Fitting the Evolution of COVID-19 Cases of China and Thailand by Applying Piecewise Linear Approximation of Compartmental Model Parameters

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Abstract

This article explains an improved method to fit the evolution dynamics of the COVID-19 pandemics in China and Thailand during January – April 2020. It is done by using a conventional compartmental model and piecewise linear approximation of the model parameters. The reported COVID-19 data of China between 22nd January and 22nd March (60 days) and Thailand between 14th March and 16th April (34 days) are considered. According to the evolution trends, estimations on the total numbers of population involved in the spreading are made and they are about 83000 for China and 3000 for Thailand. By further analyzing the data along with the Susceptible-Infected-Recovered model, relevant epidemiological parameters, which indicate the degree of the outbreak, can be extracted. For the China data, a good fit is obtained when linear time-varying functions for the parameters are assumed. In case of Thailand data, a reasonable fit is obtained with constant parameter values and it can be improved by considering the time lag of 13 days before the triggering of the recovery rate. Based on the obtained model parameters, a forecast of epidemic situation in Thailand is made. The expected end point of critical pandemic period is at the mid of June 2020. The calculated basic reproduction number of 3.39 is reported for the epidemic spreading of COVID-19 in Thailand.

Keywords: COVID-19, China, Thailand, Compartmental Model, Piecewise Linear Approximation

Introduction

Nowadays, Corona virus disease 2019 (COVID-19) is a well-known infectious disease with human-to-human transmission. It originates in Wuhan city of Hubei province in the People's Republic of China in December 2019. The outbreak of COVID-19 both inside and outside Wuhan city causes many unforeseen health and management problems that need prompt responses of Chinese government. Emergency measures were applied to slow down the outbreak. For example, the duration of Lunar New Year holiday was extended. Ultimately, Wuhan city is lockdown on 23rd January 2020. In the meantime, the outbreak of COVID-19 in other big cities of China occurred. Infected people, who is asymptomatic, can still travel to other regions and other countries. They become virus carriers. In most cases, other nearby persons were unaware and can easily got infected. This leads to the wide spreading of the COVID-19. On 12th March 2020, World Health Organization (WHO, 2020) declared it as a global pandemic as the disease rapidly spreads across the world. On 8th April 2020, Wuhan city is reopened while many countries in all continents are still being suffered from the outbreaks in the countries. Severity, duration, and controllability of the spreading are quite different in different countries. They might reflect the applied measures and the concerns of the people and government of each country.

In order to evaluation the epidemic situation, a computer modeling is typically applied to improve the understanding and to further forecast for facility preparation. Modeling can sometimes aid in determining measures. Models with various degrees of complexities have been considered for dealing with COVID-19 situation. For example, Castorina, Iorio, and Lanteri (2020) applied well-known macroscopic growth laws to estimate the cumulative number of COVID-19 cases. Pongkitivanichkul et al. (2020), who are motivated by

the renormalization group framework, have proposed a modified logistic function to fit the cumulative number. On the other hand, 'Big Data' has been created and used for helping the response made for COVID-19 in Taiwan (Wang, Ng, & Brook, 2020) while conventional compartmental models have been considered by many groups (Adam, 2020; Huang, Liu, & Ding, 2020; Singh & Adhikari, 2020). In all mentioned cases (including this work), COVID-19 data of China is first examined in order to gain a reasonable view of the handled data. In this work, we aim to do a proper forecast of COVID-19 situation in Thailand.

Concerning the modeling of infectious diseases, the classification of population into groups is generally applied first (Keeling & Rohani, 2008, Vynnycky & White, 2010). It is therefore called as compartmental models. Susceptible-Infected-Susceptible (SIS), Susceptible-Infected-Recovered (SIR), Susceptible-Exposed-Infected-Recovered (SEIR), Susceptible-Exposed-Infected-Susceptible (SEIS), and Susceptible-Infected-Recovered-Deceased (SIRD) are examples of well-formulated models in epidemiology. In general, number of considered groups is proportional to the number of model parameters. In case of COVID-19, SIR model is widely applied (Adam, 2020; Huang, Yang, Dai, Tian, & Chen, 2020; Singh & Adhikari, 2020) because it does reflect the nature of this disease with minimum parameter set. Unnecessary addition of group will increase the number of model parameters, which their values are not known beforehand. Introduction of other information of the population (spatial location, age, and individual health information) might be possible if the complete and reliable data is available (Huang et al., 2020, Li et al., 2020). Moreover, artificial intelligence might be used for forecasting the situation (Hu, Ge, Li, Jin, & Xiong, 2020).

