Mathematical Biosciences and Engineering

http://www.aimspress.com/journal/mbe

MBE, 20(8): 13849–13863.
DOI: 10.3934/mbe.2023616
Received: 01 April 2023
Revised: 16 May 2023
Accepted: 01 June 2023
Published: X June 2023

Research article

The effects of disease control measures on the reproduction number of COVID-19 in British Columbia, Canada

Meili Li[1,*], **Ruijun Zhai**[1] **and Junling Ma**[2]

[1] School of Science, Donghua University, Shanghai 201620, China

[2] Department of Mathematics and Statistics, University of Victoria, Victoria, BC V8W 2Y2, Canada

* **Correspondence:** Email: stylml@dhu.edu.cn.

Abstract: We propose a new method to estimate the change of the effective reproduction number with time, due to either disease control measures or seasonally varying transmission rate. We validate our method using a simulated epidemic curve and show that our method can effectively estimate both sudden changes and gradual changes in the reproduction number. We apply our method to the COVID-19 case counts in British Columbia, Canada in 2020, and we show that strengthening control measures had a significant effect on the reproduction number, while relaxations in May (business reopening) and September (school reopening) had significantly increased the reproduction number from around 1 to around 1.7 at its peak value. Our method can be applied to other infectious diseases, such as pandemics and seasonal influenza.

Keywords: reproduction number; transmission rate; control measure; infectious period

1. Introduction

In December 2019, a novel coronavirus (COVID-19) was discovered [1]. COVID-19 is a respiratory infectious disease caused by the severe acute respiratory syndrome coronavirus, transmitted by contact, aerosols and inhalation of virus-infected droplets [2,3]. Unfortunately, there were no effective drugs to treat the disease in 2021 [1]. Therefore, the control protocols were mainly physical isolation, such as quarantine, contact tracing and social lockdown [4–8]. Therefore, it is crucial to study the effectiveness of control measures for this disease.

The basic reproduction number $\mathcal{R}_0$ is a critical parameter in the analysis of infectious diseases. It measures the average number of secondary infections caused by a typical infectious individual in a fully susceptible population. The disease will not cause an epidemic if $\mathcal{R}_0 < 1$ [11–13]. As the epidemic progresses, or when control measures such as social distancing and vaccination are implemented, susceptible individuals are depleted and some of the contacts of the infectious individuals are

made to already infected individuals, which do not cause transmission. In this case, the threshold for disease spread is measured by the effective reproduction number $\mathcal{R}_t$, which measures the number of secondary infections caused by a typical infectious individual in the current population (with some already infected individuals). Its value is usually calculated as the product of $\mathcal{R}_0$ and the average population susceptibility [2, 4, 11]. In the initial stage of disease when the number of infected individuals is only a tiny fraction of the total population, $\mathcal{R}_t \approx \mathcal{R}_0$. Wallinga and Teunis [9] proposed a method to approximate the effective reproduction number, which studied the average number of reproduction for patients who are infected on a given day. Note that this is not the same as the number of infections caused by a patient on a given day. In addition, this method requires the time of infection of patients, which is difficult to trace. Cori et al. [14] presented a simple method for estimating the effective reproduction number, which is based on the time series of disease occurrence. However, this method's effective reproduction number $\mathcal{R}_t$ is delayed significantly. Das [4] presented a method for estimating an approximate $\mathcal{R}_t$ by taking into account both the mean generation interval and the instantaneous exponential growth rate. However, the instantaneous exponential growth rate can only be estimated from a long enough time period, preventing this method from detecting sudden changes in $\mathcal{R}_t$. In this paper, we propose a new method to directly calculate the real-time reproduction number through confirmed cases and evaluate the effectiveness of control measures.

Based on reported cases of COVID-19, we use the back-calculating method [15] to obtain the number of incidences and the number of infectious patients on each day and then we use them to estimate the change in reproduction number. Moreover, we derive the impact of control measures from the change in the reproduction numbers.

We establish the model in Section 2 and verify it using simulations in Section 3. In Section 4, we show how we applied the model to British Columbia (BC), Canada to obtain their reproduction number and the impact of control measures on the reproduction number; the results are summarized and future work is discussed in Section 5.

2. Methods

2.1. Model

In this section, we consider a discrete-time stochastic seir model in a randomly mixed population. Let S_t, E_t and I_t be the number of susceptible, latent and infectious individuals on day t. Because of the random-mixing assumption, the expected number of new infections on day t is

$$Z_t = \beta S_t I_t. \tag{1}$$

A newly infected patient goes through a latent period L and becomes infectious. Here L is a discrete random variable with a probability mass function $\{p_i\}_{i=0}^{\infty}$, i.e., the probability that the latent period has a length of i days is p_i. This patient then goes through an infectious period X and is diagnosed. Let the probability mass function of X be $\{q_i\}_{i=0}^{\infty}$. Let Q_i be the cumulative probability function of X, that is $Q_i = \sum_{j=0}^{i} q_j$, $0 \le i \le \infty$. We assume that, once diagnosed, the patient is fully isolated and stops being infectious. The course of disease Y is the sum of the latent and infectious periods, i.e., $Y = L + X$. Let

d_i be the probability mass function of Y. Then

$$d_i = \sum_{j=0}^{i} p_j q_{i-j}. \tag{2}$$

By definition, the basic reproduction number, i.e., the average number of secondary infections caused by a typical infectious individual during the infectious period in a fully susceptible population, is

$$\mathcal{R}_0 = \beta E[X],$$

where $E[X] = \sum_{i=0}^{\infty} i q_i$ is the mean infectious period.

