Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

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

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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.

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Declaration of competing interest

None.

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