In this article, we investigate of recorded temporal COVID-19 data of China and Thailand and transform them into the dataset that is suitable for further analysis. A conventional compartmental model, which is so-called SIR model, is applied to fit the evolution dynamic of the datasets from both countries. Rough estimations of total number of involved populations are made. Piecewise linear approximation is applied for the relevant model parameters in order to produce an improved modeling result and reflect the epidemic situations. This mathematical technique allows one to link between the temporal changes of the physical parameters. In case of Thailand data, the epidemic forecast is done in order to speculate the end point of COVID-19 spreading in the country. The obtained basic reproduction numbers R_0 are discussed.

Evolution Trend

Due to the severity of COVID-19 between January and March 2020, many organizations have created online database for reporting statistics of the spreading (Worldometers, 2020; Foreignpolicy.com, 2020; WHO, 2020; Johns Hopkins University, 2020). The general interested statistics are the cumulative numbers of confirmed, recovered, and death cases of each country. In this study, they are extracted from the online database of the Center for System Sciences and Engineering, Johns Hopkins University and be plotted in Figure 1. In Figure 1(a), time evolution of the epidemic spreading in China and the world are presented. Cumulative numbers have been recorded since 22nd January and updated daily. Between 22nd January and 15th February, the world data is largely overlapped with the China data since the epidemic spreading first occurs in China. To date (17th April 2020), nearly constant values of China data are reported. This indicates the end of epidemic outbreak. Good controllability of the disease spreading in China has been established. Successive measures in China might be able to adapt to other countries. Moreover, the data of China can be used to develop the test and understanding

the nature of this spreading. In contrast to China, the pandemic is ongoing worldwide and become very severe in many countries. In case of Thailand, the cumulated numbers are presented in Figure 1(b). The first COVID-19 case is reported in January 2020 and the number of cases slowly increases until the beginning of March 2020. Inset of Figure 1(b) shows the evolution during the initial spreading interval. Cumulative number of confirmed cases is more than 100 on 15th March 2020. Differently from the world situation, the cumulative number of confirmed cases in Thailand becomes nearly constant earlier. This indicates the slowdown of spreading due to the fast response measures of Thai people and government.
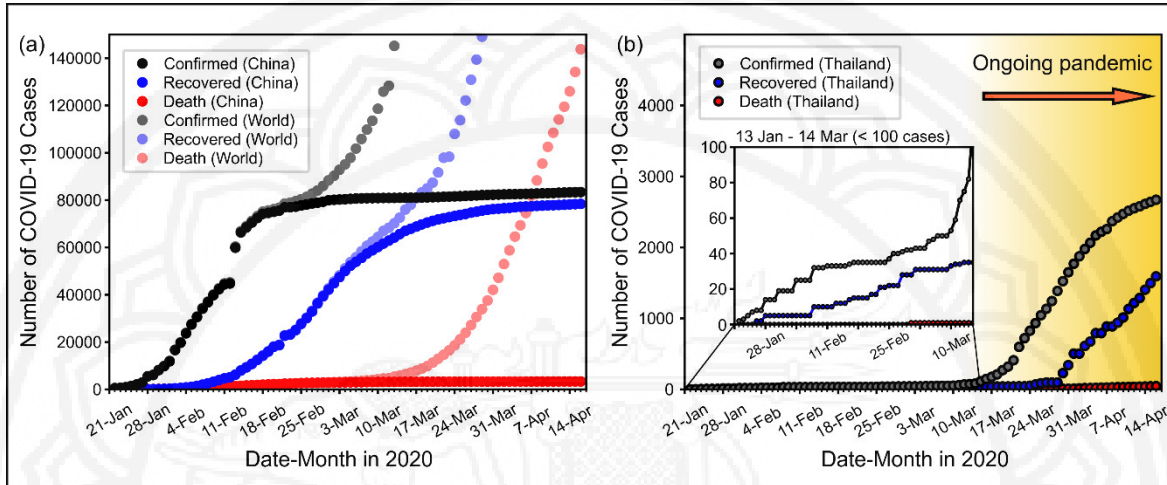

Figure 1 Time evolution of the epidemic spreading (a) in China and the world and (b) in Thailand. Inset of (b) shows the evolution during the initial spreading interval in Thailand.

