

RESEARCH ARTICLE | JULY 07 2026

Sensitivity analysis of COVID-19 epidemic mathematical model in Thailand

Sutawas Janreung; Sirachat Tipsri; Pariyaporn Roop-o ✉

AIP Conf. Proc. 3423, 080010 (2026)

<https://doi.org/10.1063/5.0338117>



Articles You May Be Interested In

Mathematical analysis of Thailand's COVID-19 model under control measures

AIP Conf. Proc. (July 2026)

Sustainability participation scientific issues to ageing the policies in Thailand

AIP Conf. Proc. (July 2026)

Developing model of charismatic leadership as small educational institution administrators in Thailand science school

AIP Conf. Proc. (July 2026)



Freedom to Innovate.

The New VHFLI 200 MHz Lock-in Amplifier.

Orchestrate pulses, triggers, and acquisition as the hub of your experiment. Discover more – run every signal analysis tool, simultaneously.

Order now

Sensitivity Analysis of COVID-19 Epidemic Mathematical Model in Thailand

Sutawas Janreung¹, Sirachat Tipsri², Pariyaporn Roop-o^{3, a)}

¹ Department of Social and Applied Science (Mathematics), College of Industrial Technology,
King Mongkut's of Technology North Bangkok 10800 Thailand

² Faculty of Science and Technology, Songkhla Rajabhat University, Muang, Songkhla 90000, Thailand

³ Faculty of Technology and Environment, Prince of Songkla University Phuket Campus,
Kathu, Phuket, 83120, Thailand

^{a)} Corresponding author, e-mail: pariyaporn.r@phuket.psu.ac.th

Abstract. This paper proposed a mathematical model for COVID-19. The reproduction number of the model is established for transmission and determined that the model has two positive equilibrium points. The disease-free equilibrium is locally asymptotically stable whenever the reproduction number is less than unity. When the basic reproduction number is greater than unity, the model has a unique endemic equilibrium, which is locally asymptotically stable. The sensitivity analysis of the model was considered. It shown that the contact rate and incubation rate are major factors in epidemic situation, as increasing those values results in increasing in the reproduction number. Additionally, numerical simulations compared the predicted model and actual data in Thailand during 2021 – 2022. It is suggested that the trend of the predicted model and the actual data are in the same direction.

Keywords: SEQIR epidemic model, Basic Reproduction Number, Stability, Sensitivity Analysis

INTRODUCTION

Due to the situation of pandemic coronavirus disease (COVID-19) transmission, there are various strategies to eliminate disease, prevention and control, i.e., wearing masks, lockdown, social distancing or isolation, and vaccines. In Thailand, COVID-19 was identified and reported cases in January 2020. Bureau of Epidemiology, Department of Disease Control, Ministry of Public Health in Thailand organized the emergency operation center (EOD) on 4 January 2020 to follow up and respond to the outbreak until the first Thai case was reported on 31 January 2020. In the later period, the number of patients continued to increase slowly, both patients traveling from abroad and patients infected within the country. It found that the spread in the later period was a cluster transmission. In addition, during that period, a city lockdown was announced in Bangkok. There was a movement of the population, causing contacts to spread out to other provinces. Consequently, the number of infected people in Thailand to increase significantly fast since mid-March 2020.

By reason of the global COVID-19 outbreak, there are many researchers attempted to understand the epidemiological behavior and dynamic of COVID-19, especially in Mathematics. Riyapan *et al.* (2021) studied a case study mathematical model in Thailand and suggested that the consistent use of face masks would go on a long way in reducing the COVID-19 pandemic. The mathematical analysis of COVID-19 is used to predict the number of infected individuals due COVID-19 virus in India proposed by Pal *et al.* (2021). It was suggested that the Indian government should take stricter measures other than quarantine, lockdown, etc. Jankhonkhan and Sawangtong (2021) proposed a mathematical model focused on social distancing and vaccination policies in Thailand to predict control techniques such as solving the limitation of ICU capacity and increasing the survival rate of patients and vaccination plan to prevent disease transmission.

