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LETTER TO EDITOR

Response to 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”


This letter refers to the recently published comments (Dhungana, 2020) on the 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” by Zhao et al. (Zhao et al., 2020). The 2019-nCoV (now known as severe acute respiratory syndrome coronavirus 2, SARS-CoV-2) is similar to the virus causing middle east respiratory syndrome (MERS) and severe acute respiratory syndrome (SARS); therefore, in the published paper (Zhao et al., 2020), the serial interval (SI) used by the authors in the study was the average of the reported SIs of MERS (Assiri et al., 2013) and SARS (Lipsitch et al., 2003). The data were obtained for 15 days, from January 10 to January 24, 2020. The study was done in the early stage of the pandemic and the estimates of the SIs from earlier published reports were 7.6 ± 3.4 days for MERS and 8.4 ± 3.8 days for SARS, with the coefficient of variation (CV) of the SIs being 44.73% and 45.23%, respectively. The author of the comment claims that the CV is high, but has misinterpreted the data shown in the report, as the data were from the early stage of the pandemic. It may also be due to sampling fluctuations, as the data came from the tail area of the curve. The author of the comment refers to the difference in the estimates given by the authors of the original study and by the World Health Organization (WHO); however, the data may only be comparable if they were derived from the similar time points. As far as the sensitivity analysis between SI and R_0 is concerned, there is a need of more data. The study in question, was from the early stage of the disease progression and obviously a sensitivity analysis and other measures would be possible, when dealing with the complete data. At that juncture, when the study was conducted, the primary concern was to calculate the R_0 in order to develop immediate and effective policies to prevent further dissemination of the infection.

The author of the comment mentioned that the authors of the original study have strongly assumed that the growth rate was exponential but did not give an estimate of this rate in the Results section. The fitting of the exponential curve is excellent, as the value of R^2 for all folds lies between 0.91 and 0.92. As far as the growth rate is concerned, this was clearly shown in the Figure 1 of the original study published (Zhao et al., 2020). Further it is stated in the original article that “Since the official diagnostic protocol was released by WHO on January 17, an increase in the diagnosis and reporting of 2019-nCoV infections probably occurred. Thereafter, the daily number of newly reported cases started increasing around January 17, see Figure 1, which implies that more

infections were likely being diagnosed and recorded.” Since the 2019-nCoV is very similar to the viruses causing SARS and MERS and the transmission chain of 2019-nCoV was unclear, the authors followed the already published probability distribution of the SIs, for the disease as the gamma distribution (Lipsitch et al., 2003; Wallinga and Lipsitch, 2007; de Silva et al., 2009; Assiri et al., 2013; Zhao et al., 2019). Thus the pattern of the probability distribution of the growth rate is very clear in the presented curve fitting (see Figure 1 in the original article) and is well established for the similar viruses. Further, the hypothetical growth did not deviate very much from the actual growth, as the curve is excellently fitted. Moreover, the incubation period of the viruses causing SARS and MERS has been reported as 5 days (Donnelly et al., 2003; Bauch et al., 2005; Lin et al., 2018); therefore it was not too early to decide on a gamma distribution of the growth rate, as it was already well established in the literature.

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Ethical approval

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Conflict of interest

There are no conflicts of interest to declare pertaining to this work.

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