

SYNOPSIS

02/07/2020

Review of “Reporting, epidemic growth, and reproduction numbers for the 2019 novel coronavirus (2019-nCoV) epidemic”

Article citation: Tuite AR, Fisman DN. Reporting, epidemic growth, and reproduction numbers for the 2019 novel coronavirus (2019-nCoV) epidemic. *Ann Intern Med.* 2020 Feb 5 [Epub ahead of print]. Available from: <https://annals.org/aim/fullarticle/2760912/reporting-epidemic-growth-reproduction-numbers-2019-novel-coronavirus-2019-ncov>

One-minute summary

- The authors created a mathematical model of the 2019-nCoV epidemic to investigate the changing nature of case finding and epidemic growth.
- The study suggests that case ascertainment is increasing and reporting lags are decreasing
 - Previous models suggest that the **proportion of cases reported increased from 2.4%** (2020 Jan 12) **to 11.0%** (2020 Jan 18). The current model suggests that the **proportion of cases reported increased to 59%** by 2020 Jan 31, assuming that the effective reproduction number (R_e , the number of secondary cases from an infection), in the presence of control measures remains near 2.3 after quarantine (2020 Jan 24).
 - The model suggests that **reporting times are decreasing**, from **> 10 days** (2020 Jan 27) to **~4 days** (2020 Feb 3).
- Large increases in cases reported are likely due to: **1) increased disease activity** and **2) increased surveillance efforts**.
- Based on both reported cases and modelled estimates, the authors state that by 2020 3 Feb, a **R_e of 1.5** is plausible.
- Authors provide readers with interactive model: https://art-bd.shinyapps.io/nCov_control

Additional information

- The disease-transmission model uses an initial epidemic start date in mid-November 2019, with a **basic reproduction number (R_0) of 2.3** and a **serial interval of 7 days**.
- The model is based on publicly available data (as of 2020 Feb 3).
- The model estimates case counts based on the number of internationally exported cases.
- **Limitations:**
 - The model focuses on disease activity in China. Should 2019-nCoV spread more widely, the epidemiology in other countries may be different.
 - The model under-represents mild infections

PHO reviewer's comments

- Modelled case counts based on internationally exported case counts may be under-estimated as the genetic sequence of 2019-nCoV was made available on January 12, 2020, meaning that until then a specific diagnostic test was not available, which may have led to under-ascertainment.

Citation

Ontario Agency for Health Protection and Promotion (Public Health Ontario). Review of “Reporting, epidemic growth, and reproduction numbers for the 2019 novel coronavirus (2019-nCoV) epidemic”. Toronto, ON: Queens’s Printer for Ontario; 2020.

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