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Estimation of Reproduction Number of COVID-19 Spread Patterns in Thailand

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Abstract

Coronavirus disease 2019 (COVID-19) caused by severe acute respiratory syndrome–coronavirus 2 (SARS-CoV-2) and was declared as *a pandemic*. The purpose of this study was to estimation the reproduction number of COVID-19 Spread Patterns by using the data from 22 January to 30 June 2020. We applied the exponential growth rate to estimate the basic reproduction number (R_0) according to the status of lockdown. The exponential growth model results during lockdown period indicate the basic reproduction number is 0.58 (95% CI: 0.55-0.60), whereas the basic reproduction number is 0.98 during easing of lockdown. The highest value of the basic reproduction number is 2.48 (95% CI: 2.21-2.77) during pre-lockdown phase II. The reduction of basic reproduction numbers (R_0). suggested that timely implementation of control measures. The estimation of reproduction numbers could be used to analyze and evaluate the effectiveness of control measures and also used as a guide for public health policymakers for future COVID-19 outbreak. Moreover, with COVID-19 cases still present in Thailand, an estimation of basic reproduction number (R_0) would be helpful for continuous monitoring of the effectiveness of the current public health policies implemented in Thailand.

Keywords: Estimation, COVID-19, Exponential growth rate, Reproduction number, Emergency Decree and lockdown, Thailand

What was Known

- COVID-19 is a global pandemic caused by the pathogen severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)
- COVID-19 can be severe, and has caused millions of deaths around the world

What's New and Next

- The exponential growth rate model can provide the insight and predictions of predictions of the spread of COVID-19
- The high reproduction number suggest that an extraordinary combination of control measures is needed for halting COVID-19

Introduction

The coronavirus diseases 2019[1] was first detected in Wuhan city, Hubei Province, China and has rapidly progressed to pandemic level. The World Health Organization (WHO) reported that in worldwide, 10,185,374 cases have been confirmed, and 503,862 deaths on 30 June 2020[2]. The epidemiologists and infectious disease experts have expected the steady trend of increasing in confirmed COVID-19 case throughout the world.

Thailand's Ministry of Public Health announced the first patient infected with the new Coronavirus 2019 (2019-nCoV) – a 61-year-old Chinese woman from Wuhan city on 13 January 2020[3]. Confirmed COVID-19 cases was increased steadily and the number of cases reported on 24 March 2020 was 827 cases[4]. The rise in case numbers was attributed to the boxing match at Lumpinee stadium on 6 March 2020. Therefore, the number of new COVID-19 confirmed cases increased to over a hundred per day over the following week, and public venues and businesses were ordered to close in Bangkok and several other provinces. Consequently, Thai government invoked national Emergency Decree and massive lockdown on 26 March 2020[5]. Foreign non-residential nations were banned from entering country at all points, business types and activities were shut down and people were requested to remain inside their homes and to strictly limit all social contacts during implementation of the measure[6, 7]. Due to gradual decrease in new reported COVID-19 cases between 1 April 2020 and 28 April 2020 (Table 1), Thai government approved the easing of lockdown on 2 May 2020 such as the reopening of businesses and activities under health and public safety rules and regulations[8]. The Ministry of Public Health declared COVID-19 a communicable disease under surveillance was effective from 1 October

2022 onwards to provide public health services includes surveillance and preventative measures, risk communication, medical treatments, and other measures to control the disease[9].

Mathematical modeling is a useful application to control disease spread effectively. Several mathematical models have been proposed and formulated in the last decades to study the epidemiology of infectious diseases and develop helpful strategies for the efficient control of the infection. Mathematical modelling now plays avital role in policy making, including health-economic aspects. In research, it is essential in study design, analysis (including parameter estimation) and interpretation.