Thus, the effective reproduction number on day t is

$$\mathcal{R}_t = \mathcal{R}_0 S_t = \beta S_t E[X] = \frac{Z_t}{I_t} E[X]. \tag{3}$$

Note that the last step is from (1).

Given the mean infectious period $E[X]$, we need to estimate the number of new infections Z_t and the number of infectious individuals I_t so that we can estimate the effective reproduction number $\mathcal{R}_t$.

Note that Z_t and m_t have the following relationship

$$m_t = \sum_{i=0}^{\infty} Z_{t-i} d_i \,. \tag{4}$$

With the m_t given, we need to solve Z_t. Unfortunately, this is a deconvolution problem, and it is difficult to solve (see, e.g., [16]). Instead of solving it, we use the following method to approximate Z_t. Suppose that the number of diagnosed cases on day t, namely m_t, is observed for days $t = 0, 1, \ldots, T$. A patient who is diagnosed on day $t + i$, $0 \le i \le T - t$ was infected on day t if and only if the serial interval $Y = i$, i.e.,

$$Z_t = \sum_{i=0}^{T-t} m_{t+i} d_i = \sum_{i=0}^{T-t} \sum_{j=0}^{i} m_{t+i} p_j q_{i-j}. \tag{5}$$

Note that (5) does not solve the deconvolution problem given by (4). However, we will show that this can give a good approximation for Z_t, especially if m_t is approximately exponentially growing or decaying and the change in the exponential growth rate is slow (measured on the time-scale of the mean serial interval). To see this, assume that $Z_t = Z_0 \mu^t$ for a constant $\mu > 0$ (the exponential growth rate is thus $\log \mu$); then, (4) becomes

$$m_t = \sum_{i=0}^{\infty} Z_0 \mu^{t-i} d_i = Z_0 \mu^t g(1/\mu) \,, \tag{6}$$

where $g(x) = \sum_{i=0}^{\infty} x^i d_i$ is the probability generating function of the serial interval distribution d_i. Substitute this into the right hand side of (5) and assume $T \gg 1$; then,

$$\sum_{i=0}^{\infty} m_{t+i} d_i = Z_0 \mu^{t+i} g(1/\mu) d_i = Z_0 \mu^t g(\mu) g(1/\mu) = Z_t g(\mu) g(1/\mu). \tag{7}$$

Table 1. Explanations of nouns appearing in the paper.

Symbols	Significance
S_t	susceptible at time t
E_t	latent at time t
I_t	infectious at time t
C_t	the number of individuals who are infected on day t
L	latent period
X	infectious period
Y	the sum of the latent and infectious periods
q_i	the probability that the infectious period has a length of i days
p_i	the probability that the latent period has a length of i days
d_i	the probability mass function of the disease course Y
m_t	the number of cases reported on day t

Thus, if the change in Z_t is slow, i.e., $\mu \approx 1$, then $g(\mu)g(1/\mu) \approx 1$.

Using a similar approximation, a patient who is diagnosed on day $t + i$ was infectious on day t because the infectious period $X \geq i$. That is,

$$I_t = \sum_{i=0}^{T-t} m_{t+i}\text{Prob}\{X \geq i\} = \sum_{i=0}^{T-t} m_{t+i}(1 - Q_{i-1}). \tag{8}$$

Thus, from (3),

$$\mathcal{R}_t = \frac{\sum_{i=0}^{T-t}\sum_{j=0}^{i} m_{t+i}p_j q_{i-j}}{\sum_{i=0}^{T-t} m_{t+i}(1 - Q_{i-1})}E[X]. \tag{9}$$

The symbols used in this article are described in detail in Table 1.

2.2. Confidence interval

Given the mean infectious period E[X], in order to find the 95% confidence interval of $\mathcal{R}_t$, we will get a random sample of Z_t and I_t by using the Monte Carlo method. For the patients who are diagnosed on day t, let $\tilde{Z}_{t,t-i}$ be the number of those who are infected on day $t - i$ for $i = 0, 1, \ldots$. Then, the approximation given by (5) is equivalent to the following two steps:

a) Assume that $\tilde{Z}_{t,t-i}$ is multinomially distributed according to

$$\tilde{Z}_{t,t-i} \sim \text{multinomial}(m_t, d_i). \tag{10}$$

b) The number of individuals who are infected on day t is

$$Z_t = \sum_{i=0}^{T-t} \tilde{Z}_{t+i,t}. \tag{11}$$

Note that the mean of (11) is given by (5).

