Modelling of Reproduction number for COVID-19 in India and high incidence states

ARTICLE INFO

Keywords

Reproduction number
COVID-19
R0-package
Disease modelling

Dear Editor in Chief

Clinical Epidemiology and Global Health.

We have read the original article “Modelling of Reproduction number for COVID-19 in India and high incidence states” which is recently published in your esteemed journal, “Clinical Epidemiology and Global Health”. Firstly, we would like to congratulate the authors for a successful publication and for a contribution to insight into the transmissibility of the Coronavirus (COVID -19) in India.

We have read the article carefully and have pointed out some significant issues that lack to address by the authors. In the introduction section (line 11–14), the authors have wrongly introduced the basic reproduction number and effective reproduction number. It is described that the basic reproduction number can be estimated at the beginning of the epidemic (a couple of days to 1–2 weeks), and effective reproduction can be estimated for an ongoing epidemic (few weeks to months). However, the interpretation of the basic and effective reproduction number is purely based on the nature of the population and the existence of immunity in the population, which has nothing to do with the time span of the virus.¹ In addition to this, the authors also assume that the effective reproduction number termed as time-dependent reproduction number (Introduction section, line 14), which should be correctly interpreted.

Authors have followed one of the highly cited papers published by Obadia et al. based on the application of “R0” package for the estimation of reproduction number. The authors lack to mention the time period for which the daily incidence is the best fit of exponential growth rate, which is the most important assumption in the exponential growth rate (EG) method. Moreover, the growth rate of the daily incidence is also missing in the paper, which should be clearly mentioned.²

In the methodology section, the authors should either develop a methodology or follow some well-developed sensitivity analysis tools to explore the variation in reproduction number due to arbitrary choice of serial interval (SI) and to insight the best time period of exponential growth in incidence. Additionally, it might be more apparent if the authors could provide the analysis of goodness of fit to see the proximity between the predicted number of cases and observed number of cases by using the model that estimates reproduction number. Without the analysis of goodness of fit for the model, it is unrealistic to say whether

the estimated transmissibility of COVID-19 is close to the true transmissibility estimation. The calculation of R^2 may provide a rough estimation of the goodness of fit, whereas the heatmap analysis or Latin Hypercube Sampling (LHS) can be used to perform the sensitivity analysis.^{3,4}

By estimating the initial growth rate, estimating the growth rate time-period, a goodness of fit analysis, and the sensitivity analysis of the model, the application of “R0” package is more useful and appropriate. In addition to this, if the authors provide the information mentioned above's, it will increase the acceptability of the paper in terms of further citations. The reproduction number is super useful transmissibility parameter in epidemiology so disease modelers and epidemiologist must be careful about the choice of appropriate methodology before its estimation.

Funding

Authors have no fund for this work.

Declaration of competing interest

None.

References

1. Delamater PL, Street EJ, Leslie TF, Yang YT, Jacobsen KH. Complexity of the basic reproduction number (R_0). *Emerg Infect Dis.* 2019;25(1):1–4. <https://doi.org/10.3201/eid2501.171901>.
2. Wallinga J, Lipsitch M. How generation intervals shape the relationship between growth rates and reproductive numbers. *Proc Biol Sci.* 2007;274(1609):599–604. <https://doi.org/10.1098/rspb.2006.3754>.
3. Dhungana HN. Comments on “Preliminary estimation of the basic reproduction number of novel Coronavirus (2019-nCoV) in China, from 2019 to 2020: a data-driven Analysis in the early phase of the outbreak”. *Int J Infect Dis.* 2020;94:72–73. <https://doi.org/10.1016/j.ijid.2020.02.024>.
4. Obadia T, Haneef R, Boëlle PY. The R0 package: a toolbox to estimate reproduction numbers for epidemic outbreaks. *BMC Med Inf Decis Making.* 2012;12:147. <https://doi.org/10.1186/1472-6947-12-147>. Published 2012 Dec 18.

Hom Nath Dhunagna*

School of Mathematical Science, University of Technology Sydney, Australia

<https://doi.org/10.1016/j.cegh.2020.07.004>

Received 6 July 2020; Accepted 12 July 2020

Available online 15 July 2020

2213-3984/© 2020 The Authors. Published by Elsevier, a division of RELX India, Pvt. Ltd on behalf of INDIACLEN. This is an open access article under the CC

BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

Saroj Ghimire
School of Public Health, Torrens University, Australia
E-mail address: Saroj.ghimire199@gmail.com.

* Corresponding author.
E-mail address: homnath.dhungana@uts.edu.au (H.N. Dhunagna).