The exponential growth rate model is one of the mathematical models for analyzing the spread of COVID-19. The number of reported cases varied depending on each country because of the COVID-19 testing and contact tracing. Therefore, the number of infected cases reported by each country might significantly differ from reality. Several academic institutes have endeavored to build the mathematical model to predict the number of infected cases, reported deaths or recovered cases in various condition at global or country levels based on available current data. For example, Musa et al.[10] used the exponential growth rate model to predict the patterns of the epidemic of COVID-19 in Africa since the first case appearance on 14 February 2020. The study showed that the peak of. exponential growth rate as 0.22 per day (95% CI 0.20–0.24), and the basic reproduction number, R_0, as 2.37 (95% CI: 2.22–2.51) based on the assumption that the exponential growth starting from 1 March 2020. Moreover, Yuan et al.[11] estimated the exponential growth rate of the spread of COVID-19 in Europe during 21st 2020 through Match 9th 2020. The study showed that effective reproduction number (R_t) was 3.27 (95% confidence interval (CI) 3.17–3.38) for Italy, 6.32 (95% CI: 5.72–6.99) for France, 6.07 (95% CI: 5.51–6.69) for Germany, and 5.08 (95% CI: 4.51–5.74. Therefore, it seemed obviously that the exponential growth rate model could also explain the spread of COVID-19.

Many news sources stated that the number of COVID-19 cases in Thailand would exponentially increase, and some researchers reported that the growth rate of 33% infection would remain[12, 13]. Chawarat et al.[14] reported the estimated basic reproduction number by using exponential growth rate model based on gamma distribution for COVID-19 outbreak during January 12th 2020 through June 30th 2020 ranged from 2.81–4.36. [15]

We presented a prediction scheme based on the exponential growth rate model to estimate the basic reproduction numbers. The purpose of this study is to give the prediction of the growth and trend of COVID-19 epidemic in Thailand, which could be useful for the modelling for possible future COVID-19 outbreak.

Materials and Methods

To estimate basic reproduction number (R_0) and effective reproduction number (R_t), we retrieved Thailand daily confirmed COVID-19 case counts between the dates 22 January 2020 and 30 June 2020 from the database collected by the Center for Systems Science and Engineering, Johns Hopkins University. This database has been updated on a daily basis which can download the CSV files link: https:/github.com/CSSEGISandData/COVID-19.git[4] (Table 1).

Table 1 Cumulative number of reported COVID-19 cases in Thailand until 30 June 2020

Week	Number of Reported cases	Number of Cumulative cases
22 January – 28 January	14	14
29 January – 4 February	11	25
5 February – 11 February	8	33
12 February – 18 February	2	35
19 February – 25 February	2	37
26 February – 3 March	6	43
4 March – 10 March	10	53
11 March – 17 March	124	177
18 March – 24 March	650	827
25 March – 31 March	824	1651
1 April – 7 April	607	2258
8 April – 14 April	355	2613
15 April – 21 April	198	2811
22 April – 28 April	127	2938
29 April – 5 May	50	2988

6 May – 12 May	29	3017
13 May – 19 May	16	3033
20 May – 26 May	12	3045
27 May – 1 June	38	3083
2 June – 9 June	38	3121
10 June – 16 June	14	3135
17 June – 23 June	21	3156
24 June – 30 June	15	3171

The basic reproduction number (R_0)

The R_0 is an indicator the transmission potential of a disease at the beginning of the pandemic, R_0 represents the average number of secondary infections occurred by a general case of an infection in a population where everyone is susceptible. If $R_0 < 1$, the disease-free equilibrium point is stable indicating the absence of COVID-19 outbreak. On the other hand, if $R_0 > 1$, the epidemic equilibrium point is stable indicating the presence of COVID-19 outbreak[16-18].

Generation time

The serial interval is the incubation period of the cases from infection to symptoms and an infectious period from exposure to infection[19, 20]. As it cannot be measured directly that time between symptoms onset. The "generation time" function in the R0 package is used to find the best-fitting generation time distribution by parametric distributions “gamma”. In this case, the mean and standard deviation must be indicated in the desired time units[21].

Model parameter

The empirical distribution could be used from raw data however only the point estimates of mean and standard deviation were reported in previous studies and eligible serial-interval distributions are those with positive values. A range of positive-valued distributions were applied to estimate COVID-19 serial interval and the Gamma distribution was commonly applied to estimate serial interval times[22]. In this study, the serial interval distribution was assumed to be a gamma distribution with a mean and standard deviation of 6.3 days of 4.2 days[23].