The view of the evolution trends can be widened by plotting the data in logarithmic scale. Figure 2 shows the China (Figure 2(a)) and Thailand (Figure 2(b)) data in this scale. Relevant variables are defined in the figure. They are $N_C(t)$ for the cumulative number of confirmed cases, $N_R(t)$ for the cumulative number of recovered cases, and $N_D(t)$ for the cumulative number of death cases. For the data at the initial stage (the first 8 days) of the disease outbreak, exponential fits of the numbers of confirmed cases $N_C(t)$ are done. The applied function is in the form:

$$N_C(t) \approx N_{C,0} \cdot e^{\alpha t}, \tag{1}$$

where $N_{C,0}$ and α are the fitting parameters. Good fits (with least squares optimization) are obtained with the parameters shown in the figure and plotted as solid lines at the initial stages. The parameter α indicates the speed of initial spread. Well linear fits in logarithmic scale are obtained since the disease outbreak at initial stage is naturally multiplicative. However, they do not longer follow the multiplicative law after the initial stage. In the later stage (after ~8 days), the increase rate is reduced. Dashed lines in Figure 2 show the extrapolated curves from the good fits of the initial stage. Clear discrepancies are observed.
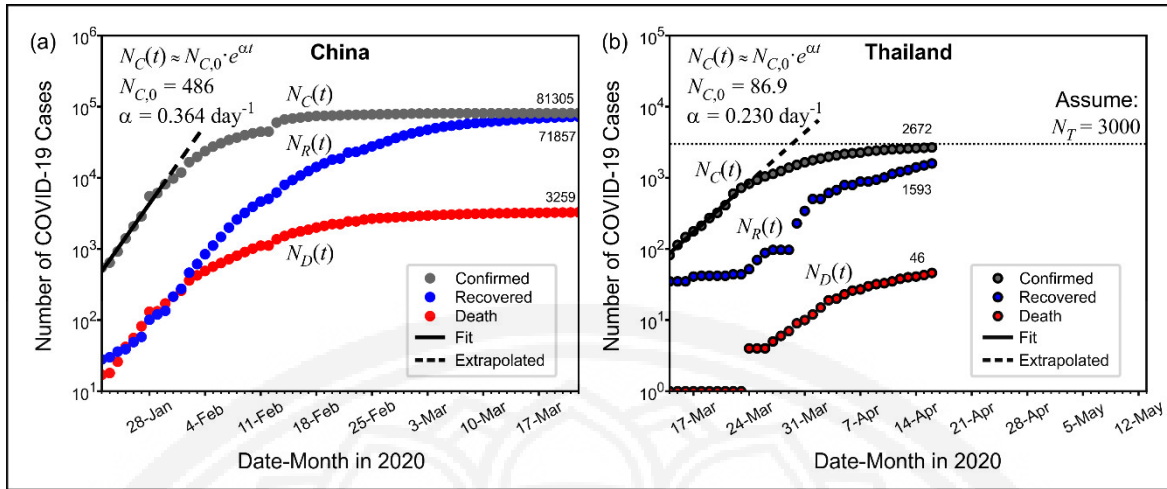
Figure 2 Time evolution of the epidemic spreading (a) in China and (b) in Thailand. Solid and dashed lines show the fitting of the data at initial stages (first 8 days) and the extrapolated, respectively. The variables $N_C(t)$, $N_R(t)$, and $N_C(t)$ are defined in the figure. Dotted line in (b) indicates the level of the assumed total number of population N_T (= 3000) for Thailand.

