

Letter to the Editor

Serial interval in determining the estimation of reproduction number of the novel coronavirus disease (COVID-19) during the early outbreak

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To the Editor

Coronavirus disease 2019 (COVID-19), caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), emerged in Wuhan, China in the end of 2019 and soon spread overseas. A comprehensive and timely review summarized the scientific research in estimating the basic reproduction number (R_0) released from 1 January to 7 February 2020 [1]. During the early outbreak, when the key epidemiological features of COVID-19 were uncovered, the R_0 estimation largely relied on the growth rate of the epidemic curve and the estimation of the serial interval (SI). Here, we demonstrated that an overlarge SI would lead to overestimation of R_0 .

We adopted the growing process proposed in [2] deterministically with a population of 11 million in Wuhan, one case onset on 5 December 2019 initially and a fixed step at 1 day. We consider two values of the mean serial interval (SI) that are

- SI at 4.6 days estimated based on 28 records of transmission chains [3], which was largely consistent with the SI estimate at 4.4 days based on 71 records [4]; and
- SI at 8 days, which was closer to the SI of the severe acute respiratory syndrome (SARS, 8.4 days), SI of the Middle East respiratory syndrome (MERS, 7.6 days).

As for demonstration that a larger SI could lead to overestimation in R_0 , we conducted the simulation with two schemes that are

- Scheme (I): $R_0 = 2$, and SI = 4.6 days; and
- Scheme (II): $R_0 = 2, 3, 4$ and 3.3 as summarized in [1], and SI = 8 days.

We also compared the simulation results with the previous estimates of the cumulative number of COVID-19 infections in Wuhan. In Fig 1, the simulation results of the scheme (I) had almost the same growing trends as those of scheme (II) with $R_0 = 3.3$. Although a higher R_0 could force the epidemic curve increasing rapidly, a shorter SI could increase iteration of transmission generation, i.e. transmission may occur shortly post infection.

According to the simply approximated formula that $R_0 = \exp(\gamma \cdot \text{SI})$, where γ was the exponential growth rate calculated from the incidence data directly, a longer SI would lead to a higher R_0 estimate theoretically. With a shorter SI at 4.6 days, which was supported by richer datasets in [3, 4], the R_0 of COVID-19 could be lower than previous estimates based on longer SI. By using the growth rate (γ) at 0.15 per day, the R_0