Exponential growth rate (EGR) method

The exponential growth method was introduced for calculating R_0 by Wallinga and Lipsitch [24, 25]. This method during the early phase of an outbreak can be linked to the initial reproduction ratio, where M is the moment generating function of the generation time distribution and r indicates the growth rate (changes in the number of new cases per capita per unit time). As incidence data are integer, Poisson regression is used to estimate the parameter, rather than linear regression of the logged incidence[26, 27]. The R_0 is computed by the following formula:

$$R_0 = \frac{1}{M(-r)} \tag{1}$$

In this study, a function ("est.R0.EG") in the R0 package is used to estimate R_0[21]. In the next step, we presented the real-time estimation of R_t the daily outbreak of COVID-19.

The effective reproduction number (R_t)

The R_t is the average number of infections generated during the infectious period from a single infected person at time t. The R_t may vary across locations due to contact rate between individuals may differ. As population density, cultural differences, level of immunity and restrictions imposed on the movement of the people have a different. When R_t >1, the outbreak of diseases will spread more quickly to a large part of the population. If R_t < 1, the outbreak of disease will slow the spread before it infects many people. Therefore R_t <1 can control the situation of outbreak. The goal of epidemiology is reduced the value of R_t to manage the transmission of the communicable disease. Moreover, R_t is useful who policy planning for control and prevention the transmission effectively[28].

Estimate the effective reproduction number (R_t) using EpiEstim

The EpiEstim method[29] is used to generate an estimate for R_t. An approximate value is the average number of infections generated that each during the infectious period from a single person infected people at time t. The method can be measured using the formular below.

$$R_t = \frac{I_t}{\sum_{s=1}^{t} I_{t-s} w_s} \tag{2}$$

where I_t is the cumulative incidence at time t, I_{t-s} is the sum of infected incidence up to time t-1, and w_s is the infectivity function represented as probability dependent on time since infection by estimating from serial interval which assumed to be a gamma distribution[28, 30].

Model parameters

The goal is to make as few assumptions as possible to make reasonable forecasts without relying on the assumptions being correctly specified. We were unable to explicitly compute the parameters of the serial interval distribution because we did not have access to more specific infector-infected data pairs (e.g. contact tracing patient data). The serial interval distribution is the most essential assumption to make. Bi et al.[23] investigated the serial interval and transmission dynamics during SARS-CoV-2 predominance in China, and reported the estimated mean and standard deviation of the serial interval distribution. For this study, we assumed a discrete gamma-distributed serial for SARS-CoV-2 infection with mean of 6.3 days and a standard deviation of 4.2 days following the reported results of 15[23]. We also used the reporting delay adjusted incidence curve on sliding weekly windows ($\tau = 7$).

EpiEstim used to estimate and evaluate the time-variant (or instantaneous) reproduction numbers of the ongoing COVID-19 epidemic for different countries[31-33].

We divided the COVID-19 infection situation into three periods according to the status of lockdown as followings:

1. Pre-lockdown period
   Pre-lockdown period was further divided into two phases:
   1.1 Pre-lockdown phase I: the number of cumulative cases less than 100 cases starting from 22 January 2020 to 14 March 2020.
   1.2 Pre-lockdown phase II: the number of cumulative cases higher than 100 cases starting from 15 March 2020 to 25 March 2020.
2. Lockdown period starting from 26 March 2020 to 2 May 2020.
3. Easing of lockdown period starting from 3 May 2020 to 30 June 2020.

Therefore, the number of confirmed COVID-19 cases from 22 January 2020 to 30 June 2020 was also divided into three periods: pre-lockdown period, lockdown period, and easing of lockdown period (Figure 1).

