



Modeling the Transmission Dynamics of the COVID-19 Outbreak in Thailand

Ekkachai Thawinan^{1,2} and Somchai Sriyab^{1,2,*}

¹ *Department of Mathematics, Faculty of Science, Chiang Mai University, Chiang Mai, Thailand*
e-mail : ekkachai.thawinan@cmu.ac.th (E. Thawinan); somchai.sriyab@gmail.com (S. Sriyab)

² *Research Center in Mathematics and Applied Mathematics, Department of Mathematics, Faculty of Science, Chiang Mai University, Chiang Mai, Thailand*

Abstract The ongoing Corona Virus Disease 2019 (COVID-19) outbreak is currently one of the largest problems in the world. In Thailand, the disease has affected all Thai people, with implications for the economy, living standards, tourism etc. In this work, we propose a mathematical model to explain the number of cases in Thailand, including exposed, symptomatic infected, asymptomatic infected, hospitalized, recovered and deceased, and compare these numbers with data reported by the Department of Disease Control, Ministry of Public Health, Thailand. The basic reproduction number has been computed to show how the disease spreads. The effect of transmission coefficient explaining the transmission from asymptomatic patients demonstrates the most important factor in this outbreak. The numerical results show that the number in each population category is consistency with the reported data before the lock down measurements start on March 26, 2020. Therefore, we can predict the number of each population category in the future without any government actions. The model shows that each symptomatic infected case reported, there are still 6 - 13 asymptomatic infected cases in Thailand.

MSC: 92B05

Keywords: mathematical model; COVID-19; transmission dynamics; basic reproduction number

Submission date: 02.09.2012 / Acceptance date: 07.10.2020

1. INTRODUCTION

The recent outbreak of infectious disease COVID-19 was caused by the SARS-CoV-2 strain of coronavirus that appeared in Wuhan, China in late December 2019. It was declared a global pandemic on March 2020 by the World Health Organization (WHO) [1]. As of April 28, 2020, the deadly COVID-19 virus had infected 2,878,196 people globally and resulted in 198,668 deaths [2]. As of April 28, 2020, there were 2,938 infections and 54 deaths in Thailand [3]. Gaining an understanding of COVID-19 transmission is vital to being able to predict and control the outbreaks of this disease. Mathematical models are crucial tools for studying the behavior of infectious diseases [4, 5]. Therefore, there have been several research projects focusing on mathematical models of COVID-19

transmission [6]-[13]. Some researchers have studied the early transmission of this disease from its original source, Wuhan, Hubei Province, China, including a conceptual model and clinical patient features [6, 8, 9, 12]. Tian-Mu-Chen and his coworkers proposed a Bat-Host-Reservoir-People transmission network model for simulating the potential transmission from source to human infection [7]. Many researchers studied the pneumonia that has been associated with several COVID-19 patients [10, 11, 13]. Thailand is the first country outside China that had confirmed COVID-19 cases. The first case appeared on January 13, 2020 [14] and the coronavirus has now spread throughout most of the country. In order to describe the transmission dynamics of the COVID-19 outbreak in Thailand, we propose a deterministic SEIAHRD model to study this disease among humans. The individuals in the SEIAHRD model population have been divided into following categories: susceptible, exposed, symptomatic infected, asymptomatic infected, hospitalized, recovered and deceased. We compute the basic reproduction number to show how the disease has been transmitted in Thailand. The numerical results, reported data and discussion are presented in Section 3. Finally, we conclude our study in the last section.

2. MATERIALS AND METHODS

MATHEMATICAL MODEL

We developed a mathematical model of COVID-19 to describe the transmission of COVID-19 in Thailand. This model was based on the transmission patterns of COVID-19 in Wuhan and Middle East Respiratory Syndrome (MERS) in South Korea [4, 6]. Since we would like to study the number of asymptomatic infected, hospitalized and deceased population so we add these population categories to SEIR model. Therefore, the population in our model is divided into seven categories of people: susceptible ($S(t)$), exposed ($E(t)$), symptomatic infected ($I(t)$), asymptomatic infected ($A(t)$), hospitalized ($H(t)$), recovered ($R(t)$) and deceased ($D(t)$). Susceptible means those people who may become infected while the exposed are those who have had contact with symptomatic or asymptomatic infected people. The symptomatic infected includes the population who are currently infected and have developed symptoms of this disease, such as fever, fatigue and dry cough. The asymptomatic infected are the people who are infected but haven't developed any symptoms [15]. The hospitalized are the population who need hospital treatment. The recovered and deceased are those who have recovered or died from COVID-19 respectively.

