

# Monitoring the COVID-19 Situation in Thailand

1<sup>st</sup> Isarapong Eksinchol

Government Big Data Institute

Thai Ministry of Digital Economy and Society

Bangkok, Thailand

<https://orcid.org/0000-0003-3047-1850>

**Abstract**—The real-time reproduction number ( $R_t$ ) of COVID-19 in 77 provinces of Thailand during January–May 2020 are obtained by fitting a modified SEIR model to the actual data reported by the Thai Ministry of Public Health (MoPH). The spread of COVID-19 in Thailand is the most rapid in March 2020, when the number of daily new confirmed cases (DNCC) rises to above 100 cases per day. During this period, the calculated  $R_t$  is above 3. At the beginning of April 2020 following the lock-down, the calculated  $R_t$  drops sharply to below 1 and the number of DNCC decays progressively until it reaches a single digit in mid-May 2020. The model is also used to forecast the COVID-19 situation of every province in Thailand under different scenarios. It is scheduled to automatically re-fit to new data reported daily by MoPH so that  $R_t$  and the forecast results keep the users up-to-date in near real-time.

**Index Terms**—SARS-CoV 2, COVID-19, pandemic, Thailand, real-time reproduction number, forecast, modelling, python, scipy

## I. INTRODUCTION

In December 2019, Coronavirus Disease 2019 (COVID-19) originated in Wuhan, China [1]. The human-to-human transmission of this virus was first confirmed in January 2020 [1]. The transmissibility of asymptomatic cases and symptomatic cases during the pre-symptomatic phase makes it hard to identify and isolate all the infectious cases from susceptible population [2]–[4]. This allows the disease to spread rapidly and widely across the globe.

The first symptomatic case in Thailand, a 61-year-old Chinese female tourist from Wuhan, was found on 8<sup>th</sup> January 2020. One week later, on 15<sup>th</sup> January 2020, the first Thai symptomatic case, a 73-year-old female who just came back from a trip to Wuhan, was reported. On 31<sup>th</sup> January 2020, the first Thai who had never been abroad was found infected. This person, a 50-year-old male taxi driver, infected the COVID-19 from a symptomatic Chinese passenger he took to the hospital.

In January–February 2020, the COVID-19 situation in Thailand remained stable with  $\approx 1$  newly symptomatic case per day on average, most of which were foreign tourists from China. Thai people with positive COVID-19 lab test during this period were all infected from either travelling abroad or foreign visitors in Thailand. No Thai-to-Thai transmission was reported until March 2020, when there were 3 super-spreading events originated from the following 3 clusters:

1. *Nightclub in Thonglor, Bangkok*: The first positive lab test was on 12<sup>th</sup> March 2020, soon after which Bangkok found more than 50 cases infected from night clubbing and drinking.

2. *Lumpinee boxing stadium, Bangkok*: There was a major boxing event on 6<sup>th</sup> March 2020 with thousands of participants. The first positive lab test found among these participants was on 14<sup>th</sup> March 2020 in one of the event organizers, followed by more than 150 other positive cases. By the time they knew they were infected, these positive cases had already spread the disease widely in multiple provinces during their pre-symptomatic phase.
3. *Jhor Qudamak & Ulamak Malaysia 2020 in Kuala Lumpur, Malaysia*: This event was held from 27<sup>th</sup> February to 2<sup>th</sup> March 2020. There were 132 Thai participants in the event, around 50 of which were later found to have positive COVID-19 test. The majority of them returned back home in southern Thailand immediately after the event and had already spread the disease widely (mostly in Yala province) by the time the first positive lab test among them was reported on 16<sup>th</sup> March 2020.

During these 3 super-spreading events, the cumulative number and the number of Daily New Confirmed Cases (hereafter DNCC) soared up and reached 1,000 cases and 100 cases/day respectively in late March 2020. On 25<sup>th</sup> March 2020, the Royal Thai Government (RTG) declared the national state of emergency, which became effective on 26<sup>th</sup> March 2020 followed by multiple measures in order to take the COVID-19 situation under control. These measures mainly focused on preventing the spread of COVID-19 in public areas and any new super-spreading event from happening.

Since then, Thai people strictly follow the rules and recommendations from the Thai Ministry of Public Health (MoPH), including the implementation of social distancing. Public health professionals actively perform case investigations and contact tracing in order to quickly identify and isolate suspect cases from susceptible population. Within 5 weeks, the number of DNCC declines very rapidly to a single digit by early-May 2020.

Following the COVID-19 recovery in Thailand, there are debates about possibilities of easing the lock-down measures to recover the economic activity. The RTG has to make decisions on what measures should be eased at what time, and stay prepared for any situation that may happen after the lock-down easing. It is therefore essential to have a tool that helps RTG monitor and forecast the COVID-19 situation in near real-time.