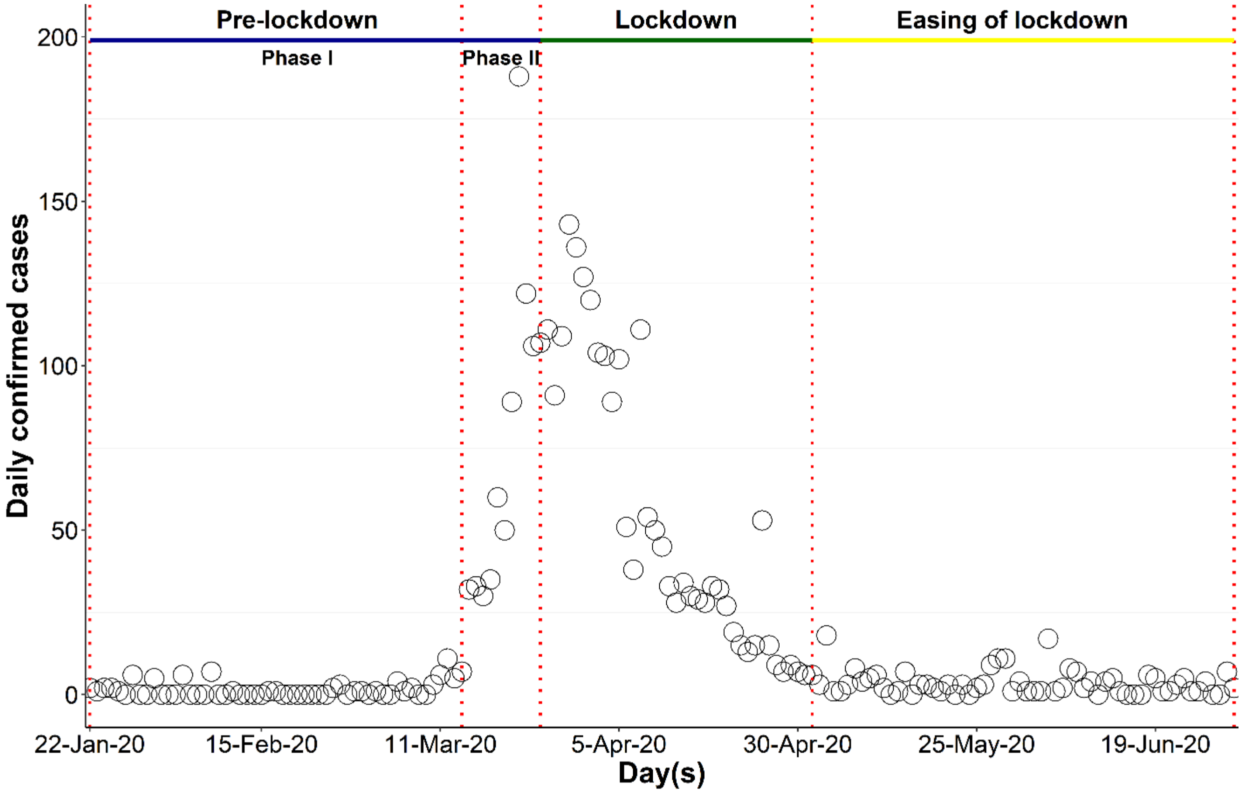

Figure 1 Confirmed case across three stages during COVID-19 outbreak in Thailand

Results

Estimation of basic reproduction number (R_0)

We estimated the basic reproduction number (R_0) based on exponential growth rate model for COVID-19 infection situation in Thailand starting from 22 January 2020 to 30 June 2020. The COVID-19 outbreak was divided into three periods according to the status of lockdown: pre-lockdown period, lockdown period, and easing of lockdown period.

Estimation of basic reproduction number (R_0) in pre-lockdown

The pre-lockdown period was further divided into two phases: pre-lockdown phase I (22 January 2020 to 14 March 2020and) pre-lockdown phase II (15 March 2020 to 25 March 2022). In pre-lockdown phase I, the results from exponential growth rate model represented the basic_reproduction number (R_0) was 1.17 (95% CI: 1.06–1.28) (Table 2). In Pre-lockdown phase II: Cumulative cases > 100.The estimation results from exponential growth rate model represented the basic reproduction number (R_0) was 2.48.17 (95% CI: 2.21–2.77) (Table 2).

Estimation of basic reproduction number (R_0) in lockdown period

After rapid surge in confirmed COVID-19 cases across Thailand, the government has announced national Emergency Decree and massive lockdown on 26 March 2020 to control the spread of COVID-19 infection. The results from exponential growth rate model represented the basic reproduction number (R_0) was 0.58 (95% CI:0.55–0.60) (Table 2).

Estimation of basic reproduction number (R_0) in easing of lockdown period

For the easing of lockdown period starting from 2 May 2020 to 30 June 2020, we found that the basic reproduction number (R_0) was 0.93 (95% CI: 0.88–0.98) (Table 2).

