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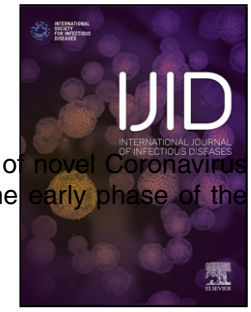

Comments on P̈reliminary estimation of the basic reproduction number of novel Coronavirus (2019-nCoV) in China, from 2019 to 2020: A data-driven Analysis in the early phase of the outbreak¨90pt plus1fill

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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"

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Dear Editor in Chief,

I have read the original article "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" which is recently published in your esteemed journal "International Journal of Infectious Diseases". Firstly, I would like to congratulate the authors for a successful publication and for making some contributions.

The methodology used in the paper for the estimation of the reproduction number strongly assumes that the growth rate is exponential. However, in the result section, the growth rate and its estimate are missing. The estimation of the reproduction number is likely to change significantly if the hypothetical growth rate differs from the actual growth rate [1]. It is too early to say about the pattern of any specific distribution regarding growth rate, new incidence cases and the cumulative number of cases of novel Coronavirus (2019-nCoV). It would be great if authors address this as a limitation of the study and provide more details about the estimation of intrinsic growth rate.

Table 1 provides the results (reproduction number estimates) for different folds of reporting rate by using three different Serial intervals (SI). Since limited studies are available in details about SI for novel coronavirus so it is obvious to use the serial interval of MRES and SARS but many studies show wide variation in their serial interval [2]. The estimates of serial intervals used in the paper are 7.6 ±3.4 and 8.4 ±3.8 (in days) respectively for MEES and SARS hence the coefficient of variation (CV) of SI for MERS and SARS seems higher (44.73 % and 45.23 % respectively). Due to this variation, it is highly recommended to a perform sensitivity analysis between SI and reproduction number so that variation between SI and reproduction number for novel Coronavirus (2019-nCoV) can be obtained.

There is a significant difference between the estimates of reproduction number reported by WHO and the findings of Shi Zhao et al. and this variation could be due to many reasons including the parameters used in the model (SI) this can be also understood by sensitivity analysis [3].

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Conflict of Interest: No conflict of interest to declare.

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