Figure 1 shows a flow diagram of a compartmental model of COVID-19. The susceptible cases become exposed cases by the transmission coefficients of symptomatic infections (β_1), asymptomatic infections (β_2) and hospitalizations (β_3). The exposed cases become symptomatic or asymptomatic infections with rates of $\gamma\sigma$ and $(1 - \gamma)\sigma$ respectively, in which γ is clinical outbreak rate and $\frac{1}{\sigma}$ is incubation period. Symptomatic infected cases become hospitalized cases with rate λ where $\frac{1}{\lambda}$ is the average time from symptom onset to the date of hospitalization. Asymptomatic infected cases can recover through their natural immunity with rate k_1 which $\frac{1}{k_1}$ being the average recovery time of asymptomatic infected cases. The hospitalized cases may either end with recovery or death with a rate of k_2 or δ which $\frac{1}{k_2}$ is average recovery time of symptomatic infected cases and $\frac{1}{\delta}$ is average time from hospitalization to death. All population categories have a natural death rate μ .

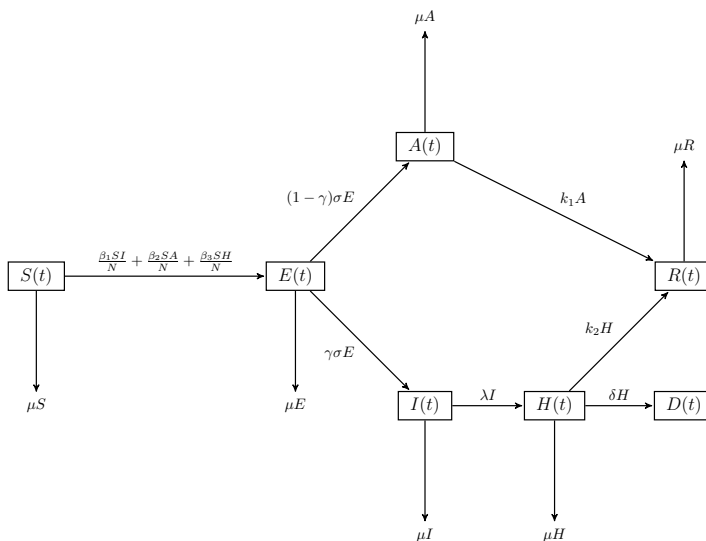


FIGURE 1. Flow diagram of the model

Therefore, the human to human transmission of COVID-19 can be formulated in a mathematical model as follows:

$$\frac{dS}{dt} = -\beta_1 \frac{SI}{N} - \beta_2 \frac{SA}{N} - \beta_3 \frac{SH}{N} - \mu S \tag{2.1a}$$

$$\frac{dE}{dt} = \beta_1 \frac{SI}{N} + \beta_2 \frac{SA}{N} + \beta_3 \frac{SH}{N} - \sigma E - \mu E \tag{2.1b}$$

$$\frac{dI}{dt} = \gamma\sigma E - \lambda I - \mu I \tag{2.1c}$$

$$\frac{dA}{dt} = (1 - \gamma)\sigma E - k_1 A - \mu A \tag{2.1d}$$

$$\frac{dH}{dt} = \lambda I - k_2 H - \delta H - \mu H \tag{2.1e}$$

$$\frac{dR}{dt} = k_1 A + k_2 H - \mu R \tag{2.1f}$$

$$\frac{dD}{dt} = \delta H \tag{2.1g}$$

MODEL ANALYSIS

Through simple calculation, we found a disease-free equilibrium $(0, 0, 0, 0, 0, \bar{D})$ in which \bar{D} is arbitrary constant. Then, we used a spectral radius of a next generation matrix to evaluate the basic reproduction number [16]. Firstly, we only considered the infected category, as shown in equations (1b) – (1e). We defined the appearance rate of new infections and the rate of individual transfer.

