

Supplementary Information for “Hotspot analysis of COVID-19 infection in Tokyo based on influx patterns”

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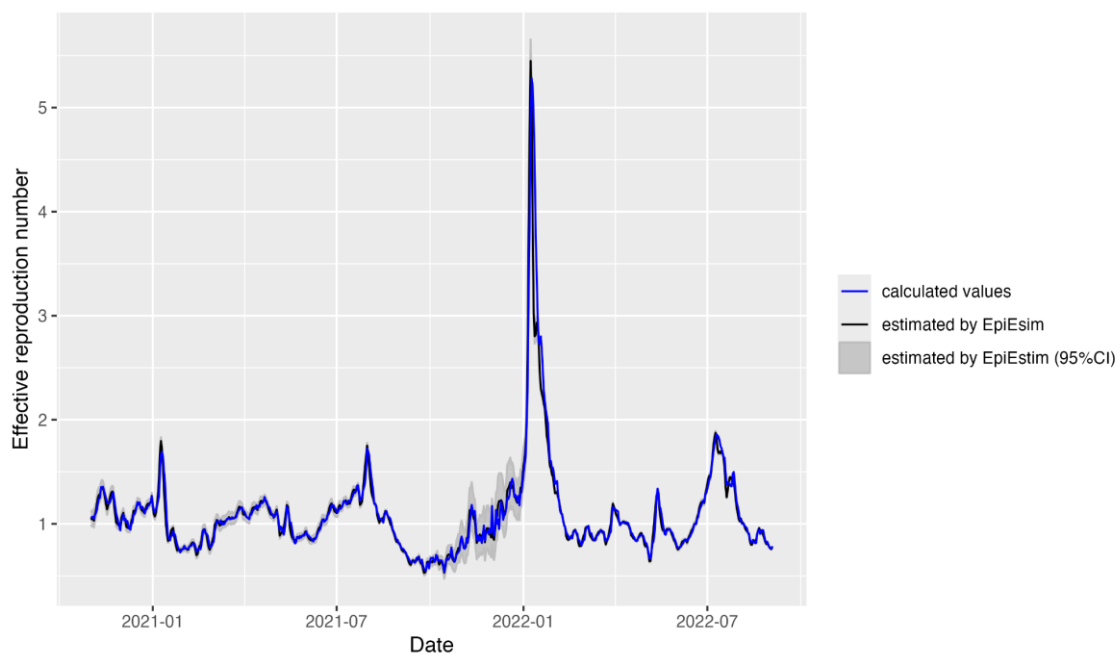
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Calculation of the effective reproduction number

Calculated values in this study

The effective reproduction number calculated in this study is compared with the estimated effective reproduction number calculated using the EpiEstim package in the R language. The results are shown in Supplementary Figure 1. According to this graph, the calculated values in this study and the values estimated by EpiEstim seem to be approximate.



Supplementary Figure 1: Comparison of the effective reproduction number calculated in this study with the estimated effective reproduction number calculated by EpiEstim. The blue line shows the effective reproduction number calculated in this study. The black line shows the estimated effective reproduction number calculated by EpiEstim. The grey colour range shows the 95% confidence interval of the estimated effective reproduction number calculated by the EpiEstim.

Note that we set values of 5.0 and 1.9 for the mean and standard deviation of the generation time parameters in EpiEstim, respectively, based on a paper by Ferretti et al.¹. The data on the number of new COVID-19 cases, which are the basis for the effective reproduction number, contain some outliers that are assumed to be due to aggregation errors. We supplement them by converting outliers to average values for the previous and following days with EpiEstim since the effective reproduction number cannot be estimated if there are empty values, as in the case of EpiEstim. Moreover, we convert outliers to empty values in the effective reproduction number calculated in this study.

References

1. Ferretti, L., et al. Quantifying SARS-CoV-2 transmission suggests epidemic control with digital contact tracing, *Science* **368**, 6491 (2020).