Similarly, for patients who show symptoms on day t, the number of those who were infected on day $t - i$ is

$$\tilde{C}_{t,t-i} \sim \text{multinomial}(m_t, q_i). \tag{12}$$

Thus, the number of individuals who are infected on day t is

$$C_t = \sum_{i=0}^{T-t} \tilde{C}_{t+i,t}. \tag{13}$$

Note that, here, C_t is a random variable, the mean of which is given by

$$E[C_t] = \sum_{i=0}^{T-i} m_{t+i} q_i, \tag{14}$$

which uses a similar approximation as (5).

The expected number of individuals I_t who are infectious on day t is the total number of people who have become infectious but have not been removed from transmission (via recovery or isolation). Thus, I_t can be calculated as

$$I_t = \sum_{i=0}^{t} C_i - \sum_{i=0}^{t} m_i, \tag{15}$$

where the first term on the right-hand side is the number of patients who have become infectious before (or on) day t, while the second term is the number of patients who have been diagnosed and isolated before (or on) day t.

To generate one sample of Z_t and I_t, for each m_t, $t = 0, 1, \ldots, T$, we use (12) to generate a sample for $\tilde{C}_{t,t-i}$, and then use (13) to calculate C_t. We then use the calculated C_t to generate a sample of Z_t using (10) and (11), and we use the calculated C_t to generate a sample of I_t using (10), (11) and (15). We can then use (3) to calculate a sample of the curve $\mathcal{R}_t$.

We generate 10^5 samples for $\mathcal{R}_t$. For each $t = 0, 1, \ldots, T$, we use these samples to estimate the 95% confidence interval.

3. Model validation

To verify that our model can correctly estimate the reproduction number, we apply (9) to a dataset generated from stochastic simulations by using the method in Section 2.2 to estimate the 95% confidence interval of the reproduction number.

Non-pharmacological intervention (NPI) measures reduce the transmission rate [17]. The latent period and infectious period are specific to the disease, and are not affected by NPI measures. Thus, we consider the following two cases.

Case 1 Seasonal variation in the transmission rate is sometimes approximated by a sinusoidal function [10, 18, 19]. Here we assume β to be sinusoidal to verify that our method can detect continuous change in $\beta(t)$. Specifically,

$$\beta = 0.2[\cos(\frac{2\pi t}{365}) + 1]. \tag{16}$$

In this case, the infectious period is assumed to be gamma-distributed with a shape parameter of 3 and a rate parameter of 0.2; the latent period is assumed to be gamma-distributed with a shape parameter of 3 and a rate parameter of 0.3. Note that these choices only serve as a numerical example and are (no comma) not tied to a specific disease.

Case 2 The transmission rate is assumed to be a step function to simulate a sequence of control measures that cause sudden change in β, that is,

$$\beta = \begin{cases} 0.5, & t \in [0, 40), \\ 0.4, & t \in [40, 60), \\ 0.3, & t \in [60, 80), \\ 0.2, & t \in [80, 100), \\ 0.3, & t \in [100, \infty). \end{cases} \tag{17}$$

In this case, the infectious period is assumed to be gamma-distributed with a shape parameter of 3 and a rate parameter of 0.25; the latent period is assumed to be gamma-distributed with a shape parameter of 3 and a rate parameter of 0.2.

In both cases, the simulated population size is 10^6. During the simulated time periods, the number of infected individuals is only a small fraction of the population size; thus, $S(t) \approx 1$ and the effective reproduction number is approximately the basic reproduction number.

Figure 1 shows the comparison of the estimated reproduction number $\mathcal{R}_t$ as a function of time with the true value for Case 1. Figure 2 shows the comparison for Case 2. In both cases, our method can correctly estimate the reproduction number. In addition, these figures also show that the confidence interval narrows with a larger case count.

4. Application to the COVID-19 outbreak in BC, Canada in 2020

Now that we have validated our method, in this section, we apply the method to study the change of the reproduction number as a function of time for the COVID-19 outbreak in BC, Canada in 2020.

In BC, we consider the following policy changes:

- Provincial state of emergency was declared on March 17;
- Businesses reopened on May 19;
- Provincial state of emergency was declared on July 7;
- Provincial state of emergency was declared on August 5;
- Public K-12 schools reopened on September 10;
- Provincial state of emergency was declared on October 28;
- Provincial state of emergency was declared on December 23.

We used the daily reported case count data for the period of March 1 to December 31, 2020 that were released from the BC Centre for Disease Control (BCCDC) as a spreadsheet. This spreadsheet has been taken offline. However, the data can still be accessed via the COVID-19 dashboard on the BCCDC website [20].