Comparison between China and Thailand data reveals that the disease spreading in Thailand is slower (smaller value of α). Not only the number of cases in Thailand is much smaller (e.g. 2672 << 81305) but also the percentage number (i.e., the number of cases divided by the total number of population in the country) is also smaller. These might be due to the high awareness of people to this disease before the outbreak event in the country. At present, the number of confirmed cases in China (Thailand) is about 81300 (2700). According to the trends and these numbers, we assume that the total numbers of population N_T, who involves in this epidemic, are 83000 and 3000 for China and Thailand, respectively.

Compartmental Model

A conventional model used to describe the number of people involved in an outbreak is so-called SIR model (Adam, 2020, Li et al., 2020, Keeling & Rohani, 2008). It is a kind of compartmental model where the total population is divided into 3 groups. They are Susceptible S: the group of people who have the possibility to get infected, Infected I: the group of infected people, and Recovered R: the group of people who get recovered from the disease and is assumed to gain immunity. In case of fatal disease, the last group (R) is the sum of those who have recovered and those who die from the disease. The numbers of people in each group are first normalized by the assumed total number of involved population N_T. Population ratios of people in each group are defined as $S(t)$, $I(t)$, and $R(t)$, respectively. The modeling of epidemic situation is essentially the study of dynamics of people moved from the group S to the I and then to the R. The continuous-time homogeneous SIR model describes the change in population of each group by using differential equations (Keeling & Rohani, 2008, Linge & Langtangen, 2020):

$$\frac{dS}{dt} = -\beta \cdot I \cdot S,$$

$$\frac{dI}{dt} = \beta \cdot I \cdot S - \gamma \cdot I, \qquad (2)$$

$$\frac{dR}{dt} = \gamma \cdot I,$$

where β and γ are model parameters. The β is so-called mass-action term and it indicates average number of contact events multiplied by the virus transmission probability for each contact. The γ is the recovery rate. Reciprocal of this γ term (i.e. $1/\gamma$) represents the average infectious period. According to the model, the basic reproduction number R_0 can be defined as the ratio of β and γ ($R_0 = \beta/\gamma$). The outbreak condition of any epidemics can be mathematically expressed as $R_0 > 1$ (Keeling & Rohani, 2008, Kermack & McKendrick, 1927). This R_0 parameter is thus an important indicator for the epidemic spreading. In order to solve Eqs. (2), initial conditions must be set. For this model, they generally are $R(0) = 0$, $I(0) = \delta$ ($0 < \delta \ll 1$) and $S(0) = 1 - \delta$ (because $S(t) + I(t) + R(t) = 1$, see Eqs. (2)). In this work, we first transform the reported data into $S(t)$, $I(t)$, and $R(t)$ and then fit the infected data $I(t)$ with its numerical solution (obtained by solving Eqs. (2)). Temporal scale is in the unit of day while β, γ and δ are treated as the fitting parameters.

Figure 3 shows the time evolution of the numbers of members in S, I and R group for China (Figure 3(a)) and Thailand (Figure 3(b)) data. In case of China (Thailand) data, total number of involved population N_T of 83000 (3000) is assumed for calculating the population ratios. According to the plot, China has obviously passed the peak of spreading period (between 12th February and 18th February) and the number of present infected people is now rather small and decay slowly. In case of Thailand, it has passed the peak spreading period (between 2nd April and 10th of April). Formula for the variable transformation from $N_C(t)$, $N_R(t)$, $N_D(t)$ and N_T to $S(t)$, $I(t)$, and $R(t)$ for SIR model are shown in the inset of Figure 3(b). It is noteworthy that the group R is the combination of the number of recovered and death cases ($R(t) = (N_R(t) + N_D(t))/N_T$), we therefore do not account for the death rate within this model and the $S(t)$, $I(t)$, and $R(t)$ cannot directly conversed back to $N_C(t)$, $N_R(t)$, and $N_D(t)$. Interestingly, the observed $R(t)$ of Thailand data show an abrupt change on 29th March. This is generally an indication of a nonlinear step-like behavior of the model parameter. In this case, it is the recovery rate γ.

