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Letter to the Editor

A re-analysis to identify the structural breaks in COVID-19 transmissibility during the early phase of the outbreak in South Korea

Exploring the temporal patterns of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) transmission is of importance in understanding the features of coronavirus disease 2019 (COVID-19) and developing control strategies (Chong et al., 2020). By using the ‘SIR’-based compartmental model, one breakpoint with a drop in the transmission rate, i.e., 7 March 2020, was estimated in the COVID-19 outbreak in South Korea (Kim et al., 2020). In this study, a re-analysis of the outbreak in South Korea was performed, and we argue that there was likely more than one structural break in the local SARS-CoV-2 transmission.

The daily numbers of new COVID-19 cases in time-series were collected from the public surveillance platform released by the World Health Organization (WHO); see https://covid19.who.int/region/wpro/country/kr and Figure 1A. We adopted the time-varying reproduction number ($R_t$) to quantify the instantaneous COVID-19 transmissibility. Following the estimation framework of Cori et al. (2013), $R_t$ is the ratio of $C(t)$ over $\int_0^t w(k)C(t-k)dk$, where $C(t)$ denotes the number of new COVID-19 cases on the $t$-th date. The $w(\cdot)$ is the distribution (function) of the generation time (GT) of COVID-19 that is set as a gamma distribution having mean ($\pm$ standard deviation) of 5.3 ($\pm$2.1) days (Ferretti et al., 2020; Ganyani et al., 2020). The estimated $R_t$ series are shown in Figure 1B.

To explore and examine the structural breaks in the changing patterns of $R_t$, generalized regression models with segmentation are employed to fit the time index $t$ (independent variable) to $R_t$ (dependent variable) with a Poisson likelihood framework. The structural break is (mainly) determined by the knot parameters in the segmented regression. The number of knot parameters indicates the counts of the occurrence of the structural breaks in COVID-19 transmissibility, and the value of the knot determines when the structural break occurs (on the timeline). The numbers and values of the knot parameters are selected according to fitting performance in terms of the AIC.

It was found that the model with two knots (AIC = −151) outperformed the model with only one knot (AIC = −34). Additionally, the models with three and four knots had AIC of −162 and −166, respectively, both of which improved the fitting performance. Considering the large difference in AICs between the models with one and two knots, their fitting results are shown in Figure 1B for comparison.

The modelling framework of Kim et al. (2020) is equivalent to assuming that $R_t$ changes as a discontinuous function, i.e., in a ‘step’

![Figure 1](https://example.com/figure1.png)

**Figure 1.** The number of daily new COVID-19 cases (panel A) and time-varying reproduction number ($R_t$, panel B) from 16 February to 15 April 2020 in South Korea. In panel B, the light blue dots are the estimated $R_t$ series, the black dashed curve is the fitted $R_t$ series with one breakpoint, and the red bold curve is the fitted $R_t$ series with two breakpoints. The vertical pink lines highlight the two breakpoints (for the red curve).

https://doi.org/10.1016/j.ijid.2020.08.061

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function scheme. In this study, with a continuous modelling scheme in $R_t$, there may be more than one structural break in the changing patterns of COVID-19 transmissibility, which appears to be more statistically reasonable.

**Author contribution**

SZ conceived study, collected the data, conducted the analysis, discussed the results, drafted, and critically revised manuscript. All authors read the manuscript and approved for publication.

**Ethics approval and consent to participate**

Not applicable.

**Data availability**

The COVID-19 surveillance data used in this work are collected in the public domain from https://covid19.who.int/region/wpro/country/kr.

**Funding**

This work is not funded.

**Conflict of interests**

The authors declare no competing interests.

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Received 25 June 2020