For this reason, the author, as part of the Royal Thai Government COVID-19 modelling team, has constructed a mathemat-

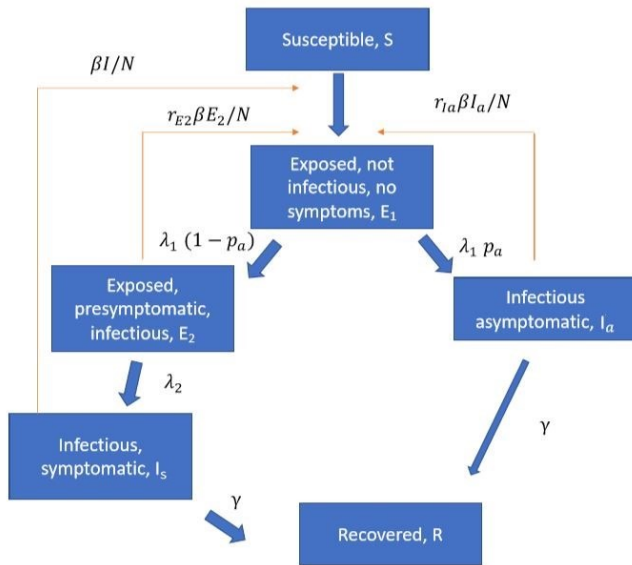


Fig. 1. From [9]. Diagram illustrating the model used in this study.

ical model of COVID-19 based on actual epidemiological data updated daily to calculate the real-time reproduction number ( $R_t$ ) and forecast the number of infected people in every province in order to provide early indicators of the COVID-19 situation in Thailand to the decision makers in near real-time.

## II. METHODOLOGY

This work constructs a modified Susceptible-Exposed-Infectious-Removed (SEIR) model and fit it to the actual DNCC data of every province in Thailand reported publicly by MoPH. In this section, we describe how values of  $R_t$  and the forecast results are obtained. We will first begin with details of the modified SEIR model in sections II-A and II-B. Then, section II-C will explain how we fit the model to the data.

### A. Forward Modelling

The forward model is a modified deterministic SEIR model, which has been used in several studies for modelling the COVID-19 (e.g. [5]–[8]). In addition to what the classical SEIR model implements, we divide each of the Exposed (E) and Infectious (I) phases further into 2 phases “E1 and E2” and “Is and Ia” respectively where E1 = exposed, not infectious, no symptoms; E2 = exposed, pre-symptomatic, infectious; Is = infectious, symptomatic; and Ia = infectious, asymptomatic. This is similar to what the Norwegian Institute of Public Health (NIPH) implemented [9] (as shown in Fig.1).

In Fig.1, phase S (susceptible) refers to anyone who has never been exposed to the disease. Phase E1 is when anyone from phase S gets exposed to the disease but is not infectious and shows no symptom of infection. After phase E1, there are two possible routes the disease can develop: either route E2–Is–R or route Ia–R.

We let the probability of entering route E2–Is–R be  $= 1 - p_a$  and the probability of entering route Ia–R be  $= p_a$  (these two add up to 1). An infected person entering route Ia–R

will never show any symptom (asymptomatic) but will be infectious during phase Ia. On the other hand, An infected person going through route E2–Is–R will show symptoms in phase Is and he/she will be infectious during phases E2 and Is. Both routes will eventually terminate at phase R (recovered), which is not infectious and no longer susceptible.

We let the phase-changing rate from E1 to E2 be  $\lambda_1 (1 - p_a)$  and from E1 to Ia be  $\lambda_1 p_a$  where  $\lambda_1$  is the decay constant of phase E1; the recovery rate from either phase Is to R or phase Ia to R be  $\gamma$ ; and, the decay constant of phase E2 be  $\lambda_2$ .

The susceptibles (phase S) can get infected from 3 different ways: 1.) from E2 at a rate  $= r_{E2} \beta E_2 / N$ ; 2.) from Ia at a rate  $= r_{Ia} \beta I_a / N$ ; and 3.) from Is at a rate  $= \beta I_s / N$  where  $N$  is the number of population in the system we are modelling.

According to the MoPH report, the COVID-19 mortality rate in Thailand is at around 2%. We therefore assume that the death proportion can be neglected in the model calculation. We also assume that  $p_a$ ,  $\lambda_1$ ,  $\lambda_2$ ,  $\gamma$ ,  $r_{E2}$ , and  $r_{Ia}$  are time-independent and each of them is the same for every province in Thailand. Whereas,  $\beta$  (which is the main parameter that determines the COVID-19 transmission rate) depends on the population density, behaviour, and culture in each province including the local government measures and policies, which can change with time. We hence let each province has its own numerical values of  $\beta$ , which is time-dependent that changes every 7 days.