Table 2 Estimation of basic reproduction number (R_0) of the spread of COVID-19

Status of lockdown	**Date**	R_0	95%CI
Pre-lockdown period			
Phase I	22/01/2020 – 14/03/2020	1.17	1.06–1.28
Phase II	15/03/2020 – 25/03/2020	2.48	2.21–2.77
Lockdown period	26/03/2020 – 2/05/2020	0.58	0.55–0.60
Easing of lockdown period	3/05/2020 – 30/06/2020	0.93	0.88–0.98

Estimation of effective reproduction number (R_t)

The effective reproduction number was estimated by Cori et al.[29] method. This method required the incidence data consisting of daily counts of onset of symptoms. The effective reproduction number was estimated by the ratio of the number of newly diagnosed cases at time step t. (R_t). The available data on the confirmed cases at country-level were used to estimate the effective reproduction numbers (R_t) and their 95% confidence interval bands, as depicted by the red curves and bands, respectively in Figure 2.

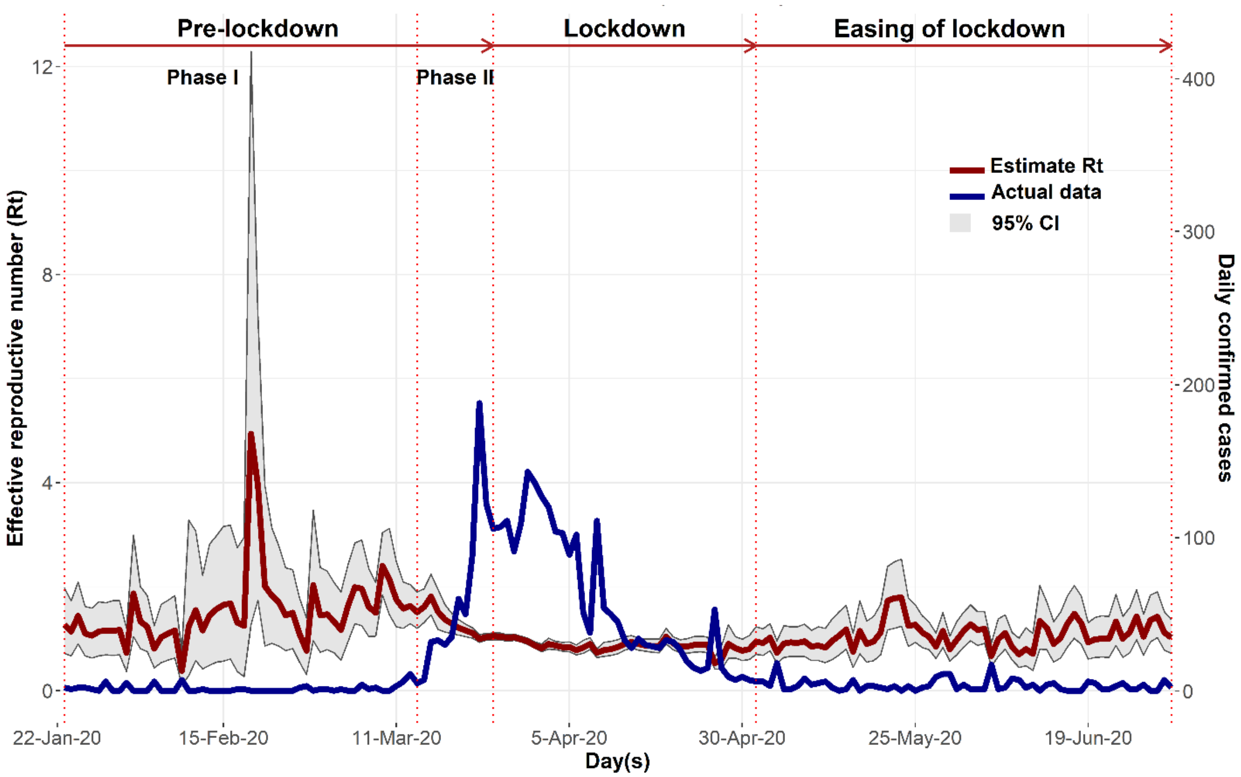

Figure 2 The effective reproduction number (R_t) based on COVID-19 case in Thailand

Estimation of basic reproduction number (R_0)

For current COVID-19 situation, we also retrieved Thailand daily confirmed COVID-19 case counts between the dates 1st August 2020 and 30th September 2022 from the database collected by the Center for Systems Science and Engineering, Johns Hopkins University. This database has been updated on a daily basis which can download the CSV files link: https:/github.com/CSSEGISandData/COVID-19.git[4]. The results from exponential growth rate model represented the basic reproduction number (R_0) was 0.85 (95% CI:0.85–0.86)

Estimation of effective reproduction number (R_t)

The effective reproduction number for current COVID-19 situation was estimated by the ratio of the number of newly diagnosed cases at time step t. (R_t). The available data on the confirmed cases at country-level were used to estimate the effective reproduction numbers (R_t) and their 95% confidence interval bands, as depicted by the red curves and bands, respectively in Figure 3.