The reproduction number is essential in the study of the epidemiological behavior of epidemic model. Some researchers interested in the effect of changing model parameters. Samsuzzoha *et al.* (2013) suggested that the basic reproduction number and endemic equilibrium are important factors. They represent the nature of disease transmission and prevalence. Moreover, the sensitivity analysis of the model depicted the basic reproduction

number as the most sensitive to the transmission rate of disease. Das *et al.* (2021) proposed the SEIQR model for COVID-19. The sensitivity analysis of the model recommended how to control the spread of coronavirus and investigated the elasticity of the basic reproduction number as a measure of control parameters of the dynamic system.

In this work, the mathematical model for COVID-19 is developed by introducing a quarantine state class. The model focused on the effect of parameters changing on the dynamic behavior of the model. The paper is organized as a model formulation, analysis of the model, sensitivity analysis, and numerical simulation as follows.

OBJECTIVES

To investigate the effect of the parameters sensitive to the spread of COVID-19 in Thailand during 2021 – 2022.

METHODS

Formulation of the SEQIR model

In this paper, the entire population can be separated into five classes; i.e., susceptible (S), exposed (E), quarantine (Q), infected (I), and recovered (R), with the total population considered $N = S + E + Q + I + R$. The flowchart of the SEQIR model is depicted in Figure 1, and the system of differential equations is introduced with standard incidence rate as follows. Additionally, all parameters of the model with their description are provided in Table 1.

The susceptible population is introduced with the recruitment rate, Π , into the community, and the recovered population are added to the class S . Susceptible populations who are infected at the rate β but do not show symptoms become exposed and move to the quarantine class at the rate α . After the complete incubation period, the exposed move to the infected class at the rate σ . The quarantine and infected population are removed from Q and I added to the recovered class at the rate γ_2 and γ_1 , respectively and die from infection at the rate d . The population will be removed from all population classes at the same natural death rate μ . It is assumed that the recovered population has temporary immunity that can be moved to the susceptible class again.

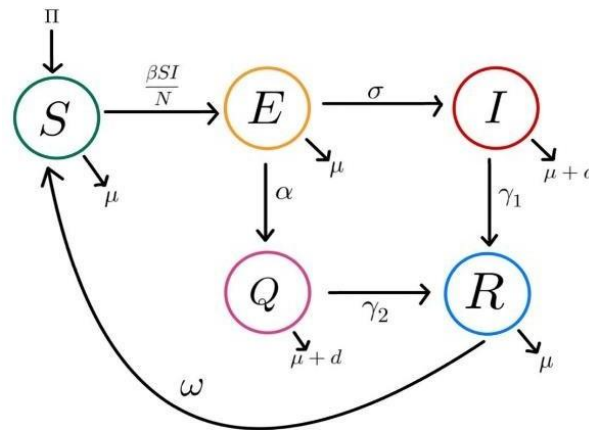


FIGURE 1. Flowchart of model

Applying above assumption, the SEQIR model is formulated as follow:

$$\begin{aligned}
\frac{dS}{dt} &= \Pi + \omega R - \frac{\beta SI}{N} - \mu S \\
\frac{dE}{dt} &= \frac{\beta SI}{N} - k_1 E \\
\frac{dQ}{dt} &= \alpha E - k_2 Q \\
\frac{dI}{dt} &= \sigma E - k_3 I \\
\frac{dR}{dt} &= \gamma_1 I + \gamma_2 Q - k_4 R
\end{aligned} \tag{1}$$

where $k_1 = \sigma + \alpha + \mu$, $k_2 = \gamma_2 + \mu + d$, $k_3 = \gamma_1 + \mu + d$, $k_4 = \omega + \mu$.

Analysis of the model

1. The reproduction number and disease-free equilibrium

The reproduction number is the threshold number that is used to measure the spread of disease in the population; in other words, it shows the risk of infection or the contact rate effectiveness. It is defined as the average number of cases produced if one infected person or individual is introduced into the population. The basic reproduction number of the model is given by the next-generation method (Driessche & Watmough, 2002) as follows.

$$R_0 = \frac{\beta \sigma}{k k} \tag{2}$$

1 3

2. Local stabilities of disease-free equilibrium (DFE)

In case of no infection process scenario, that is $E = I = 0$, the first steady stage of the model (1), called disease-free equilibrium obtained by setting the right-hand sides of the system (1) to zero is given by

$$E_0 = \begin{pmatrix} \Pi \\ \mu \\ 0, 0, 0, 0 \end{pmatrix}. \tag{3}$$

In accordance with the next-generation method, the linear stability of the system can be considered as follow.

Lemma 1. The SEQIR model at DFE, E_0 , is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.