We emphasize on monitoring the situation as a whole in real-time, which requires fast and efficient calculations rather than very complicated detailed algorithms. In order for the model to run fast enough so that it can update and fit to the actual data daily, we therefore do not divide different age groups further into multiple models.

Our forward model has the governing system of ordinary differential equations (ODEs) as follows:

$$\dot{S} = -\frac{\beta S}{N} (I_s + r_{E2} E_2 + r_{Ia} I_a) \quad (1)$$

$$\dot{E}_1 = -\lambda_1 E_1 + \frac{\beta S}{N} (I_s + r_{E2} E_2 + r_{Ia} I_a) \quad (2)$$

$$\dot{E}_2 = -\lambda_2 E_2 + \lambda_1 (1 - p_a) E_1 \quad (3)$$

$$\dot{I}_a = -\gamma I_a + \lambda_1 p_a E_1 \quad (4)$$

$$\dot{I}_s = -\gamma I_s + \lambda_2 E_2 \quad (5)$$

$$\dot{R} = \gamma I_s + \gamma I_a \quad (6)$$

$$N = S + E_1 + E_2 + I_a + I_s + R \quad (7)$$

We numerically integrate this system of ODEs using the odeint method in scipy.integrate library in python [10]. The initial conditions we use are:

$$S(0) = N - E_1(0)$$

$$E_2(0) = I_a(0) = I_s(0) = R(0) = 0$$

where  $E_1(0)$  is an unknown parameter that can be found by fitting the model to the actual data. This set of initial conditions means that we define time  $t = 0$  to be the date that the infection in phase  $E_1$  is first present with no one in any of the phases  $E_2$ ,  $I_a$ ,  $I_s$  and  $R$ .

Hence, our forward model has unknown parameters as follows:  $p_a$ ,  $\lambda_1$ ,  $\lambda_2$ ,  $\gamma$ ,  $r_{E2}$ ,  $r_{Ia}$ ,  $\beta$ , and  $E_1(0)$ . We let the numerical value of each of  $p_a$ ,  $\lambda_1$ ,  $\lambda_2$ ,  $\gamma$ ,  $r_{E2}$ , and  $r_{Ia}$  be the same for every province. But,  $\beta$  and  $E_1(0)$  are not the same.  $\beta$  of each province also changes every 7 days.

### B. Mobility between Provinces

People can travel across provinces. This causes the disease to spread from one province to another. Our model takes this factor into account by allowing people to move between provinces once daily. The model takes the daily number of people travelling across provinces as an input, which can change everyday.

We assume that the prevalence of each of the SEIR phases (S, E1, E2, Ia, Is, and R) in travelers departing from a province each day is equal to that found in the population of that province on the same day. That is, suppose a province A (with number of population =  $N$ ) on one day has the number of people in phases S, E1, E2, Ia, Is, and R equal to  $S$ ,  $E_1$ ,  $E_2$ ,  $I_a$ ,  $I_s$  and  $R$  respectively and the number of people departing from this province is =  $M$ , our model will assume that in these  $M$  travellers there are  $S \frac{M}{N}$ ,  $E_1 \frac{M}{N}$ ,  $E_2 \frac{M}{N}$ ,  $I_a \frac{M}{N}$ ,  $I_s \frac{M}{N}$  and  $R \frac{M}{N}$  individuals in phases S, E1, E2, Ia, Is, and R respectively.

### C. Data-Model Fitting

We use the `curve_fit` method from `scipy.optimize` library in python [10] to fit the model to the actual data. The `curve_fit` method seeks optimal values of the model's unknown parameters by minimizing the root mean square (RMS) error.

We define the error as the difference of the number of DNCC between the actual data and the model results. The actual number of DNCC comes from the MoPH daily report. And, the modelled number of DNCC is calculated from the phase-changing rate from phase E2 to phase Is, which is =  $\lambda_2 E_2$  (see the right-hand side of (3) and (5)). This is based on the assumption that the MoPH report has taken all the symptomatic cases into account.