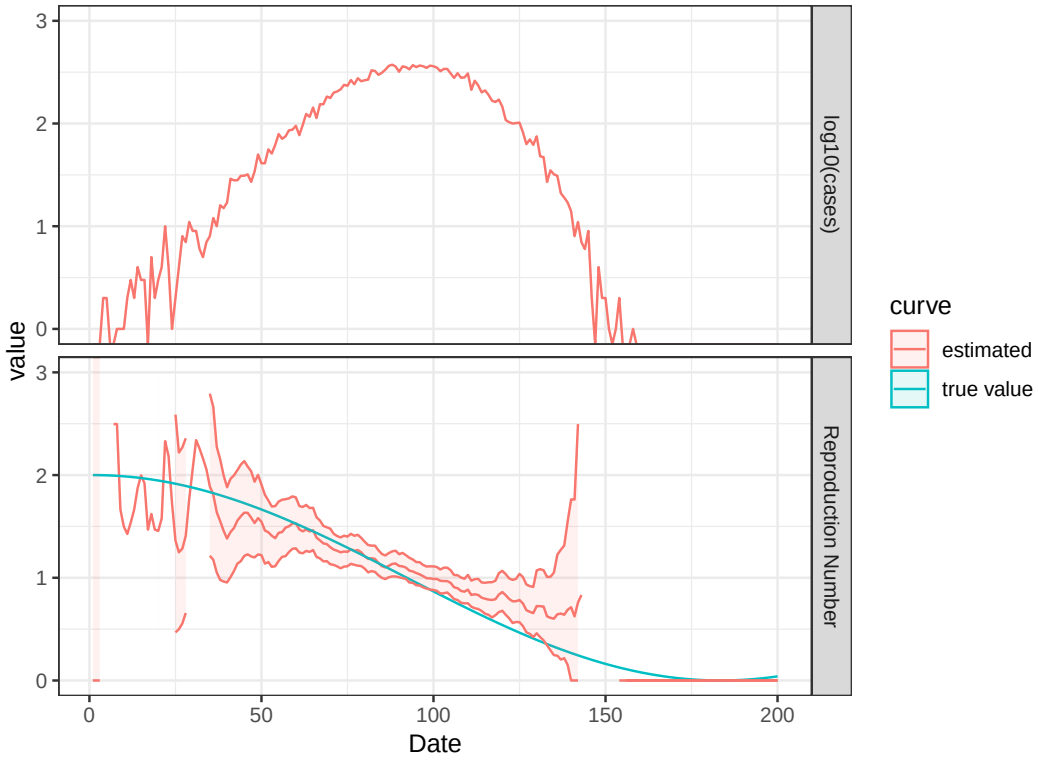

Figure 1. Model validation for Case 1. The top panel shows the simulated epidemic curve (in $\log_{10}$), while the lower panel shows the comparison of the estimated reproduction number and its confidence interval with the true value in blue. Note that, when the case count is low, the confidence interval becomes very large, causing the upper and lower bounds of the confidence interval to disappear on some days.