3. Local stabilities of endemic equilibrium

Let S^*, E^*, Q^*, I^*, R^* represent the arbitrary steady state of S, E, Q, I and R , respectively. By setting the right-hand sides of the system (1) to zero, the positive endemic equilibrium can be expressed as

$E_1 = (S^*, E^*, Q^*, I^*, R^*)$ where

$$\begin{aligned}
S^* &= \frac{-k_1 \Pi k_3 (k_2 k_3 k_4 + k_2 \sigma (k_4 + \gamma_1) + k_3 \alpha (k_4 + \gamma_2))}{(k_1 k_3 - \beta \sigma) (k_1 k_2 k_3 k_4 - \omega (k_3 \alpha \gamma_2 + k_2 \alpha \gamma_1)) - k_1 k_3 \mu (k_2 \sigma (k_4 + \gamma_1) + k_3 \alpha (k_4 + \gamma_2))} \\
E^* &= \frac{\Pi k_2 k_3 k_4 (k_1 k_3 - \beta \sigma)}{(k_1 k_3 - \beta \sigma) (k_1 k_2 k_3 k_4 - \omega (k_3 \alpha \gamma_2 + k_2 \alpha \gamma_1)) - k_1 k_3 \mu (k_2 \sigma (k_4 + \gamma_1) + k_3 \alpha (k_4 + \gamma_2))}
\end{aligned}$$

$$I^* = \frac{\sigma \Pi k_2 k_4 (k_1 k_3 - \beta \sigma)}{(k_1 k_3 - \beta \sigma)(k_1 k_2 k_3 k_4 - \omega(k_3 \alpha \gamma_2 + k_2 \alpha \gamma_1)) - k_1 k_3 \mu (k_2 \sigma (k_4 + \gamma_1) + k_3 \alpha (k_4 + \gamma_2))}$$

$$Q^* = \frac{\alpha \Pi k_3 k_4 (k_1 k_3 - \beta \sigma)}{(k_1 k_3 - \beta \sigma)(k_1 k_2 k_3 k_4 - \omega(k_3 \alpha \gamma_2 + k_2 \alpha \gamma_1)) - k_1 k_3 \mu (k_2 \sigma (k_4 + \gamma_1) + k_3 \alpha (k_4 + \gamma_2))}$$

$$R^* = \frac{\Pi(k_1 k_3 - \beta \sigma)(k_2 \gamma_1 \sigma + k_3 \alpha \gamma_2)}{(k_1 k_3 - \beta \sigma)(k_1 k_2 k_3 k_4 - \omega(k_3 \alpha \gamma_2 + k_2 \alpha \gamma_1)) - k_1 k_3 \mu (k_2 \sigma (k_4 + \gamma_1) + k_3 \alpha (k_4 + \gamma_2))}$$

Let consider the following results on existence of the endemic equilibrium.

Lemma 2 The model (1) has a unique endemic equilibrium whenever $R_0 > 1$.

Analysis of the local stability of the model (1) using the center manifold theory (Carr, 1981) is given as follows.

Let $S = X_1$, $E = X_2$, $Q = X_3$, $I = X_4$, $R = X_5$, and $N = \sum_{n=1}^5 X_n$, respectively. Next, by using the vector notations $X = (X_1, X_2, X_3, X_4, X_5)^T$ and $F = (f_1(X), f_2(X), f_3(X), f_4(X), f_5(X))^T$, then, the SEQIR model is written in the form $\frac{dx}{dt} = F(X)$, where

$$f_1 = \Pi + \omega X_5 - \beta \frac{X_1 X_4}{\sum_{n=1}^5 X_n} - \mu X_1, \quad f_2 = \frac{\beta X_1 X_4}{\sum_{n=1}^5 X_n} - k_1 X_2, \quad f_3 = \alpha X_2 - k_2 X_3,$$

$$f_4 = \sigma X_2 - k_3 X_4, \text{ and } f_5 = \gamma_1 X_4 + \gamma_2 X_3 - k_4 X_5.$$

From $R_0 = \frac{\beta \sigma}{k k}$, we choose $\beta^* = \frac{k_1 k_3}{\sigma}$ for bifurcation parameter of the model.