We first construct a forward model for the whole country and fit it to the actual data from January to mid-May 2020 to find optimal parameters of  $p_a$ ,  $\lambda_1$ ,  $\lambda_2$ ,  $\gamma$ ,  $r_{E2}$ ,  $r_{Ia}$ ,  $\beta$ , and  $E_1(0)$ , where  $\beta$  can change every 7 days. During the rapid spread of COVID-19 in Thailand in March 2020, most foreigners were banned from entering the country. We therefore assume in the model that the country can be approximated as a closed system during January–May 2020 (i.e. no entering to and departing from Thailand). To find optimal parameters, we run the `curve_fit` method using the initial guess and the upper and lower bound values of the model's unknown parameters as given in Table I. The initial guess values are similar to those in the NIPH's modelling [9]. Optimal parameters obtained will be shown and discussed later in Section III (Table II).

Different province has different measures and policies for COVID-19 prevention and control. Population density, culture, and behaviour are also different. This results in a different transmission rate, hence, a different value of  $\beta$ . In the next step, we therefore model 77 provinces with 77 different

TABLE I  
INITIAL GUESS VALUES OF THE MODEL PARAMETERS WITH THE LOWER AND UPPER BOUNDS USED FOR RUNNING THE `SCIPY.OPTIMIZE.CURVE_FIT` METHOD.

Parameter	Initial Guess	Lower Bound	Upper Bound
$p_a$	0.40	0	1
$\lambda_1$	1/3	0	50
$\lambda_2$	1/2	0	50
$\gamma$	1/10	0	50
$r_{E2}$	1.00	0	10
$r_{Ia}$	1.00	0	10
$\beta$	0.15	0	1
$E_1(0)$	2.60	1	20

models, each of which has its own values of  $\beta$  and  $E_1(0)$ . But, every province will still use the same numerical values of  $p_a$ ,  $\lambda_1$ ,  $\lambda_2$ ,  $\gamma$ ,  $r_{E2}$ , and  $r_{Ia}$  obtained earlier from the whole-country modelling (see later in Section III Table II). To find optimal values of  $\beta$  and  $E_1(0)$  for each province, we fit the province's model to the actual provincial DNCC data (reported by MoPH) using the `curve_fit` method similar to what was implemented previously in the whole-country model. The initial guess and the upper and lower bound values of  $\beta$  and  $E_1(0)$  are also the same (as listed in Table I).

### D. Reproduction Number

By definition,  $R_t$  is the mean number of infections infected directly from a single infective [11]. We can decompose  $R_t$  into 2 components (multiplying together):

1. The mean infectious period: How many days on average an infective can transmit the disease to others, and
2. The mean transmission rate: how many, per day, on average there are new cases infected from an infective.

In the model, phases E2, Is, and Ia are infectious with the mean lifetime (mean infectious period) =  $1/\lambda_2$ ,  $1/\gamma$ , and  $1/\gamma$  respectively (see (3), (5), and (4)), and the transmission rate =  $r_{E2}\beta$ ,  $\beta$ , and  $r_{Ia}\beta$  respectively (see (1)). Multiplying these two components together gives the mean number of new cases infected from an infective in phase E2, Is, and Ia =  $r_{E2}\beta/\lambda_2$ ,  $\beta/\gamma$ , and  $r_{Ia}\beta/\gamma$  respectively. We add these three terms together, each weighted by the probability of its route (E2–Is–R route =  $1 - p_a$  and Ia–R route =  $p_a$ ), to obtain the mean number of infectious infected directly from an infective:

$$\begin{aligned} R_t &= (1 - p_a) \left[ \frac{r_{E2}\beta}{\lambda_2} + \frac{\beta}{\gamma} \right] + p_a \frac{r_{Ia}\beta}{\gamma} \\ &= \beta \left[ \frac{p_a r_{Ia} + 1 - p_a}{\gamma} + \frac{(1 - p_a) r_{E2}}{\lambda_2} \right]. \end{aligned} \quad (8)$$

i.e.,  $R_t$  can be calculated directly from the model parameters fitted to the actual data.

## III. RESULTS AND DISCUSSION

The optimal parameters obtained from fitting the model to the actual data are listed in Table II. These are slightly different from the values reported by [12] probably due to the diversity

TABLE II

OPTIMAL PARAMETER VALUES OBTAINED BY FITTING THE MODEL TO THE ACTUAL DATA USING THE SCIPY.OPTIMIZE.CURVE\_FIT METHOD.

Parameter	Optimal Value
$p_a$	0.41
$\lambda_1$	1.82
$\lambda_2$	1.26
$\gamma$	0.13
$r_{E2}$	1.31
$r_{Ia}$	0.80
$E_1(0)$	2.83

of several factors among different countries such as climate (e.g. temperature and humidity) and genetic differences, which may respond/react to COVID-19 differently.