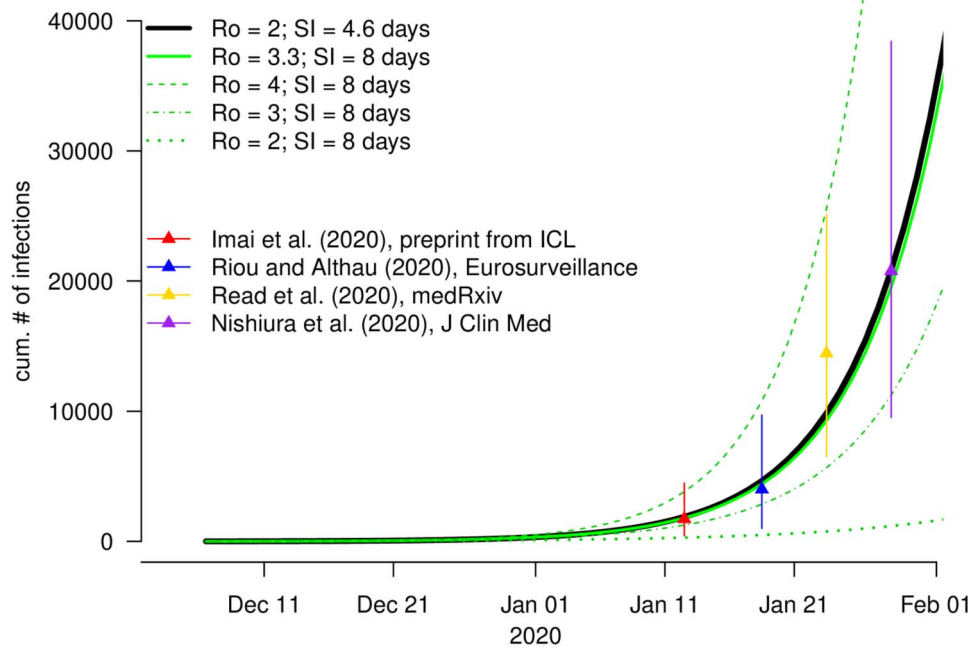


Figure 1. The simulated (curves) and previously estimated (dots and bars) cumulative number of COVID-19 cases in Wuhan, China. The bold (main results) and dashed (alternative scenarios) curves are the simulation results. The curves in green are the simulation with SI at 8 days. The curve in black is the simulation with SI at 4.6 days. The triangular dots are the previously estimates of the COVID-19 infections, and the details can be found in the [Supplementary Material S1](#)

was found at 2.0 with SI at 4.6 days, whereas 3.3 with SI at 8 days. Although the effects of public health control were ignored in this analysis, our model could be extended by introducing an effective reproduction number accounting for the effectiveness of the control measures, and we remarked this modification would not affect the main conclusion. Furthermore, as pointed out in [3], provided that the SI of COVID-19 might be shorter than its incubation period, pre-symptomatic transmission may occur shortly after being infected [5]. This implies that a fraction of transmissions cannot be prevented solely through isolating the symptomatic cases, since the time when contact tracing is conducted, they might have already been infectious and generated secondary cases. Therefore, the effective quarantine of suspected (and probable) cases, as well as close contacts, and timely contact tracing were crucial in successful outbreak mitigation.

Supplementary Data

[Supplementary data](#) are available at *JTM* online.

Ethics Approval and Consent to Participate

Since no real-world data were used in this work, neither ethical approval nor individual consent was not applicable.

Availability of Materials

There were no real-world data used in this work, the estimates from previous studies can be found in the [Supplementary Material S1](#), and the key R code was attached in [Supplementary Material S2](#).

Consent for Publication

Not applicable.

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Conflict of Interest

D.H. declares receiving funding from Alibaba (China)-Hong Kong Polytechnic University Collaborative Research project. Other authors declare no conflict of interest.

Disclaimer

The funding agencies had no role in the design and conduct of the study; collection, management, analysis, and interpretation of the data; preparation, review, or approval of the manuscript; or decision to submit the manuscript for publication.

Authors' Contributions

S.Z. and D.H. conceived the study, carried out the analysis and drafted the first manuscript. All authors discussed the results,

critically read and revised the manuscript and gave final approval for publication.

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References

1. Liu Y, Gayle AA, Wilder-Smith A, Rocklöv J. The reproductive number of COVID-19 is higher compared to SARS coronavirus. *J Travel Med* 2020. doi: [10.1093/jtm/taaa021](https://doi.org/10.1093/jtm/taaa021).
2. Tuite AR, Fisman DN. Reporting, epidemic growth, and reproduction numbers for the 2019 novel coronavirus (2019-nCoV) epidemic. *Ann Intern Med* 2020. doi: [10.7326/M20-0358](https://doi.org/10.7326/M20-0358).
3. Nishiura H, Linton NM, Akhmetzhanov AR. Serial interval of novel coronavirus (2019-nCoV) infections. *medRxiv* 2020. doi: [10.1101/2020.02.03.20019497](https://doi.org/10.1101/2020.02.03.20019497).
4. You C, Deng Y, Hu W *et al*. Estimation of the time-varying reproduction number of COVID-19 outbreak in China. *medRxiv* 2020. doi: [10.1101/2020.02.08.20021253](https://doi.org/10.1101/2020.02.08.20021253).
5. Jung SM, Akhmetzhanov AR, Hayashi K *et al*. Real-time estimation of the risk of death from novel coronavirus (COVID-19) infection: inference using exported cases. *J Clin Med* 2020; 9. doi: [10.3390/jcm9020523](https://doi.org/10.3390/jcm9020523).