The Jacobian of $\frac{dx}{dt} = F(X)$ evaluated at E with $\beta^* = \frac{k_1 k_3}{\sigma}$ is given by

$$J(\beta^*) = \begin{bmatrix} -\mu & 0 & 0 & -\frac{k_1 k_3}{\sigma} & \omega \\ 0 & -k_1 & 0 & \frac{k_1 k_3}{\sigma} & 0 \\ 0 & \alpha & -k_2 & 0 & 0 \\ 0 & \sigma & 0 & -k_3 & 0 \\ 0 & 0 & \gamma_2 & \gamma_1 & -k_4 \end{bmatrix}$$

It can be shown that $J(\beta^*)$ has at least one eigenvalue with zero real part. Hence, the center manifold theory can be used to analyze the dynamics of the SEQIR model with $\beta = \beta^*$.

The right eigenvector of $J(\beta^*)$ associated with the zero eigenvalue at $\beta = \beta^*$ is given by $w = [w_1, w_2, w_3, w_4, w_5]^T$, where

$$w_1 = -\frac{(k_1 k_2 k_3 k_4 - \omega(k_2 \gamma_1 \sigma + k_3 \alpha \gamma_2)) w_5}{\mu(k_2 \gamma_1 \sigma + k_3 \alpha \gamma_2)}, \quad w_2 = \frac{w_3 w_4 w_5}{k_2 \gamma_1 \sigma + k_3 \alpha \gamma_2},$$

$$w_3 = \frac{k_3 k_4 \alpha w_5}{k_2 \gamma_1 \sigma + k_3 \alpha \gamma_2}, \quad w_4 = \frac{\sigma k_2 k_4 w_5}{k_2 \gamma_1 \sigma + k_3 \alpha \gamma_2}, \quad w_5 = w_5.$$

Similarly, the components of the left eigenvector of $J(\beta^*)$ is associated with the zero eigenvalue at $\beta = \beta^*$, denoted by $v = [v_1, v_2, v_3, v_4, v_5]^T$ where

$$v_1 = 0, \quad v_2 = v_3 = 0, \quad v_4 = \frac{v_5 k_1}{\sigma}, \quad v_5 = 0.$$

The coefficients a and b defined in Center manifold Theorem are given by

$$a = \sum_{k,n,m=1}^k v_k w_n \frac{\partial^2 f_k}{\partial x_n \partial x_m}(0,0)$$

$$= -\frac{2v_2 k_2 k_4 w_5^2 \sigma \beta \mu (k_2 k_3 k_4 + k_2 k_3 \alpha + \sigma k_2 k_4 + k_2 \gamma_1 \sigma + k_3 \alpha \gamma_2)}{(k_2 \gamma_1 \sigma + k_3 \alpha \gamma_2)^2 \Pi}$$

and

$$b = \sum_{k,n=1}^k v_k w_n \frac{\partial^2 f_k}{\partial x_n \partial \beta^*}(0,0)$$

$$= \frac{v_2 \sigma k_2 k_4 w_5}{k_2 \gamma_1 \sigma + k_3 \alpha \gamma_2}$$

Clearly, the coefficient b is always positive and a is always negative.

Theorem 1 The endemic equilibrium of the SEQIR model is locally asymptotically stable whenever $R_0 > 1$.

Sensitivity analysis of reproduction number

Based on the concept of sensitivity analysis of reproduction number presented by Chitnis *et al.* (2008), the relative importance of model parameters to COVID-19 transmission and prevention is investigated by computing the sensitivity indices of the reproduction number R_0 to six model parameters at the baseline values given in Table 1 defined by

$$\theta_p^{R_0} = \frac{\partial R_0}{\partial p} \frac{p}{R_0},$$

where $\theta_p^{R_0}$ denotes the sensitivity indices of R_0 to a model parameter p . The study results are shown in Figure 2. It is found that the sensitivity indices $\theta_{\gamma_1}^{R_0}$, $\theta_{\alpha}^{R_0}$, $\theta_d^{R_0}$, $\theta_{\mu}^{R_0}$ are negative, while the sensitivity indices $\theta_{\beta}^{R_0}$, $\theta_{\sigma}^{R_0}$ are positive. The positive sign of $\theta_p^{R_0}$ means increasing the value of model parameter p would increase the value of R_0 which is an impact to increase COVID-19 infection. These study results indicate that the most

sensitive parameter to COVID-19 transmission is β and followed by σ respectively. Meanwhile, the most sensitive parameter to COVID-19 controlling is γ_1 and followed by α , d , and μ , respectively. It is found that the recovered rate of infected population, the progression from E to Q , especially people who are carriers of COVID-19 but they have not shown symptoms are major factors in controlling COVID-19 as increasing those values resulted in decreasing R_0 . On the other hand, it is found that the contact rate and incubation rate are major factors in epidemic situation, as increasing those values resulted in increasing R_0 .