Fitting Procedure and Results

The SIR model is applied to fit the observed infected data $I(t)$. The fit is done by numerically solving Eqs. (2) with Euler forward difference method (Linge & Langtangen, 2020). Time resolution of 0.01 day is chosen for this numerical integration as it gives negligible numerical errors for the obtained solution. The relevant parameters (δ, β and γ) are first estimated from the observed dataset and obtained α from the exponential fit of the initial stage (Initially, $\beta - \gamma \approx \alpha$). Computational code is developed in Python 3.7 language with the aid of Scipy and Numpy packages (Johansson, 2019). The model parameters are then optimized with *optimize.leastsq* method in Scipy package. Basically, the optimization is done by minimizing the sum of the squares of errors *SSE* between the observed population ratio of infected $I(t)$ and the calculated one $\hat{I}(t)$:

$$SSE(\delta,\ \beta,\ \gamma) = \sum_t (I(t) - \hat{I}(t))^2 \qquad (3)$$

In our model validation, other ratios ($S(t)$ and $R(t)$) are considered as well. For improving the fit of the observed data, time-varying parametric values of β and γ is tested. In the numerical experiment, we have performed the fit with constant, linear time-dependent, and step-like function for β and γ values. Only relevant and meaningful results are presented.
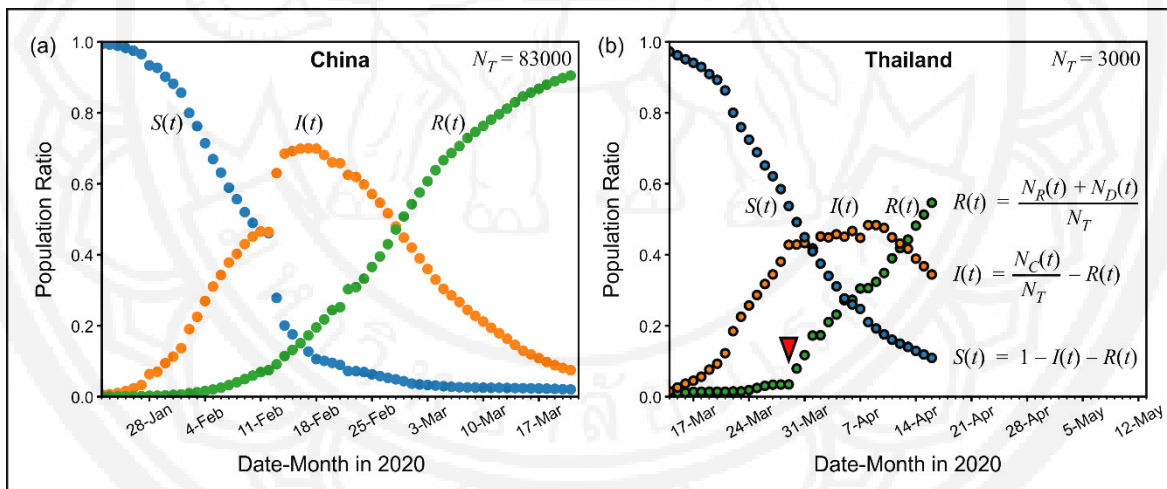

Figure 3 Time evolution of the numbers of people in S, I and R groups for (a) China and (b) Thailand data. Formula for the variable conversion are shown in the inset of (b). Upper red triangle in (b) marks the onset of the abrupt recovery (from I to R).

Figure 4(a) shows the results from the fitting of the China data (60 days, 22nd January − 22nd March) with constant model parameters. It is obvious that the fit with constant values does not produce the correct numerical values while the tentative trends of all functions ($S(t)$, $I(t)$, and $R(t)$) are correct. The obtained SSE is 0.265. In case of linear time−dependent parameters, it provides a good fit and the optimized result is shown in Figure 4(b). The calculated SSE is reduced to 0.0352. In this case, both β and γ are changed to time−dependent parameters $\beta(t)$ and $\gamma(t)$ and they are linearly varied from β_i and γ_i (at the 0th day) to β_f and γ_f (at the 59th day), respectively. All β_i, β_f, γ_i and γ_f are treated as the fitting parameters. The time−dependency of both β and γ reflects the change of control measures during the epidemic spreading in China. The trends of these parameters provide the decrease of R_0 over time. The obtained numerical values of the optimized parameters are presented as graphs in Figure 6 and discussed below.