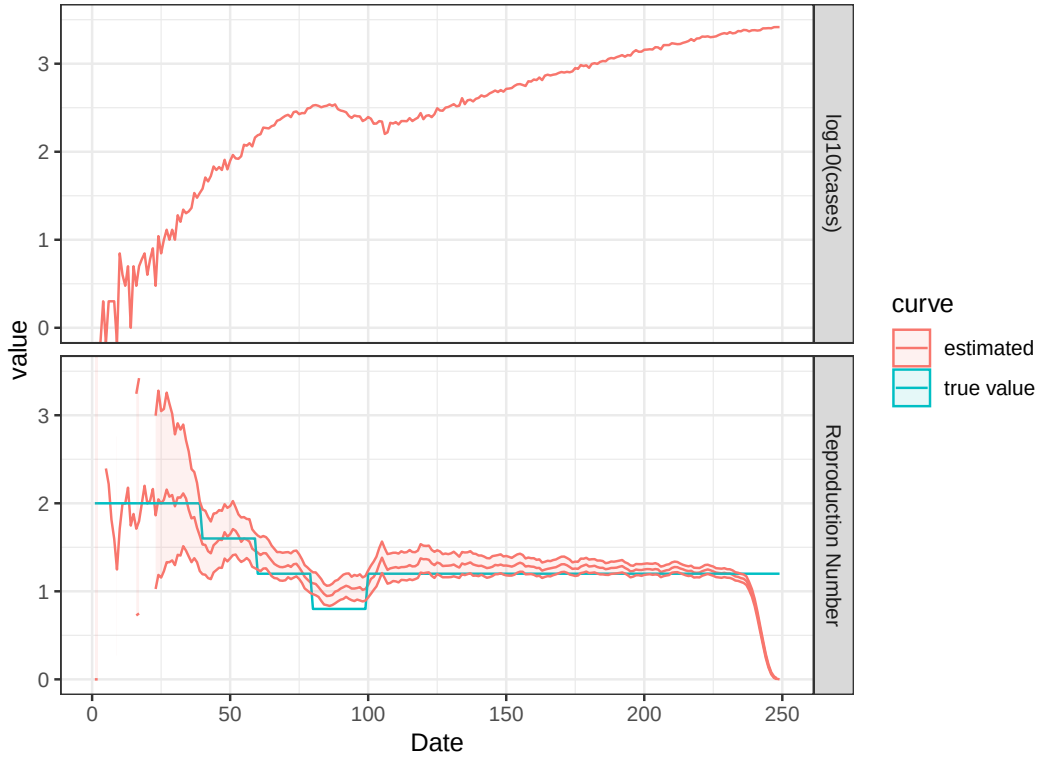

Figure 2. Model validation for Case 2. The top panel shows the simulated epidemic curve (in $\log_{10}$), while the lower panel shows the comparison of the estimated reproduction number and its confidence interval with the true value in blue.

Table 2. The estimated parameters for the gamma-distributed COVID-19 infectious period in BC, Canada in 2020.

Parameter	Mean	Sd	95% confidence interval
α	4.791	1.074	(3.133, 7.358)
ε	1.815	0.373	(1.143, 2.610)

To apply our method, we need to know the latent period distribution and the infectious period distribution. We use the latent period distribution estimated by [21], which is gamma-distributed with a mean of 5.48 days and a standard deviation of 2.72 days.

On the other hand, regional differences in testing policy and human behavior in voluntary testing may affect when a patient is diagnosed and isolated, and, in turn, affect the infectious period. In Subsection 4.1, we estimate the infectious period distribution in BC from the daily number of diagnosed cases and symptom onsets.

4.1. Estimate the infectious period

We assume that the patients will be isolated after being diagnosed. Therefore, the end of their infectious period is marked by diagnosis, not recovery. We assume that the infectious period is gamma-distributed [22–26], with a shape parameter α and a scale parameter ε.

We digitized and tabulated the daily number of symptom onsets for the period of January 15 to June 7, 2020 from the British Columbia COVID-19 Daily Situation Report released on June 9 [27].

Using an approximation similar to (5), the expected number of patients showing symptoms on day t can be calculated from the diagnosed cases on day $t + i$ (m_{t+i}) as

$$\lambda_t = \sum_{i=0}^{T-t} m_{t+i} q_i. \tag{18}$$

We assume that C_t is the observed symptom onset count on day t; it follows a Poisson distribution with the mean λ_t, i.e.,

$$C_t \sim \text{Poisson}(\lambda_t) \tag{19}$$

We use the Markov chain Monte Carlo method via the R package "R2jag" to estimate the distribution parameters α and ε. The prior distributions of the parameters are chosen to follow a uniform distribution with wide intervals:

$$\alpha \sim \text{U}(0, 10)\,, \varepsilon \sim \text{U}(0, 5) \tag{20}$$

The results are given in Table 2. Figure 3 shows the point estimate and 95% confidence interval of the estimated density function of the infectious period distribution.

4.2. Estimate the effective reproduction number

Using the point estimate of the infectious period distribution in Subsection 4.1, we estimate the reproduction number as a function of time in BC, Canada.

Figure 4 shows both the epidemic curve (reported cases) and the estimated reproduction number. This figure shows that, since the provincial state of emergency on March 17, the reproduction number

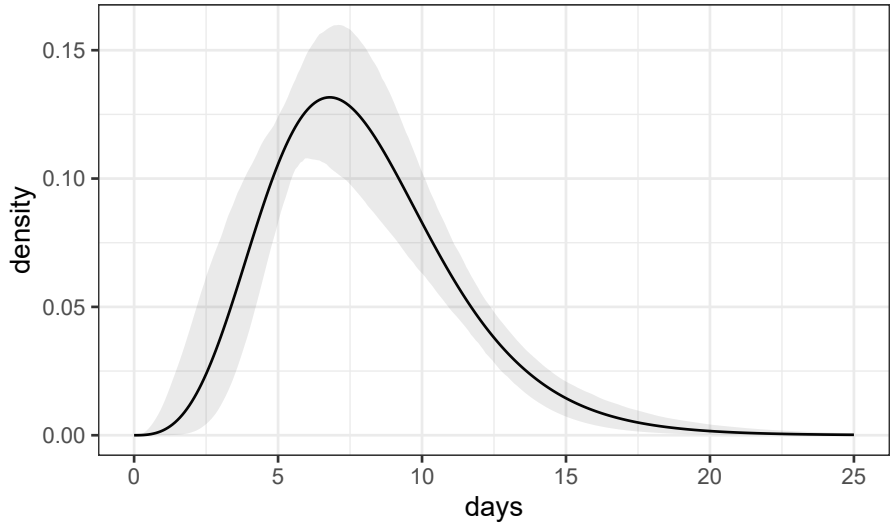

Figure 3. The point estimates and 95% confidence interval of the probability density function of the infectious period distribution in BC, Canada.

was controlled to below 1 until the relaxation (business reopening) announced on May 19. The reproduction number then increased gradually after the relaxation to 1.76 in June, being largely maintained until August 1st, at which point it was about 1.60. The strengthening of control measures on August 5 reduced the reproduction number and eventually controlled it to around 1 on September 10. It then increased again to a peak value of 1.67 on October 10. It was then brought back to about unity beginning on November 13.

