts long awaited COVID-19 vaccination drive Reuters. 2021. https://www.reuters.com/world/asia-pacific/thailand-starts-long-awaited-covid-19-vaccination-drive-2021-06-07/.
5. Classification of Omicron (B.1.1.529): SARS-CoV-2 Variant of Concern. 2021. https://www.who.int/news/item/26-11-2021-classification-of-omicron-(b.1.1.529)-sars-cov-2-variant-of-concern.
6. National Geographic How booster shots can help protect you from Omicron. 2021. https://www.nationalgeographic.com/science/article/how-booster-shots-can-help-protect-you-from-omicron.

7. Alvarez M, Bravo-González S, Santiago T.-dG. Modeling the effect of vaccination strategies in an Excel spreadsheet: The rate of vaccination, and not only the vaccination coverage, is a determinant for containing COVID-19 in urban areas. *medRxiv* 2021.

8. Yavuz M, Coşar F, Günay F, Özdemir F. A new mathematical modeling of the COVID-19 pandemic including the vaccination campaign. *Open Journal of Modelling and Simulation* 2021; 9(3): 299–321.

9. Angeli M, Neofotistos G, Mattheakis M, Kaxiras E. Modeling the effect of the vaccination campaign on the COVID-19 pandemic. *Chaos, Solitons and Fractals* 2021; 111621.

10. Mumtaz G, El-Jardali F, Jabbour M, A H, Abu-Raddad L, M M. Modeling the impact of COVID-19 vaccination in Lebanon: A call to speed-up vaccine roll out. *Vaccines* 2021; 9(7): 697.

11. Bartsch S, O'Shea K, Ferguson M, et al. Vaccine efficacy needed for a COVID-19 coronavirus vaccine to prevent or stop an epidemic as the sole intervention. *Am J Prev Med* 2020; 59(4): 493–503.

12. Acuña-Zegarra M, Díaz-Infante S, Baca-Carrasco D, Olmos-Liceaga D. COVID-19 optimal vaccination policies: A modeling study on efficacy, natural and vaccine-induced immunity responses. *Math Biosci* 2021; 337(108614).

13. Riyapan P, Shuaib S, Intarasit A. A mathematical model of COVID-19 pandemic: a case study of Bangkok, Thailand. *Computational and Mathematical Methods in Medicine* 2021; 2021: 11 pages.

14. Nishiura H. Correcting the actual reproduction number: a simple method to estimate R_0 from early epidemic growth data. *Int J Environ Res Public Health* 2010; 7(1): 291–302.

15. Diekmann O, Heesterbeek J, Metz J. On the definition and the computation of the basic reproduction ratio R_0 in models for infectious diseases in heterogeneous populations. *J Math Biol.* 1990; 28(4): 365–382.

16. Iboi E, Sharomi O, Ngonghala C, Gumel A. Mathematical modeling and analysis of COVID-19 pandemic in Nigeria. *Math Biosci Eng* 2020; 17(6): 7192–7220.

17. Eikenberry S, Mancuso M, Iboi E, et al. To mask or not to mask: modeling the potential for face mask use by the general public to curtail the COVID-19 pandemic. *Infect Dis Model* 2020; 5: 293–308.

18. Ferguson N, Laydon D, Nedjati-Gilani G. Report 9: impact of non-pharmaceutical interventions (NPIs) to reduce COVID19 mortality and healthcare demand. Tech. Rep. May 2020, Imperial College London; 2020.

19. Ferguson N, Laydon D, Nedjati-Gilani G, et al. Impact of non-pharmaceutical interventions (NPIs) to reduce COVID-19 mortality and healthcare demand. tech. rep., Imperial College COVID-19, Response Team, London; 2020.

20. Bernal J, Andrews N, Gower C, et al. Effectiveness of COVID-19 vaccines against the B.1.617.2 (Delta) variant. *N Engl J Med* 2021: 585–594.

21. Verity R, Okell L, Dorigatti I, et al. Estimates of the severity of coronavirus disease 2019: a model-based analysis. *Lancet Infect Dis.* 2020; 20(6): 669–677.

22. Moriarty L, Plucinski M, Marston B, et al. Public health responses to COVID-19 outbreaks on cruise ships—worldwide, February–March 2020. *Morbidity and Mortality Weekly Report* 2020; 69(12): 347–352.

23. Center of Disease control, Thailand. 2021. https://covid19.ddc.moph.go.th/en.

24. Number of people who received the COVID-19 vaccine. 2021. https://www.mhesi.go.th/index.php/content_page/item/3547-share-of-people-who-received-at-least-one-dose-of-covid-19-vaccine.html.

25. Liu X, Shaw R, Stuart A, et al. Safety and immunogenicity report from the com-COV study-a single blind randomised non-inferiority trial comparing heterologous and homologous prime-boost schedules with an adenoviral vectored and mRNA COVID-19 vaccine. 2021.

26. Schmidt T, Klemis V, Schub D, et al. Immunogenicity and reactogenicity of a heterologous COVID-19 prime-boost vaccination compared with homologous vaccine regimens. *medRxiv* 2021.

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