Figure 5(a) shows the results from the fitting of available Thailand data (34 days, 14th March − 16th April) by using SIR model with constant parameters. The calculated SSE is 0.0172 in this fit. The optimized constant parameters can well fit the observed $I(t)$ and they also provide correct trends for both $S(t)$ and $R(t)$ as well. However, the discrepancy of the numerical values between observed $S(t)$ and $R(t)$ and the calculated ones is clearly observed in this case. Because the smooth increasing function is a general solution of $R(t)$ from the Eqs. (2), it is hard to represent a piecewise linear trend of the observed $R(t)$. We therefore consider the piecewise constant function of γ in this fitting case. The assumed γ is in the form

$$\gamma(t) = \begin{cases} 0, & t < t_0 \\ \gamma_c, & t \geq t_0 \end{cases}, \tag{4}$$

where t_0 and γ_c are constants. Both parameters are treated as the fitting parameters. Note that the parameter β is still considered as a constant since the inclusion of the β variation does not improve the fit (not shown).
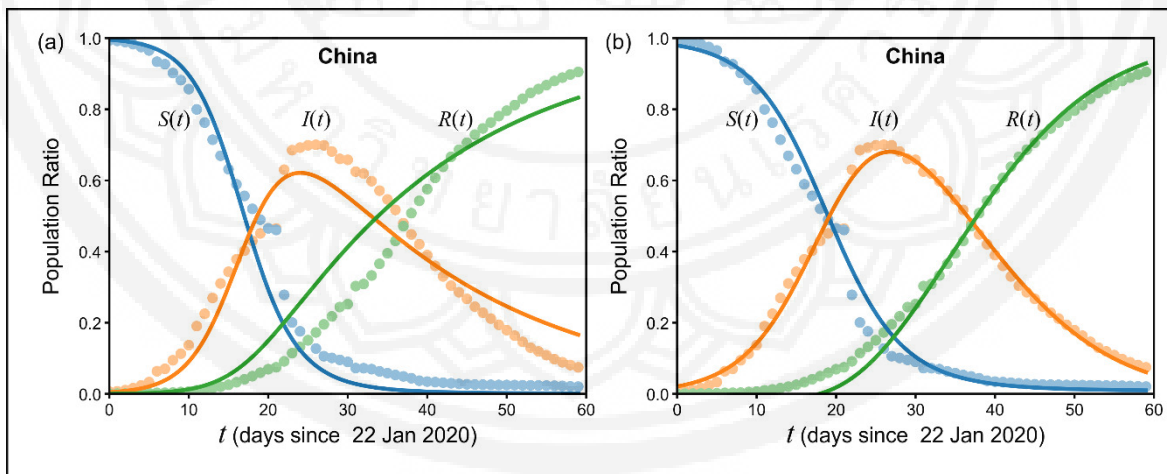