5. Concluding remarks

We have developed a novel method to estimate the change of the reproduction number with time. Using simulated data, we have shown that our method can estimate the change in the reproduction number due to either seasonal forcing or control measures. This means that our method is widely applicable to understand the change of the transmission rate.

Applying our method to the COVID-19 outbreak in BC, Canada in 2020 shows that the strengthening of control measures such as social distancing, restricting gathering and closing schools from March 20 to the end of May successfully reduced the reproduction number to below 1, except for a period in early April (may be due to clustered cases in long-term care facilities [28], or the gathering activities of the Easter holiday). However, the reproduction number gradually increased to above 1 after business reopening in May, even though the case counts did not exhibit an immediate increase. This shows that our method is very sensitive as a tool to detect the changes in reproduction number. The same increase also happened after the school reopening in September, which eventually triggered the fast increase of cases in October and early November. Note that, during this time, the variants of concern had not shown up yet, that is, no variants of concern appeared in 2020 [29, 30]. Thus, the increase of cases is mostly likely due to the relaxation of control measures.

Not surprisingly, our estimation yields a narrower confidence interval with a larger case count. Our method also relies on reliable estimation of the latent and infectious periods, which may be difficult to

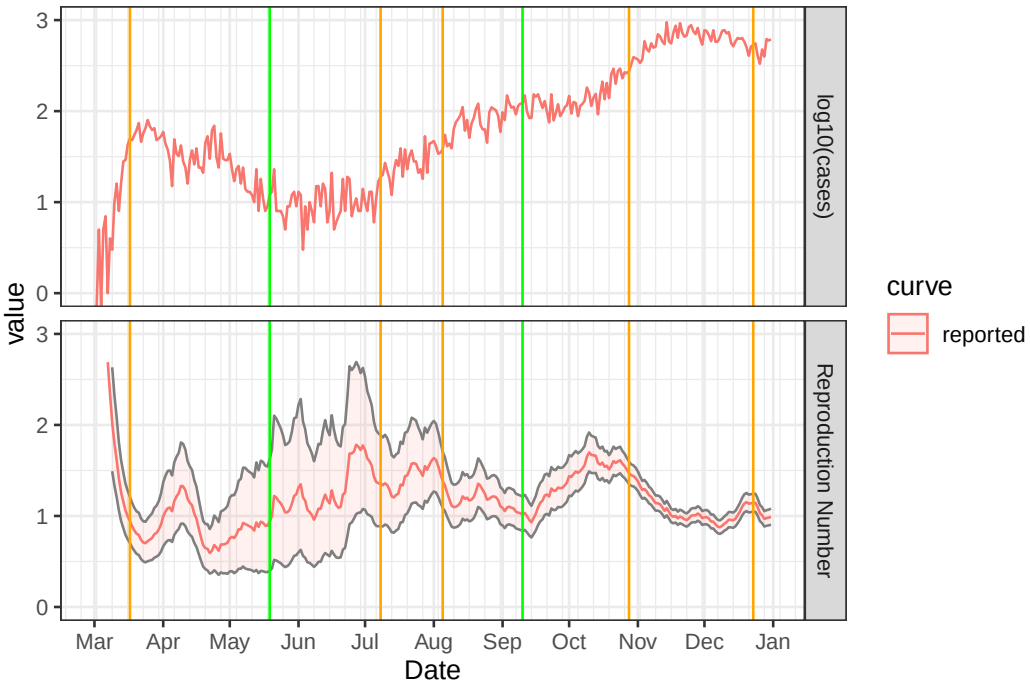

Figure 4. The top panel shows the daily reported cases (in $\log_{10}$). The lower panel shows the estimated reproduction number and the confidence interval on each day. The vertical lines show the dates of the implementation of epidemic control measures, where the orange lines show the declaration of a state of emergency, and the green lines show the dates of relaxation.

estimate during the early stage of a disease outbreak. However, we have also demonstrated that our method can be adapted to estimate the infectious period from the daily counts of symptom onset and diagnosed cases.

Another limitation of our method is that it ignores asymptomatic and pre-symptomatic transmissions, which may be an important factor driving the COVID-19 transmission. However, this may not significantly affect our method if the ratio of asymptomatic cases to all cases remains roughly constant, as the proportional fact is canceled in our formulation.