#### A. Fitting model to the historical data

The bottom panel of Fig.2 shows  $R_t$  obtained from fitting the model to the actual data (shown in Fig.2, top panel) of Thailand viewed as a single system. This graph shows that  $R_t > 1$  before the lock-down begins at the end of March. Especially in early-March, there were 3 super-spreading events happening simultaneously (see section I), during which the number of DNCC soared up from below 10 to above 100 per day (Fig.2, top panel). The calculated  $R_t$  also has a sharp rise from around 1.5 to above 3 during the super-spreading events in early-March 2020.

As stated in several studies (e.g. [11], [13], [14]),  $R_t$  is a key indicator for monitoring pandemics including the COVID-19. Fig.2 shows that  $R_t$  trend leads the trend of DNCC number. In early-March 2020,  $R_t$  has risen sharply (from  $\approx 1.5$  to  $\approx 3$ ) one week prior to a significant increase of the number of DNCC around mid-March 2020.

On 25<sup>th</sup> March 2020, the RTG announced the national state of emergency, night curfew, and ban on incoming international flights, which become effective on 26<sup>th</sup> March 2020. Social gatherings and community events were prohibited. People implemented social distancing and stayed at home. From then,  $R_t$  calculated by the model suddenly dropped to below 1 (Fig.2, bottom panel), meaning that the epidemic was fading out as shown in the top panel of Fig.2 where the number of DNCC began to drop.

In addition to the whole-country view, we also calculate  $R_t$  for every individual province updated daily. Fig.3 shows the model results in two example provinces: Bangkok (left column) and Phuket (right columns).

The COVID-19 outbreak in Thailand originated in Bangkok, the capital city. Bangkok also has the highest total number of confirmed cases in Thailand at around one half of the whole country. The disease then spreads to other provinces due to travel. In Fig.3, by comparing Bangkok (left column) to Phuket (right column), we can see that both the number of DNCC and  $R_t$  in Bangkok begin to rise one week before Phuket (early-March vs. mid-March 2020).

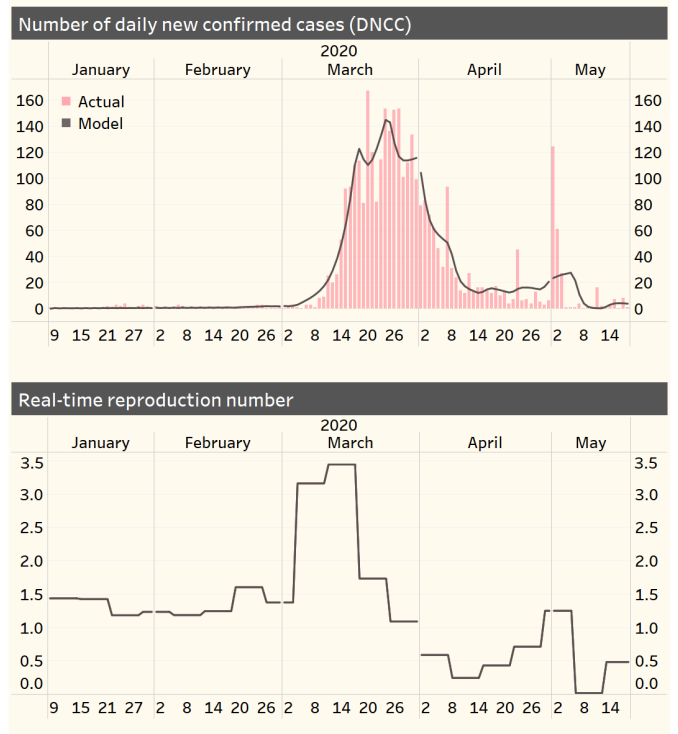


Fig. 2. **Top:** number of daily new confirmed cases (DNCC) as reported by the Thai Ministry of Public Health (MoPH) (pink bars) and as calculated from the model (dark grey line). **Bottom:** real-time reproduction number of COVID-19 in Thailand obtained by fitting the whole-country model to the actual data during January–May 2020.

Nevertheless, the reason why we see the number of DNCC and  $R_t$  in Bangkok rise before Phuket could also be because the lab test for COVID-19 available in Phuket could begin later than in Bangkok. If this was the case, it would result in a delay of confirmed case findings in provinces outside Bangkok.

#### B. Forecasting

Once the optimal model parameters are obtained, we can use the model to forecast time evolution of the number of people in different SEIR phases ( $S$ ,  $E_1$ ,  $E_2$ ,  $I_a$ ,  $I_s$ , and  $R$ ) in several different scenarios. From April 2020, Thailand can control the COVID-19 situation very well.  $R_t$  stays below 1 and the number of DNCC keeps declining until it is below 10 in mid-May 2020 (as seen in Fig.2).