Figure 4 Fit of China data by using SIR model with (a) constant parameters and (b) linear time−varying parameters. Observed data are shown as background.
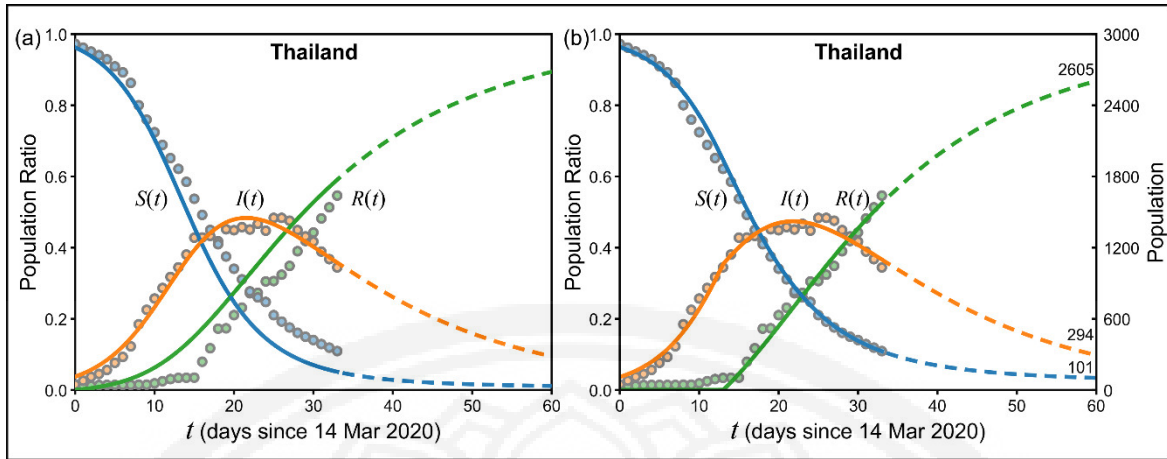
Figure 5 Fits of available Thailand data by using SIR model with (a) constant parameters and (b) 13-day-delayed constant parameter for γ. Observed data are shown as background. Dashed lines show the forecast of these values. Right axis of (b) shows the unnormalized scale. Numerical values near the right axis of (b) shows unnormalized numbers of population in each group after 60 days (on 13th May).

Figure 5(b) shows the results from the fitting with 13-day-delayed parameter for γ ($t_0 = 13$ days). The good fit of $I(t)$ is preserved while the matched trends and values of both $S(t)$ and $R(t)$ are clearly observed. The calculated SSE is reduced to 0.0133 in this fit. This result and the fit of China data confirm the advantage of the mathematical model proposed in this work. Piecewise linearity of the $R(t)$ can well be reproduced with the piecewise constant γ value proposed in Eq. (4). This might response to the delayed recovery of the COVID-19 patients in Thailand because all infected persons need some reasonable time to recover. In addition, due to the small number of infected cases in Thailand, the smooth function cannot represent the trend of $R(t)$.

According to the obtained optimized parameters of Thailand data, the forecast of $S(t)$, $I(t)$ and $R(t)$ can be made and it is shown as dashed lines in Figure 5. Numerical values the right axis of Figure 5(b) shows unnormalized numbers of population in each group after 60 days (on 13th May). According to the applied SIR model and its assumptions, least than 101 people will involve in the epidemic spreading after the date. Number of infected cases is below 300 and most of population are recovered. By further extrapolating the function, the expected end point of critical pandemic in Thailand at the mid of June 2020 (~123 days after the starting day) is predicted. After that date, the occurrence of new infected cases is much less than 1, the number of infected cases is below 10 and 97% of the total population becomes recovered. However, this predicted scenario is under the condition that the obtained epidemiological parameters, which relate to the applied public health management of the whole country, are not altered with time. If it is not the case, the epidemic spreading can prolong. Migration of patients can be another factor that extend the epidemic period in the country. In the worst scenario, another outbreak in a new group of population occurs. The number of total population N_T will increase. The cumulative numbers of all cases will go up again and they will eventually saturate at some higher values.
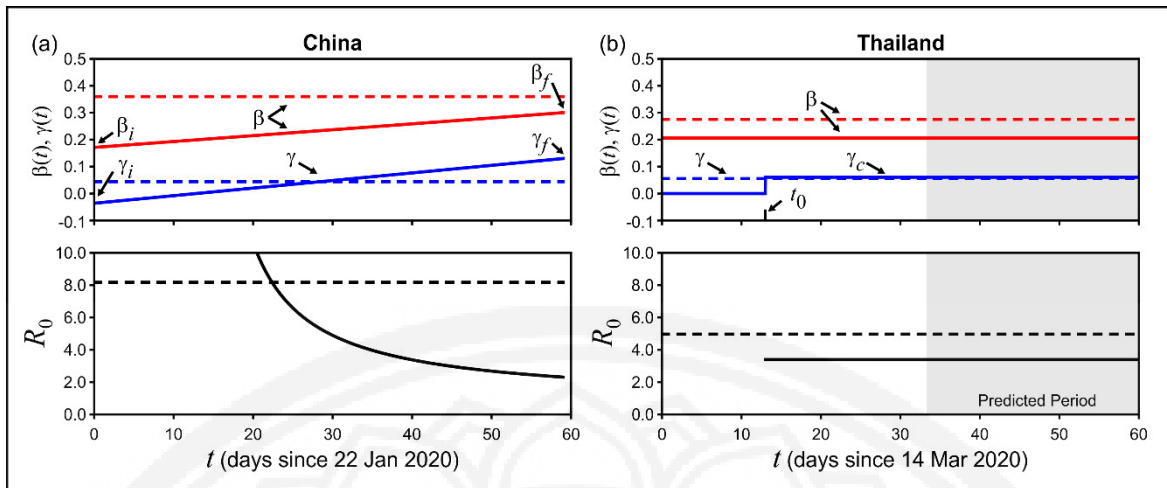
Figure 6 Evolution of the model parameters (upper panel) and the basic reproduction number R_0 (lower panel) from the fitting
of (a) China and (b) Thailand data. Dashed lines are from the fits with constant parameters and the solid lines are from
the fits with piecewise linear function. In (b), predicted period of parameter values are shaded.