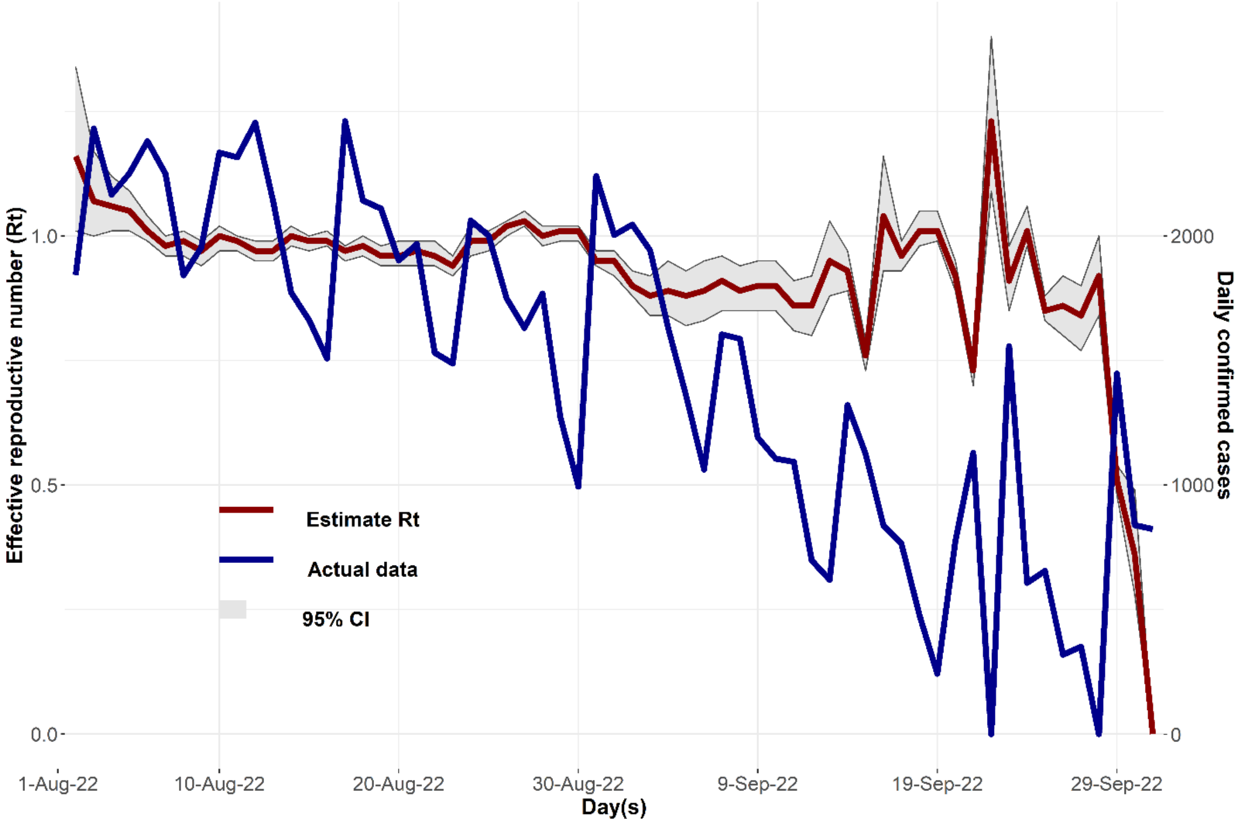

Figure 3 The effective reproduction number (R_t) based on COVID-19 case in Thailand from August 1st to 30th September 2022

Discussion

In this study, we used the exponential growth rate model on daily reported COVID-19 cases in Thailand from 22 January 2020 to 30 June 2020 to estimate the basic reproduction number (R_0) during pre-lockdown period, lockdown period, and easing of lockdown period.