$$\bar{F} = \begin{bmatrix} \beta_1 \frac{SI}{N} + \beta_2 \frac{SA}{N} + \beta_3 \frac{SH}{N} \\ 0 \\ 0 \\ 0 \end{bmatrix}, \quad \bar{V} = \begin{bmatrix} \sigma E + \mu E \\ -\gamma \sigma E + \lambda I + \mu I \\ -(1 - \gamma)\sigma E + k_1 A + \mu A \\ -\lambda I + k_2 H + \delta H + \mu H \end{bmatrix}$$

Then, calculations showed that the partial derivatives of \bar{F} and \bar{V} were about $x = (E, I, A, H)$. After that, we substituted the initial condition (E_0, I_0, A_0, H_0) into variables, and obtained:

$$F = \begin{bmatrix} 0 & \frac{\beta_1 S_0}{N} & \frac{\beta_2 S_0}{N} & \frac{\beta_3 S_0}{N} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}, \quad V = \begin{bmatrix} (\sigma + \mu) & 0 & 0 & 0 \\ -\gamma \sigma & (\lambda + \mu) & 0 & 0 \\ -(1 - \gamma)\sigma & 0 & (k_1 + \mu) & 0 \\ 0 & -\lambda & 0 & (k_2 + \delta + \mu) \end{bmatrix}$$

and so

$$FV^{-1} = \begin{bmatrix} F_1 & F_2 & \frac{\beta_2 S_0}{(k_1 + \mu)N} & \frac{\beta_3 S_0}{(k_2 + \delta + \mu)N} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \tag{2.2}$$

where

$$F_1 = \frac{\gamma \sigma \lambda \beta_3 S_0}{(\sigma + \mu)(\lambda + \mu)(k_2 + \delta + \mu)N} + \frac{(1 - \gamma)\sigma \beta_2 S_0}{(\sigma + \mu)(k_1 + \mu)N} + \frac{\gamma \sigma \beta_1 S_0}{(\sigma + \mu)(\lambda + \mu)N} \tag{2.3}$$

$$F_2 = \frac{\beta_1 S_0}{(\lambda + \mu)N} + \frac{\lambda \beta_3 S_0}{(k_2 + \delta + \mu)(\lambda + \mu)N} \tag{2.4}$$

Since the basic reproductive number (R_0) is the biggest eigenvalue of matrix FV^{-1} , one can compute that $R_0 = F_1$.

DATA

The Department of Diseases Control, Ministry of Public Health, Thailand released a time series of reported cases [3]. They provided detailed data of the endemic in Thailand, including the total number of exposed cases, symptomatic infected, hospitalized, recovered and deceased. We can analyze the relationship between numerical results using these data.

PARAMETER VALUES

According to data provided by the National Statistical Office of Thailand, the total population of Thailand (N) is approximately 65 million people, while the natural death rate is 0.076 [17]. The WHO reports that the incubation period of COVID-19 (σ^{-1}) is 7 days [15]. Since COVID-19 is a new infectious disease, exact parameter values have not been reported yet. In this research, we use some parameter values from Middle East Respiratory Syndrome (MERS), including the transmission coefficients of symptomatic infected cases (β_1), asymptomatic infected cases (β_2), hospitalized cases (β_3) and clinical outbreak rate (γ) [4]. The average time from onset of symptoms to hospitalization (k_1^{-1}) and symptomatic infected cases (k_2^{-1}), the average time from data of symptoms onset to

data of hospitalization (λ^{-1}) and the average time from hospitalization to death (δ^{-1}) are estimated. The value and source of all parameters are shown in Table 1.

Parameters	Value	Source
N	65 million	[17]
μ	0.0076	[17]
β_1	0.65	[4]
β_2	0.55	[4]
β_3	0.55	[4]
γ	0.145	[4]
σ	7 days	[15]
k_1^{-1}	30 days	Estimated
k_2^{-1}	30 days	Estimated
λ^{-1}	6.5 days	Estimated
δ	0.001	Estimated

TABLE 1. Parameters values in the system

THE EFFECT OF TRANSMISSION COEFFICIENTS

In this section, we apply two dimensional figures to explain how the transmission coefficients affect to the basic reproduction number. Figure 2 represents the relationship between the transmission coefficient of symptomatic infected cases (β_1), asymptomatic infected cases (β_2) or hospitalized cases (β_3) and the basic reproduction number (R_0). It suggests that the transmission coefficients are linearly proportional with the basic reproduction number. Since slope of β_2 is bigger than slope of β_1 and β_3 , so the transmission coefficient of asymptomatic infected cases has a stronger influence on the basic reproduction number than the transmission coefficient of symptomatic infected cases and hospitalized cases. It show us that the transmission from the asymptomatic patient is most important factor of COVID-19 outbreak.