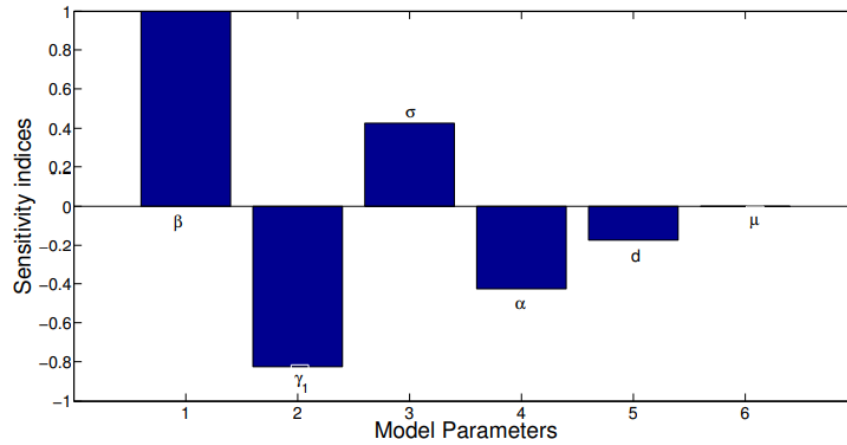


FIGURE 2. Sensitivity indices of R_0 to parameters for the SEQIR model, evaluated at the baseline parameter values given in Table 1. The parameters are ordered from most sensitive to least.

TABLE 1. Description and parameter values of SEQIR model

Parameter	Definition	Value	Reference
Π	Recruitment rate	5000	Assumed
β	Transmission rate	0.57	Assumed
σ	Rate of progression by exposed population to infected population	0.33 day ⁻¹	Patanarapeelert <i>et al.</i> (2013)
α	Rate of progression by exposed population to quarantine population	0.33 day ⁻¹	Ritraksa <i>et al.</i> (2022)
γ_1	Recovery rate for infected population	0.091 day ⁻¹	Ritraksa <i>et al.</i> (2022)
γ_2	Recovery rate for quarantine population	0.071 day ⁻¹	Ritraksa <i>et al.</i> (2022)
μ	Natural death rate	3.91×10^{-5} day ⁻¹	Ritraksa <i>et al.</i> (2022)
d	Mortality death rate by COVID-19	0.00001 day ⁻¹	Ritraksa <i>et al.</i> (2022)
ω	Rate of immune waning by recovered population	0.0001 day ⁻¹	Assumed

Numerical simulation for comparison predicted data and epidemiological COVID-19 data in Thailand

During 2021 – 2022, there were 2,837,533 cases of COVID- 19 reported by Bureau of Epidemiology, Department of Disease Control, Ministry of Public Health in Thailand (2022). In 2021, there were 2,219,082 cases, 91,646 deaths from COVID-19. And in 2022, there were 2,492,446 cases, 11,577 deaths from COVID-19. The number of cases collected from 3 January 2021 – 3 December 2022.

The associated simulation of the system (1) with parameters based on real data for COVID- 19 in Table 1 are used, which are $\Pi = 5000$, $\mu = 3.91 \times 10^{-5}$, $d = 0.00001$, $\gamma_1 = 0.09$, $\gamma_2 = 0.071$, $\alpha = 0.33$, and $\omega = 0.0001$. Further, the parameters $\beta = 0.57$ and $\sigma = 0.33$ are used for 2021, $\beta = 0.5$ and $\sigma = 0.45$

are used for 2022, respectively. The corresponding reproduction numbers with the above parameter values are $R_0 = 3.1331$ for 2021 and $R_0 = 3.1712$ for 2022. It can be seen that the reproduction number has slightly changed but is still in the range 1.4 – 6.49 (Liu *et al.*, 2020). It can be noticed that infected people are mostly spread disease 2 days before they develop symptoms and those who develop severe disease can be spread for longer.