Concerning the values of parameters obtained from the applied optimization scheme, they are plotted and
compared in Figures 6(a) and 6(b) for China and Thailand data, respectively. Since the good fit is obtained
only when the time-dependent parameters are considered for China data, we discuss mainly this case. By
allowing the time-variation of the parameters β and γ, the obtained basic reproduction number R_0 decreases with
time. At the initial stage of the outbreak, the R_0 value is very high (> 10, as shown in Figure 6(a)) because of
small and uncertain γ value. This might response to the first unforeseen event of the COVID-19 outbreak in the
country and the world. The calculated R_0 is eventually reduced to 2.31. It is rather low compared with the
recently reported value by Sanche et al. (2020) but it does agree with other studies of the similar data. For
example, Li et al. (2020) reported the R_0 value of 2.2. This value has been mentioned in many subsequent
studies.

In case of Thailand data, the small variations of obtained parameters from the fit are observed. Value of R_0
is decreased from 4.96 to 3.39 when the 13-day-delayed recovery rate is assumed. Both values are higher
than the above-mentioned R_0 value of China data. Different degree of restriction to the applied measures might
response for this difference. In case of Thailand, infection among involved people can happen easier and it
indicates the high severity of the epidemic spreading in Thailand. Fortunately, the involved population is much
lower in Thailand. It thus has less infected and death cases.

Conclusion and Suggestions

In conclusion, we have presented the reported epidemic data of COVID-19 in China and Thailand. The data are transformed for applying into SIR model. The method to fit the evolution dynamics is explained. It is done by solving the set of nonlinear differential equations. The reported COVID-19 data of China between 22nd January and 22nd March and Thailand between 14th March and 16th April are considered for the fitting with the SIR model. In case of the China data, a good fit is obtained when linear time-varying functions are assumed for the model parameters. For Thailand data, a reasonable fit is obtained with constant parameter and the fitting can be further improved by including the delay of 13 days before the starting of recovery event. A forecast is made based on the extrapolation of the model solution. The expected end point of critical pandemic period in Thailand is at the mid of June (~123 days after 14th March). Finally, the basic reproduction numbers are calculated. In case of Thailand, we report the R_0 value of 3.39, which indicates the severity of the disease spreading.

As suggestions for future researches, the considerations of data from other countries and the world data are possible within this model. Comparisons of the obtained parameter values can be used to quantitatively evaluate the effects of epidemic and forecast the situation. The scenarios might be changed according to the applied policies in each country. Further researches are needed to quantitatively evaluate the influences. In addition to the proposed model, modeling with other functional forms of parameters (e.g. exponential growth/decay or delta function) are possible and it might be done to reflect the occurred events during the observation. Since the epidemic of COVID-19 is still ongoing, new related publications are rapidly emerging. Some of them are collected by several publishers (Chen, Allot, & Lu., 2020; AAAS Science, 2020; Elsevier, 2020). The readers, who are interested in the study related to COVID-19, are suggested to explore the mentioned resources.

Acknowledgments

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