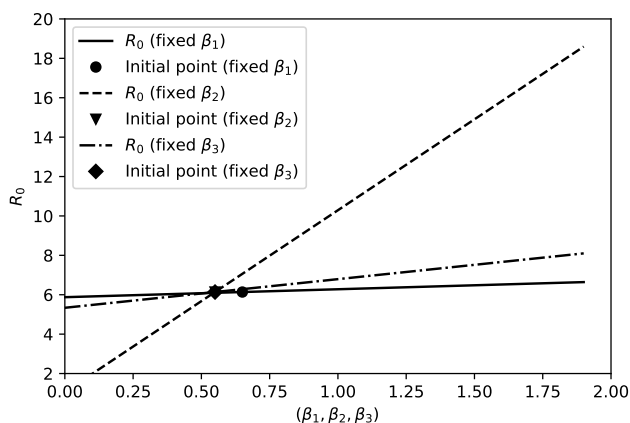


Figure 2. The influence of β_1, β_2 and β_3 on R_0

3. RESULTS AND DISCUSSION

The basic reproduction number (R_0) can be expressed such that the expected number of cases are directly generated by one case. Substituting the parameter values from Table 1 into the expression of (R_0) in the form of equation (2.3), we obtain $R_0 = 6.14$. The basic reproduction number in our research is similar to the basic reproduction numbers found by Shen M. ($R_0 = 6.49$) [18] and Tang B. ($R_0 = 6.47$) [19]. It is well-known that if R_0 is greater than one, the disease will keep spreading in the population. This would mean that the disease is likely to spread quickly throughout Thailand. Next, the numerical results from the model and the reported data for each population category have been presented. The reported data were collected from February 1 to April 28, 2020. Figure 3 shows that the number of exposed cases in our model is consistent with the reported data. It suggest that the number of exposed cases are exponential growth because susceptible people have become exposed through contact with symptomatic and asymptomatic infected people.

The number of symptomatic infected cases in the model simulation and in the reported data are illustrated in Figure 4. The simulation of symptomatic infected cases only fit with data reported from February 1 (Day 1) to April 10, 2020 (Day 70). One possible reason for this is that the Thai government declared an Emergency Situation pursuant to a March 26, 2020 Emergency Decree to control the COVID-19 outbreak. However, the data can predict the number of symptomatic infected cases that would have occurred without any government reactions. Figure 5 illustrates the hospitalized cases predicted by the model and reported in the data. It suggests that the results of the simulation model qualitatively agree with reported data from February 1 (Day 1) to April 10, 2020 (Day 70). It explains that the theoretical and real hospitalized cases both increased significantly before lockdown measures started (March 26, 2020). Following that action, the real hospitalized cases decreased dramatically while the theoretical hospitalized cases continued their exponential increase after April 10, 2020.