The comparison simulation results of the number of COVID- 19 cases using the above parameter values between the prediction of the SEQIR model (1) and the actual data as shown in Figure 3 – 4 for 2021 – 2022, respectively. It can be seen that the trend of the spread of COVID- 19 in the predicted model and actual data are in the same direction.

In 2021, the number of COVID- 19 cases started to increase in May and peaked in July. After that, the number of infected people decreased until December depicted in Figure 3.

Figure 4 shows the number of COVID-19 cases increased in January and peaked in March. Then the number of infected people dropped until December 2022.

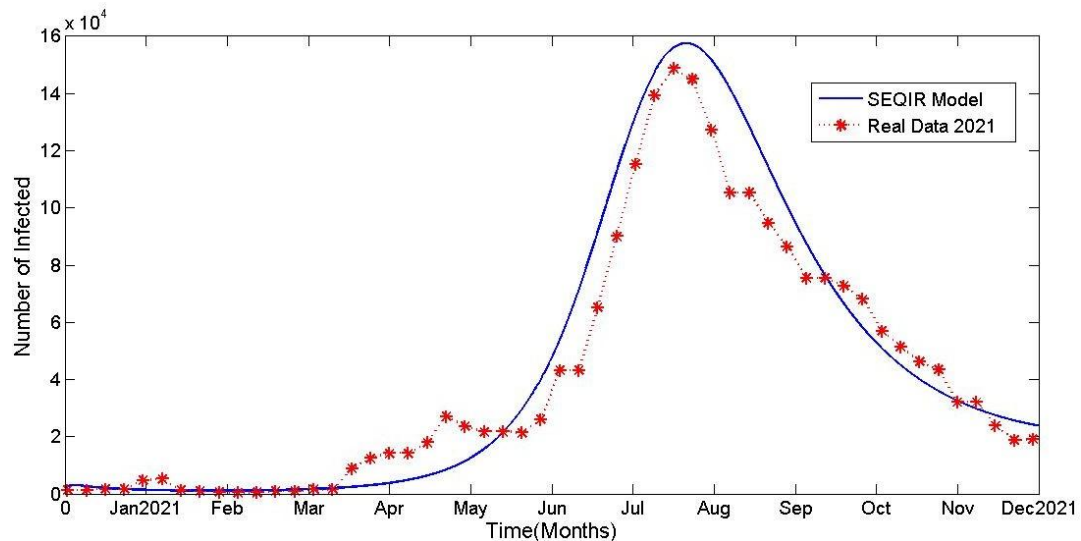


FIGURE 3. Comparison of the predicted data obtained by the SEQIR model and the actual data of number of COVID-19 cases in 2021.

It can be concluded that during the COVID outbreak, it was 3 months since the number of infected people started to increase and reached its peak. The epidemic will be continue to decrease since people have an awareness of prevention and follow the government policies such as wearing masks, lockdowns, social distancing or isolation, and vaccines.

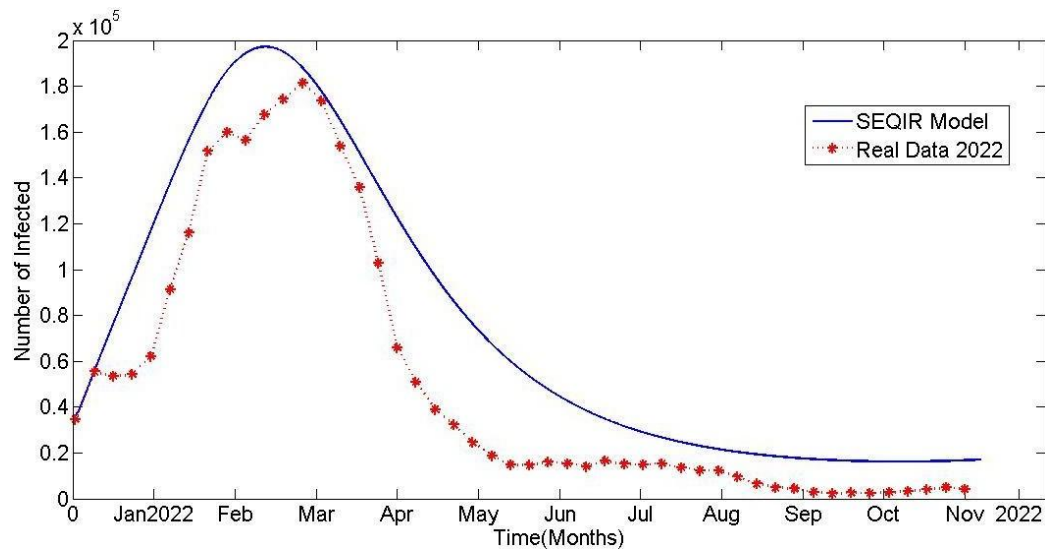


FIGURE 4. Comparison of the predicted data obtained by the SEQIR model and the actual data of number of COVID-19 cases in 2022.