Our method provides a new tool for analyzing host immunity resulting from the effective vaccinations, with and without NPI measures. At the onset of disease spread, the effective vaccination rate v is the primary factor influencing the number of susceptible individuals. In this case, the effective reproduction number can be expressed as $R_t = \beta(1-v)S_tE(X)$, which is similar to (3). If the effective vaccination rate v is known, our method can estimate the temporal changes in β. However, in the absence of information about v, it is only possible to estimate the value of $\beta(1-v)$, not the individual parameters β and v.

Our method can be used to study other infectious diseases as well. For instance, it can be used to investigate the influence of seasonality on the transmission of seasonal influenza, or to examine the effect of control measures on historical outbreaks, such as pandemic influenza, SARS and Ebola. Furthermore, our method can be applied to the study of vector-borne diseases, including those transmitted by mosquitoes, by extending our model to consider the disease transmission from person to person, with mosquitoes as the vectors. However, obtaining the specific changes in β is challenging, as the infection rate through the vector depends on the change in infected mosquitoes, resulting in a more complex dependence of β on mosquitoes than the simple $SEIR$ model. Therefore, further research is needed to address this complexity. Additionally, the same generalization can be applied to sexually transmitted infections.

Use of AI tools declaration

The authors declare that they have not used artificial intelligence tools in the creation of this article.

Acknowledgments

This research was supported by the National Natural Science Foundation of China (No. 12271088) (ML), the Natural Sciences Foundation of Shanghai (No. 21ZR1401000) (ML) and a discovery grant from the Natural Sciences and Engineering Research Council Canada (JM), as well as two NSERC EIDM grants (OMNI and MfPH) (JM).

Conflict of interest

The authors declare that there is no conflict of interest.

References

1. T. Asselah, D. Durantel, E. Pasmant, G. Lau, R. F. Schinazi, COVID-19: Dis-

covery, diagnostics and drug development, *J. Hepatol.*, **74** (2021), 168–184. https://doi.org/10.1016/j.jhep.2020.09.031

2. D. Chen, T. Zhou, Control Efficacy on COVID-19, *ArXiv Preprint ArXiv.*, (2020), 2003.00305. https://doi.org/10.1371/journal.pone.0246715
3. R. Karia, I. Gupta, H. Khandait, A. Yadav, COVID-19 and its modes of transmission, *SN Compr. Clin. Med.*, **2** (2020), 1798–1801. https://doi.org/10.1007/s42399-020-00498-4
4. A. Das, An approximation-based approach for periodic estimation of effective reproduction number: A tool for decision-making in the context of coronavirus disease 2019 (COVID-19) outbreak, *Public Health*, **185** (2020), 199–201. https://doi.org/10.1016/j.puhe.2020.06.047
5. C. Signorelli, T. Scognamiglio, A. Odone, COVID-19 in Italy: Impact of containment measures and prevalence estimates of infection in the general population, *Acta Biomed.*, **91** (2020), 175–179. https://doi.org/10.23750%2Fabm.v91i3-S.9511
6. T. Lee, H. D. Kwon, J. Lee, The effect of control measures on COVID-19 transmission in South Korea, *Plos One*, **16** (2021), e0249262. https://doi.org/10.1371/journal.pone.0249262
7. N. Scott, A. Palmer, D. Delport, R. Abeysuriya, R. M. Stuart, C. C. Kerr, et al., Modelling the impact of relaxing COVID-19 control measures during a period of low viral transmission, *Med. J. Aust.*, **214** (2021), 79–83. https://doi.org/10.5694/mja2.50845
8. L. Cirrincione, F. Plescia, C. Ledda, V. Rapisarda, D. Martorana, G. Lacca, et al., COVID-19 pandemic: New prevention and protection measures, *Sustainability*, **14** (2022), 4766. https://doi.org/10.3390/su14084766
9. J. Wallinga, P. Teunis, Different epidemic curves for severe acute respiratory syndrome reveal similar impacts of control measures, *Am. J. Epidemiol.*, **160** (2004), 509–516. https://doi.org/10.1093/aje/kwh255
10. H. Yu, W. J. Alonso, L. Feng, Y. Tan, Y. Shu, W. Yang, et al., Characterization of regional influenza seasonality patterns in China and implications for vaccination strategies: Spatio-temporal modeling of surveillance data, *PLoS Med.*, **10** (2013), e1001552. https://doi.org/10.1371/journal.pmed.1001552
11. C. You, Y. Deng, W. Hu, J. Sun, Q. Lin, F. Zhou, et al., Estimation of the time-varying reproduction number of COVID-19 outbreak in China, *Int. J. Hyg. Environ. Health*, **228** (2020), 113555. https://doi.org/10.1016/j.ijheh.2020.113555
12. I. Locatelli, B. Trächsel, V. Rousson, Estimating the basic reproduction number for COVID-19 in Western Europe, *Plos One*, **16** (2021), e0248731. https://doi.org/10.1371/journal.pone.0248731
13. Y. Alimohamadi, M. Taghdir, M. Sepandi, Estimate of the basic reproduction number for COVID-19: a systematic review and meta-analysis, *J. Prev. Med. Public Health*, **53** (2020), 151–157. https://doi.org/10.3961%2Fjpmph.20.076
14. A. Cori, N. M. Ferguson, C. Fraser, S. Cauchemez, A new framework and software to estimate time-varying reproduction numbers during epidemics, *Am. J. Epidemiol.*, **178** (2013), 1505–1512. https://doi.org/10.1093/aje/kwt133
15. H. Nishiura, Backcalculating the Incidence of Infection with COVID-19 on the Diamond Princess, *J. Clin. Med.*, **9** (2020), 657. https://doi.org/10.3390/jcm9030657