At the same time, some people demand easing of the lock-down to recover the economic activity. The RTG has to find out what measures could be eased, and how much the COVID-19 situation will change after the lock-down easing. To answer the latter question, the author (working as a Thai Government Officer in collaboration with MoPH) uses this numerical model to forecast the COVID-19 situation in 4 different scenarios:

1.  $R_t = 1$  with no one allowed to travel between provinces,
2.  $R_t = 1$  with normal travel between provinces,
3.  $R_t = 2$  with no one allowed to travel between provinces, and
4.  $R_t = 2$  with normal travel between provinces.

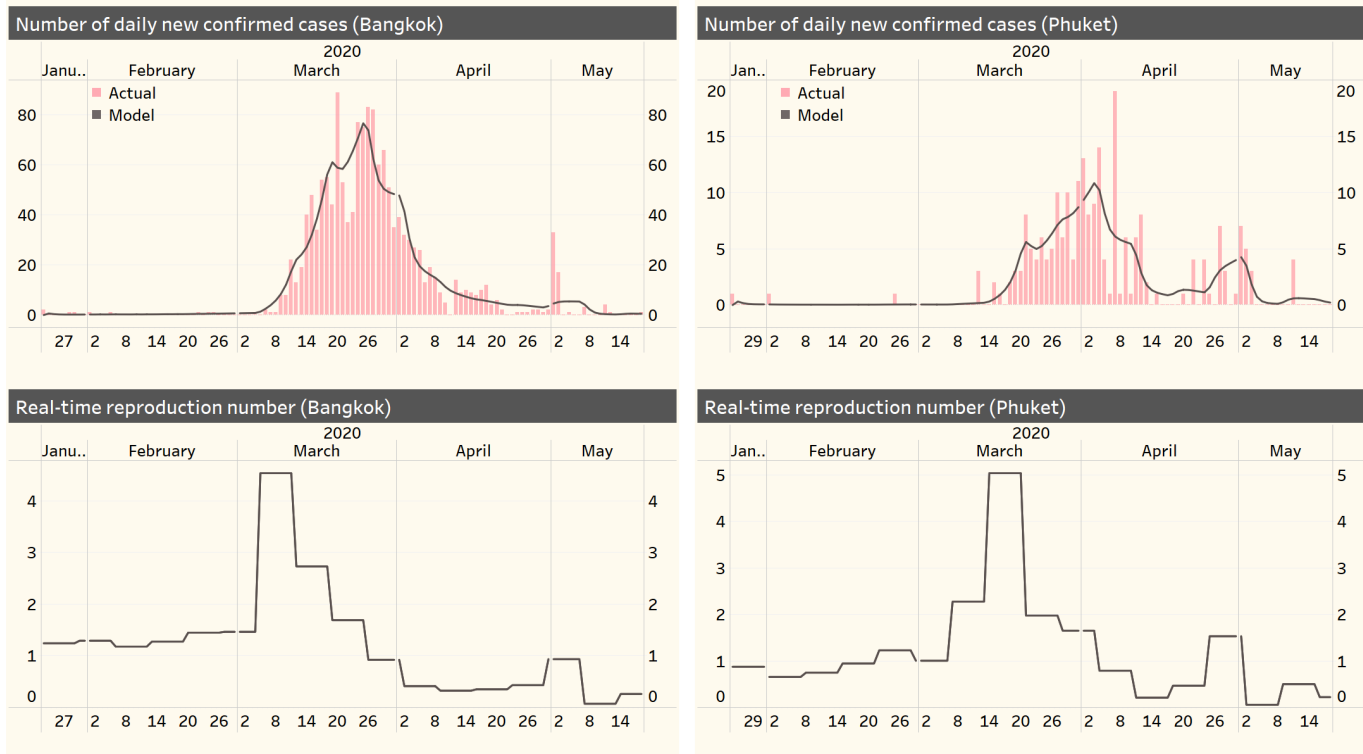


Fig. 3. Actual data and the model results for Bangkok (left column) and Phuket (right column). For details of the top and bottom row, see caption of Fig.2 (top) and 2 (bottom) respectively.

From (8), we can adjust the modelled  $R_t$  by adjusting  $\beta$ . Numerical values of the remaining parameters ( $p_a$ ,  $\lambda_1$ ,  $\lambda_2$ ,  $\gamma$ ,  $r_{E2}$ , and  $r_{Ia}$ ) are kept unchanged as listed in Table II. In the scenarios with normal travel across provinces, we estimate the daily number of travellers between provinces from the total number of visitors visiting each province in year 2018 reported by the Thai Ministry of Tourism and Sports.