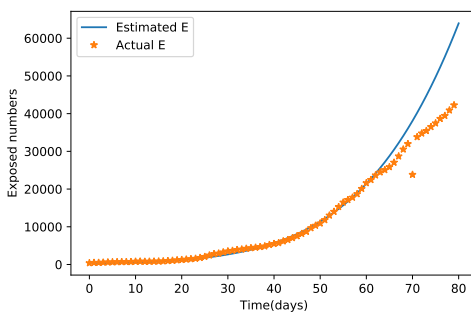


Figure 3. Exposed cases

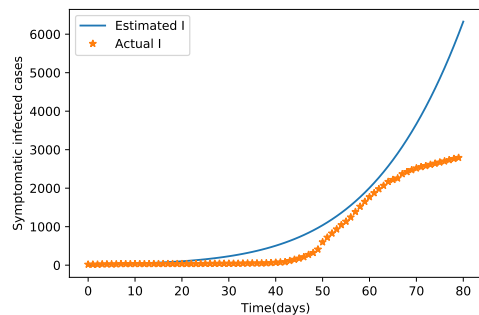


Figure 4. Symptomatic infected cases

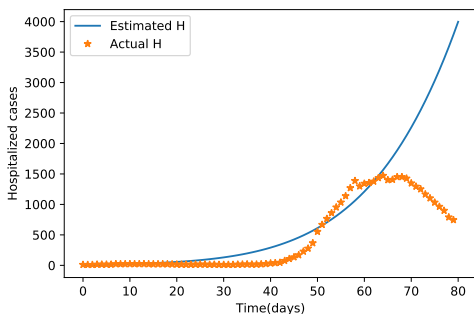


Figure 5. Hospitalized cases

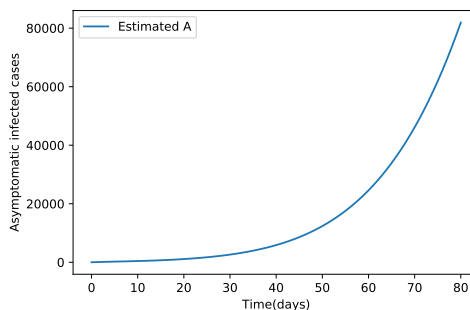


Figure 6. Asymptomatic infected cases

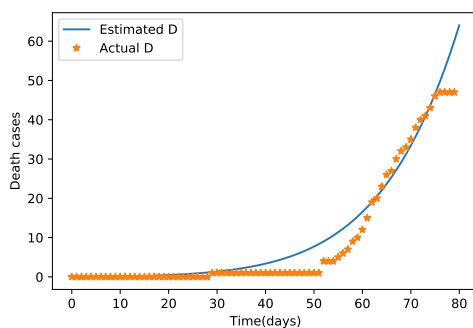


Figure 7. Death cases

Since there is no reported data of asymptomatic infected cases, so we will reveal the numerical data of this cases in Figure 6. It shows that asymptomatic cases are higher than the symptomatic infected cases and it increase exponentially. Figure 7 includes both model prediction and reported data of deceased cases. It shows that the theoretical and reported of deceased cases are exactly fit. Therefore, we can predict the number of deceased cases of Thailand in the future.

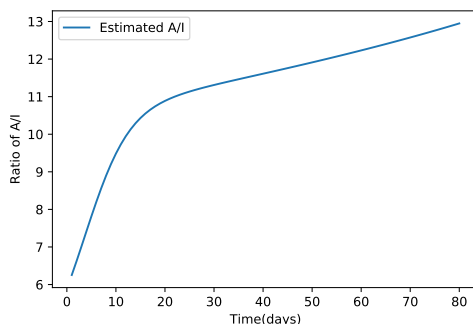


Figure 8. The ratio of asymptomatic and symptomatic cases

Figure 8 shows the ratio of asymptomatic and symptomatic infections in simulation. It indicates that there are 6 - 13 asymptomatic infected patients for each symptomatic infected case found.

4. CONCLUSIONS

We developed a mathematical model that is consist of susceptible, exposed, symptomatic infected, asymptomatic infected, hospitalized, recovered and died to explain the outbreak of COVID-19 in Thailand. The basic reproduction number (R_0) was computed using the spectral radius of next generation matrix that we obtained $R_0 = 6.17$. This value means that the COVID-19 outbreak was transmitted across the nation. However, the basic reproductive numbers have been verified by many research projects, so our basic reproduction number is quite similar to that found by Shen and Tang [18, 19]. The effect of transmission coefficient shows that transmission from asymptomatic infected cases is a major contributing factor to the COVID-19 outbreak in Thailand.

We compared the model results with the reported data for each population category. Since the susceptible cases may become exposed through contact with symptomatic and asymptomatic infected people, the model and reported data both show exponential growth in this category. The simulation of symptomatic infected people is identical to the data reported before the lockdown measures began. Moreover, the model can predict how many symptomatic infected cases would appear if no governmental action was taken . Before the lockdown measures started, the numerical and real hospitalized cases increased significantly. After the governments actions, the reported hospitalized cases decreased dramatically while the models hospitalized cases still increased exponentially. Asymptomatic infected people were included in our study because they could transmit the virus to susceptible people. For each symptomatic infected patient reported, there are about 6 - 13 asymptomatic infected cases. Finally, since the numerical and theoretical results of population category are consistency so we can use our model to predict the number of exposed, symptomatic, asymptomatic, hospitalized and deceased cases in Thailand without any government actions.