DISCUSSION AND CONCLUSION

In this paper, the mathematical model of COVID-19 is formulated. The analysis of the model shows that the model has two equilibrium points, that is, the disease-free equilibrium and endemic equilibrium. The reproduction number (R_0) is the threshold value of the model. Moreover, the results of sensitivity analysis of the reproduction number indicate that the most sensitive parameter to COVID-19 transmission is β and followed by σ respectively. These parameters are relevant to the number of infected populations, which is especially important and directly related to the number of deaths. It is found that decreasing of R_0 depends on the increase of the recovered rate of infected population, γ_1 and the rate of progress E to Q , α , which are major factors in controlling COVID-19. The numerical results show that the model can be used to predict the period of COVID-19 outbreak in Thailand. As the result, the strategy for controlling the spread of COVID-19 should be to reduce the contact rate. However, the vaccination and a booster dose of COVID-19 vaccine are the choices to recommend in decreasing your risk of infection and severe illness with COVID-19.

SUGGESTION

The proposed model (1) should be added a vaccinated class for suitable to the current situation. Furthermore, the death class should be determined to show the efficiency of the vaccine affected to decreasing of severe of the disease.

REFERENCES

1. Carr, J. (1981). *Applications of Centre Manifold Theory*. New York. Springer-Verlag.
2. Chitnis, N., Hyman, J. & Cushing, J. (2008). Determining important parameters in the spread of malaria through the sensitivity analysis of a mathematical model. *Bulletin of Mathematical Biology*, 70, 1272–1296.
3. Das, K., Kumar, G. R., Reddy, K. M. & Lakshminarayan, K. (2021). Sensitivity and elasticity analysis of novel corona virus transmission model: A mathematical approach. *Sensors International*, 2, 1–5.
4. Department of disease control. (2022). *Thailand Weekly COVID-19 Report* [Online]. Retrieved December 24, 2022, from: <https://ddc.moph.go.th/covid19-dashboard/>.
5. Jankhonkhan, J. & Sawangtong, W. (2021). Model predictive control of COVID-19 pandemic with social isolation and vaccination policies in Thailand. *Axioms*, 10, 1–17.

6. Liu, Y., Gayle, A. A., Wilder-Smith, A. & Rocklöv, J. (2020). The reproductive number of COVID-19 is higher compared to SARS coronavirus. *Journal of Travel Medicine*, 27(2), 1–4.
7. Pal, D., Ghosh, D., Santra, P. K. & Mahapatra, G. S. (2022). Mathematical analysis of a COVID-19 epidemic model by using data driven epidemiological parameters of diseases spread in India. *Biophysics*, 67(2), 301–318.
8. Patanarapeelert, K. , Songprasert, W. & Patanarapeelert, N. (2022). Modeling dynamic responses to COVID-19 epidemic: A case study in Thailand. *Tropical Medicine and Infection Disease*, 7(303), 1–16.
9. Ritaksa, S., Photphanloet, C., Shuaib, S., Intarasit, A. & Riyapan, P. (2022). Mathematical modeling to study the interactions of two risk populations in COVID-19 spread in Thailand. *Mathematics*, 8(1), 2044–2061.
10. Riyapan, P., Shuaib, S. E., & Intarasit, A. (2021). A mathematical model of COVID-19 pandemic: A case study of Bangkok, Thailand. *Computational and Mathematical Methods in Medicine*, 2021, 1-11.
11. Samsuzzoha, M. , Singh, M. , Lucy, D. (2013). Uncertainty and sensitivity analysis of the basic reproduction number of a vaccinated epidemic model of influenza. *Applied Mathematical Modelling*, 37(3), 903–915.
12. van den Driessch, P. & Wathmough, J. (2002). Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission. *Mathematical Biosciences*, 180, 29–48.