The forecast results of 2 example provinces (Bangkok and Patum-thani) are shown in Fig.4. Blue and green lines show that if  $R_t = 1$  the number of DNCC in every province will stay constant, and the effect of travel between provinces will be insignificant. i.e., the disease is in the endemic equilibrium when  $R_t = 1$  as expected.

On the other hand, if  $R_t = 2$ , the number of DNCC in each province will grow exponentially. Travel between provinces will affect different province differently depending mainly on the COVID-19 prevalence in that province relative to the others.

For example, Bangkok (left panel of Fig.4), which is one of the top 5 provinces that have the highest COVID-19 prevalence in Thailand, will see a slower growth of DNCC if travel between provinces returns to normal compared with the case when travelling across provinces is banned (red line vs. yellow line, left panel of Fig.4). The reason is because the provincial border re-opening will drain some infectives out of Bangkok. Infectives from Bangkok can then transmit the disease to people outside Bangkok instead of transmitting it to people in Bangkok themselves. This also applies to other provinces with

the COVID-19 prevalence above the average of the country.

Conversely, provinces with the COVID-19 prevalence below the average (such as Patum-thani, right panel of Fig.4) will have a faster growth of DNCC if travel between provinces returns to normal compared with the case when travelling across provinces is banned (red line vs. yellow line, right panel of Fig.4). Travel between provinces will drain infectives *out of* provinces with prevalence *above* the average *into* provinces with prevalence *below* the average.

In addition to what we have shown here, our model also forecasts the number of infected people in different SEIR phases in every province. This includes the Is phase, which can be used to estimate the hospitalization rates. This helps the RTG ensure that health-care resources are sufficient for any scenario that can happen in the near future.

#### IV. CONCLUSIONS

We develop a modified SEIR model and fit it to the actual COVID-19 data in Thailand reported by MoPH to find the trend of  $R_t$  and to forecast the COVID-19 situation in multiple different scenarios. Our main priority is given to the computational cost so that the model can re-fit to new data and re-forecast everyday, which keeps the users up-to-date. The near real-time  $R_t$  and forecast results give early warnings of potential risks so that the RTG are well-prepared for any challenge in the near future.

COVID-19 in Thailand spreads most rapidly in March 2020, during which  $R_t$  is elevated above 3 and the number of DNCC

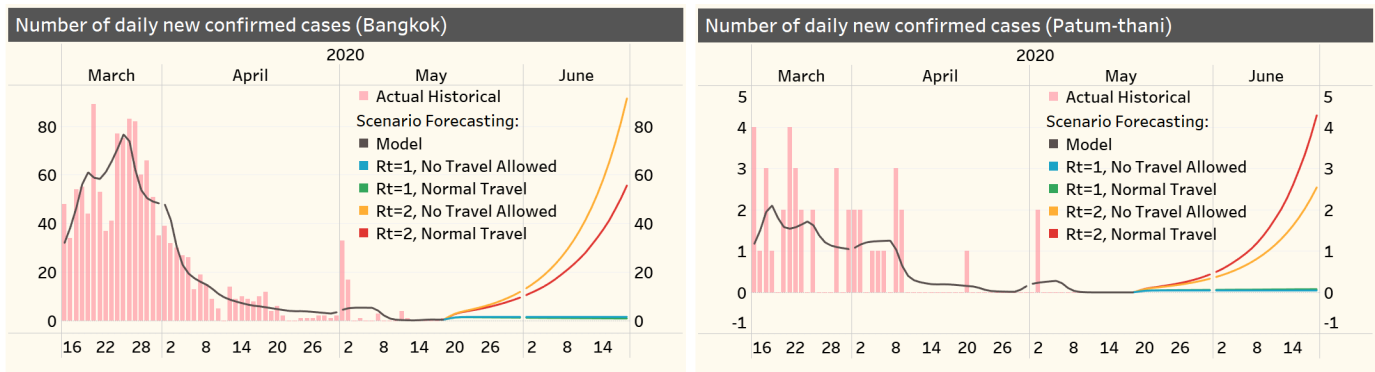


Fig. 4. The number of DNCC in Bangkok (left) and Patum-thani (right). Different coloured lines correspond to different scenarios of the model forecast results performed on 19<sup>th</sup> of May 2020: 1.) **blue line**:  $R_t = 1$  with no one allowed to travel between provinces, 2.) **green line**:  $R_t = 1$  with normal travel between provinces, 3.) **yellow line**:  $R_t = 2$  with no one allowed to travel between provinces, and 4.) **red line**:  $R_t = 2$  with normal travel between provinces. Dark grey line is the modelled number of DNCC obtained from fitting model to the actual historical data (pink bars).

is greater than 100 cases per day. By the beginning of April,  $R_t$  has dropped quickly to below 1, which stops the spread of COVID-19. Since then, the number of DNCC substantially declines to below 20 cases per day by mid-April 2020.