We hope that our study provides important insights into the transmission dynamics of the COVID-19 outbreak in all population sectors in Thailand. It is important to thoroughly understand disease transmission in order to help implement effective prevention and control programs.

ACKNOWLEDGEMENTS

This research work is supported by Chiang Mai University, Chiang Mai, Thailand.

REFERENCES

- [1] World Health Organization. WHO characterizes covid-19 as a pandemic, 2020: <https://www.who.int/dg/speeches/detail/who-director-general-s-opening-remarks-at-the-media-briefing-on-covid-19-13-april-2020> (April 28 , 2020).
- [2] World Health Organization. WHO coronavirus disease (covid-2019) situation reports, 2020: <https://www.who.int/emergencies/diseases/novel-coronavirus-2019/situation-reports> (April 28, 2020).

- [3] Department of Disease Control, Ministry of Public Health, Thailand. The situation of COVID-19: <https://covid19.ddc.moph.go.th/> (April 28, 2020).
- [4] Z.Q. Xia, J. Zhang, Y.K. Xue, Modeling the transmission of middle east respirator syndrome Corona Virus in Republic of Korea, PLOS ONE, (2015) <https://doi.org/10.1371/journal.pone.0144778>.
- [5] Y. Zhou, Z. Ma, A Discrete epidemic model for SARS transmission and control in China, *Math. Comput. Model.* 40 (2004) 1491–1506.
- [6] Q. Lin, S. Zhao, D. Gao, A conceptual model for outbreak of Coronavirus disease (COVID-19) in Wuhan, China with individual reaction and government action, *Int. J. Infect. Dis.* 93 (2020) 211–216.
- [7] T.M. Chen, J. Rui, Q.P. Wang, A Mathematical model for simulating the phase-based transmissibility of novel coronavirus, *Infect. Dis. Poverty.* 9 (2020) 1–8.
- [8] Q. Li, X. Guan, P. Wu, X. Wang, L. Zhou, Y. Tong, Early transmission dynamics in Wuhan, China, of novel coronavirus-infected pneumonia, *N. Eng. J. Med.* 382 (13) (2020) 1199–1207.
- [9] C. Huang, Y. Wang, X. Li, L. Ren, J. Zhao, Y. Hu, Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China, *Lancet.* 395 (2020) 487–506.
- [10] J.F. Chan, S. Yuan, K.H. Kok, K.K. To, H. Chu, J. Yang, A familial cluster of pneumonia associated with the 2019 novel coronavirus indicating person to-person transmission: a study of a family cluster, *Lancet.* 395 (2020) 514–523.
- [11] N. Zhu, D. Zhang, W. Wang, X. Li, B. Yang, J. Song, A novel coronavirus from patients with pneumonia in China, *N. Engl. J. Med.* 382 (2020) 727–733.
- [12] I.I. Bogoch, A. Watts, A. Thomas-Bachli, C. Huber, M.U.G. Kraemer, K. Khan, Pneumonia of unknown etiology in Wuhan, China: Potential for International Spread Via Commercial Air Travel, *J. Travel. Med.* (2020) 1–3.
- [13] J.T. Wu, K. Leung, G.M. Leung, Now casting and forecasting the potential domestic and international spread of the 2019-nCoV outbreak originating in Wuhan, China: a modelling study, *Lancet.* 395 (2020) 689–697.
- [14] E. Cheung, Thailand confirms first case of Wuhan virus outside China, *South China Morning Post*, January 13, 2020.
- [15] World Health Organization, Q&A on coronaviruses (COVID-19): <https://www.who.int/news-room/q-a-detail/q-a-coronaviruses> (2020).
- [16] P.V.D. Driessche, J. Watmough, Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission, *Math. Biosci.* 180 (2002) 29–48.
- [17] Department of Provincial Admiration, Ministry of Interior, Thailand, Office statistical system: <https://stat.dopa.go.th/stat/statnew/statTDD> (2020).
- [18] M. Shen, Z. Peng, Y. Xiao, L. Zhang, Modelling the epidemic trend of the 2019 novel coronavirus outbreak in China, *bioRxiv* 2020, medRxiv, (2020).
- [19] B.Tang, X. Wang, Q. Li, Estimation of the transmission risk of 2019-nCov and its implication for public health interventions, *J. Cli.Med.* 9 (2020) 462.