16. E. Goldstein, J. Dushoff, J. Ma, J. B. Plotkin, D. J. Earn, M. Lipsitch, et al., Reconstructing influenza incidence by deconvolution of daily mortality time series, *Proc. Natl. Acad. Sci. U S A*, **106** (2009), 21825–21829. https://doi.org/10.1073/pnas.0902958106

17. P. Nouvellet, S. Bhatia, A. Cori, K. E. Ainslie, M. Baguelin, S. Bhatt, et al., Reduction in mobility and COVID-19 transmission, *Nat. Commun.*, **12** (2021), 1090. https://doi.org/10.1038/s41467-021-21358-2

18. M. Lipsitch, C. Viboud, Influenza seasonality: Lifting the fog, *Proc. Natl. Acad. Sci. U S A*, **106** (2009), 3645–3646. https://doi.org/10.1073/pnas.0900933106

19. J. Dushoff, J. Plotkin, S. Levin, D. Earn, Dynamical resonance can account for seasonality of influenza epidemics, *Proc. Natl. Acad. Sci. U S A*, **101** (2004), 16915–16916. https://doi.org/10.1073/pnas.0407293101

20. BC Centre for Disease Control. 2020 British Columbia COVID-19 Dashboard on the BCCDC website. http://www.bccdc.ca/health-professionals/data-reports/respiratory-diseases

21. H. Xin, Y. Li, P. Wu, Z. Li, E. H. Y. Lau, Y Qin, et al., Estimating the latent period of coronavirus disease 2019 (COVID-19), *Clin. Infect. Dis.*, **74** (2022), 1678–1681. https://doi.org/10.1093/cid/ciab746

22. S. M. Moghadas, M. C. Fitzpatrick, P. Sah, A. Pandey, A. Shoukat, B. H. Singer, et al., The implications of silent transmission for the control of COVID-19 outbreaks, *Proc. Natl. Acad. Sci. U S A*, **117** (2020), 17513–17515. https://doi.org/10.1073/pnas.2008373117

23. A. W. Byrne, D. McEvoy, A. B. Collins, K. Hunt, M. Casey, A. Barber, et al., Inferred duration of infectious period of SARS-CoV-2: Rapid scoping review and analysis of available evidence for asymptomatic and symptomatic COVID-19 cases, *BMJ Open*, **10** (2020), e039856. http://doi.org/10.1136/bmjopen-2020-039856

24. Y. Xiang, Y. Jia, L. Chen, L. Guo, B. Shu, E. Long, COVID-19 epidemic prediction and the impact of public health interventions: A review of COVID-19 epidemic models, *Infect. Dis. Model.*, **6** (2021), 324–342. https://doi.org/10.1016/j.idm.2021.01.001

25. S. Zhao, B. Tang, S. S. Musa, S. Ma, J. Zhang, M. Zeng, et al., Estimating the generation interval and inferring the latent period of COVID-19 from the contact tracing data, *Epidemics*, **36** (2021), 100482. https://doi.org/10.1016/j.epidem.2021.100482

26. K. Chatterjee, K. Chatterjee, A. Kumar, S. Shankar, Healthcare impact of COVID-19 epidemic in India: A stochastic mathematical model, *Med J Armed Forces India.*, **76** (2020), 147–155. https://doi.org/10.1016/j.mjafi.2020.03.022

27. BC Centre for Disease Control. 2020 British Columbia COVID-19 Daily Situation Report. http://www.bccdc.ca/Health-Info-Site/Documents/BC-Surveillance-Summary-June%20-9-2020.pdf

28. BC Centre for Disease Control, COVID-19 Situation Report. https://bccdc.shinyapps.io/respiratory-covid-sitrep/COVID-19-outbreaks

29. BC Centre for Disease Control. Weekly Update on Variants of Concern (VOC) 30 April 2021. http://www.bccdc.ca/Health-Info-Site/Documents/VoC/VoC_weekly_04302021.pdf

30. Public Health Agency of Canada. COVID-19 Epidemiology Update: Testing and Variants. https://health-infobase.canada.ca/covid-19/testing-variants.html

AIMS Press