#### ACKNOWLEDGEMENT

I would like to acknowledge the Thai Ministry of Public Health for providing the COVID-19 data of Daily New Confirmed Cases and the computational resources for running the model and creating data visualization.

#### REFERENCES

- [1] Qun Li et al., "Early Transmission Dynamics in Wuhan, China, of Novel Coronavirus-Infected Pneumonia," *New England journal of medicine*, vol. 382, no. 13, Massachusetts Medical Society, pp. 1199–1207, 2020, DOI: 10.1056/NEJMoa2001316.
- [2] M.M. Arons et al., "Presymptomatic SARS-CoV-2 Infections and Transmission in a Skilled Nursing Facility," *New England journal of medicine*, vol. 382, no. 22, Massachusetts Medical Society, pp. 2081–2090, 2020, DOI: 10.1056/NEJMoa2008457.
- [3] Monica Gandhi, Deborah S. Yokoe, and Diane V. Havlir, "Asymptomatic Transmission, the Achilles' Heel of Current Strategies to Control Covid-19," *New England journal of medicine*, vol. 382, no. 22, Massachusetts Medical Society, pp. 2158–2160, 2020, DOI: 10.1056/NEJMe2009758.
- [4] Daihai He et al., "The relative transmissibility of asymptomatic COVID-19 infections among close contacts," *International Journal of Infectious Diseases*, vol. 94, Elsevier, pp. 145–147, 2020, DOI: 10.1016/j.ijid.2020.04.034.
- [5] Kaustuv Chatterjee, Kaushik Chatterjee, Arun Kumar, and Subramanian Shankar, "Healthcare impact of COVID-19 epidemic in India: A stochastic mathematical model," *Medical Journal Armed Forces India*, vol. 76, Elsevier, pp. 147–155, 2020, DOI: 10.1016/j.mjafi.2020.03.022.
- [6] Yaqing Fang, Yiting Nie, and Marshare Penny, "Transmission dynamics of the COVID-19 outbreak and effectiveness of government interventions: A data-driven analysis," *Journal of Medical Virology*, vol. 92, Wiley, pp. 645–659, 2020, DOI: 10.1002/jmv.25750.
- [7] Kiesha Prem et al., "The effect of control strategies to reduce social mixing on outcomes of the COVID-19 epidemic in Wuhan, China: a modelling study," *The Lancet Public Health*, vol. 5, Elsevier, pp. e261–e270, 2020, DOI: 10.1016/S2468-2667(20)30073-6.
- [8] Zifeng Yang et al., "Modified SEIR and AI prediction of the epidemics trend of COVID-19 in China under public health interventions," *Journal of Thoracic Disease*, vol. 12, pp. 165–174, 2020, DOI: 10.21037/jtd.2020.02.64.
- [9] Norwegian Institute of Public Health, "Coronavirus modelling at the NIPH," Published 17<sup>th</sup> April 2020, Updated 12<sup>th</sup> June 2020, url: <https://www.fhi.no/en/id/infectious-diseases/coronavirus/coronavirus-modelling-at-the-niph-fhi/>.
- [10] Pauli Virtanen et al., "SciPy 1.0: fundamental algorithms for scientific computing in Python," *Nature Methods*, vol. 17, pp. 261–272, 2020, DOI: 10.1038/s41592-019-0686-2.
- [11] O Diekmann, and JAP Heesterbeek, "Mathematical Epidemiology of Infectious Diseases: Model Building, Analysis and Interpretation. 1st ed.," Wiley, 2000, ISBN 0-471-49241-8.
- [12] Luca Ferretti et al., "Quantifying SARS-CoV-2 transmission suggests epidemic control with digital contact tracing," *Science*, vol. 368, 2020, DOI: 10.1126/science.abb6936.
- [13] Ta-Chou Ng, and Tzai-Hung Wen, "Spatially Adjusted Time-varying Reproductive Numbers: Understanding the Geographical Expansion of Urban Dengue Outbreaks," *Scientific Report*, vol. 9:19172, 2019, DOI: 10.1038/s41598-019-55574-0.
- [14] Roya Nikbakht, Mohammad Reza Baneshi, Abbas Bahrapour, and Abolfazl Hosseinnataj, "Comparison of methods to Estimate Basic Reproduction Number ( $R_0$ ) of influenza, Using Canada 2009, and 2017-18 A (H1N1) Data" *Journal of Research in Medical Sciences*, vol. 24:1, pp. 67, 2019, DOI: 10.4103/jrms.JRMS\_888\_18.