The exponential growth rate model represented that the basic reproduction number in pre-lockdown phase II with more than 100 cases ($R_0 = 2.48$) (95% CI: 2.21–2.77) was much higher than pre-lockdown phase I with less than 100 cases ($R_0 = 1.17$). It indicated the outbreak of COVID-19 will continue to grow. The government implemented the measures to control COVID-19 spread. In lockdown period, the model indicated that the basic reproduction number (R_0) was_smallest ($R_0 = 0.58$) (95% CI: 0.55–0.60). It indicated that COVD-19 transmission would probably wane off because one infectious case will infect less than one person. The basic reproduction number increased after lifting nation-wide lockdown but still less than 1 (R_0= 0.58) (95% CI: 0.55–0.60). It also suggests that COVID-19 transmission would probably decline. A similar study[14] on COVID-19 epidemic in Thailand showed that the basic reproduction number (R_0) during the study ranged from 2.23–5.90, with a mean of 3.75. In our study, the basic reproduction number (R_0) was similar to their results especially during pre-lockdown phase II. However, there are some differences in values because of using different prior means and standard deviations to estimate the basic reproduction number. Our results were also consistent with the studies of the epidemic of coronavirus disease (COVID-19) during the initial phase of the infection outbreak in China showed that the basic reproduction number (R_0) was varied from 2.24–3.74[15, 34-36]. However, the studies in European countries such as France Germany and Spain was varied from 5.08-6.32[10]. Our estimate was thus lower than that in European countries. This might be due to a higher number of daily contacts for a citizen in European countries than for a citizen in Thailand because of the dense populations in European cities. This might also be due to methodological such as setting up the different prior means and standard deviations as mentioned in the method section.

For current Thailand COVID-19 situation, we used the daily confirmed case from August 1st to 30th September 2022**.** The exponential growth rate model represented that the basic reproduction number (R_0) was 0.85 (95% CI:0.85–0.86). The basic reproduction number (R_0) and effective reproduction number were relatively low when compared with the early COVID-19 outbreak in 2020. Our estimate is limited. We cannot estimate the overall size of daily confirmed cases because the reported daily confirmed cases was defined as the reported cases that only required hospitalizations [37]. Another reason is the coverage of 2-dose vaccination was fifty-four out of seventy-seven provinces or approximately 76% of total Thailand population[38].

The Limitation of this study is to estimate reproduction numbers. We need data on daily counts of the disease, but our results are based on the reported confirmed cases of the disease, and these reported cases are much less than the real cases because not all cases are symptomatic to be referred for testing and not all symptomatic patients are being tested- due to laboratory limitations. There may also be some considerations in the announcement of real data. As long as there is a constant relation between the number of reported cases and the number of real cases, the estimated results are acceptable. Moreover, the number of daily confirmed cases in this study was based on the reported results of the polymerase chain reaction test, the trend of daily confirmed cases was affected by the capacity of scientific laboratory for timely reporting cases during this early epidemic in 2020.

Conclusion

Based on our estimation on basic reproduction number (R_0) we showed that timely implementation of the control measures resulted in the reduction of basic reproduction numbers and in COVID-19 transmission. The results provided some information on the future wave of the COVID-19 pandemic that could be used in the future as a guide for public health policymakers in Thailand influenced by the social distancing measure, movement control measures and non-pharmacological interventions. The results can be also applied to analyze and evaluate the effectiveness of social distancing measure, movement control measures and non-pharmacological interventions. Moreover, with COVID-19 cases still present in Thailand, an estimation of the basic reproduction number (R_0) would be helpful for continuous monitoring of the effectiveness of the current public health policies implemented in Thailand.

Ethical Approval Statement

Siriraj Institutional Review Board is in full compliance with international guidelines for human research protection indicate that this study complies with a "Research with Exemption" category under topic Prediction of the Epidemiological Patterns and reproduction number of COVID-19 in Thailand.

Author Contributions

LJ designed and formulated the research under the supervision MY. LJ collected the COVID-19 dataset form the Center for Systems Science and Engineering (CSSE) and conducted the initial analysis according to the guidance of MY. LJ wrote the manuscript and MY helped to revise the manuscript. All authors read and approved the manuscript prior to submission for publication.

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Conflicts of Interest

The authors declare to have no conflicts of interest.

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