Observations: Brief Research Reports

Reporting, Epidemic Growth, and Reproduction Numbers for the 2019 Novel Coronavirus (2019-nCoV) Epidemic

Background: Virologically confirmed cases of 2019 novel coronavirus (2019-nCoV) in China and other countries have increased sharply (1, 2), leading to concerns regarding its pandemic potential. Viral epidemiology has been characterized sufficiently to permit construction of transmission models that predict the future course of this epidemic (3).

Objective: To provide insight into the changing nature of case findings and epidemic growth.

Methods: We developed a simple disease-transmission model in which the 2019-nCoV epidemic was modeled as a branching process starting in mid-November 2019, with a serial interval of 7 days (time between cases) and a basic reproduction number ($R_0$) of 2.3 (new cases from each old case), based on available data and assuming no intervention (Figure 1). The epidemic start date aligned our modeled case counts to point estimates from international case exportation data (4). The model estimated plausible values of the effective reproduction number ($R_e$; reproductive number in the presence of control) shows the effect of introducing control measures vs. continued epidemic growth without control. The difference between the 2 curves map. Because many combinations of model parameters created a series of “contours,” similar to altitude values on a map. Because many combinations of model parameters created approximately 4 days by 3 February 2020). Contours generated by the model with intervention give us information about which (average) reproduction numbers may be plausible and which are implausible (Figure 2). If $R_e$ had fallen to 1.0 after 24 January 2020, the model predicts fewer cases than are currently being reported (as of 3 February 2020), making this level of control implausible. By contrast, reduction to an $R_e$ of 1.5 is plausible on the basis of reported cases and model estimates up to 3 February 2020, but it would also imply complete reporting.

Discussion: Using a simple model of epidemic growth that includes the representation of control efforts can provide helpful insights into the growth of the 2019-nCoV epidemic that are not directly observable in publicly reported data. Comparison of modeled and reported case counts suggests that reporting lags are decreasing and case ascertainment increasing over time. The narrowing gap between modeled and confirmed cases shows that the massive public health effort under way in China is increasing ascertainment of 2019-nCoV cases. Large leaps in reported case counts represent both disease activity and a surveillance effort that is “catching up” with an epidemic.

Contour plots can be used to indirectly estimate $R_e$ after introduction of control efforts, because case counts exceeding a given contour suggest that an $R_e$ value is implausible. Potential limitations of this model include underrepresentation of mild infections and its focus on an epidemic currently centered in China. If this epidemic becomes a pandemic, epidemiology in individual countries may diverge. Nonetheless, the tool may help policymakers by allowing inferences about likely underlying dynamics of the epidemic, even when available disease data are delayed or incomplete.

We will continue to plot case counts against such projections moving forward (with updated counts incorporated into our online tool). If cumulative case counts flatten and intersect with contour lines horizontally, either control is improving and the mean reproduction number is decreasing or (a pessimistic interpretation) case ascertainment efforts are flagging because of limited laboratory or human resources. Conversely, if
The initial growth of the epidemic is based on introduction of the pathogen in mid-November 2019, with $R_0 = 2.3$ and a serial interval of 7 d. The model reproduces estimates of case counts based on volume of internationally exported cases (green squares) (4). Daily cumulative counts of virologically confirmed cases are based on publicly available reports (1, 2) (blue circles). Case counts reported on 3 February 2020 are not compatible with reduction of $R_e$ to 1 but could be compatible with reduction to 1.5. If control is achieved, reported case counts will intersect horizontally with the contour lines on this graph. When reported cases move beyond contours vertically, the reproduction numbers represented by those contours become implausible. 2019-nCoV = 2019 novel coronavirus; $R_0 = $ basic reproduction number; $R_e = $ effective reproduction number.

reported case counts cross the contour lines above them, that would imply an ever higher minimum value for $R_e$.

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Disclaimer: The tool, available at https://art-bd.shinyapps.io/nCov_control, was developed by the authors for this article using a third-party application, which may have limited access and functionality. Neither Annals of Internal Medicine nor the American College of Physicians is responsible for the content and functionality of this online application. Questions regarding the use of the application should be addressed to the corresponding author (e-mail, david.fisman@utoronto.ca).

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References
1. BNO News. Tracking coronavirus: map, data and timeline. 2 February 2020. Accessed at https://bnonews.com/index.php/2020/02/the-latest-coronavirus-cases on 3 February 2020.
2. China Centers for Disease Control. Distribution of pneumonia in a new coronavirus infection. 2020. Accessed at http://2019ncov.chinacdc.cn/2019-nCoV on 3 February 2020.
3. Wu JT, Leung K, Leung GM. Nowcasting and forecasting the potential domestic and international spread of the 2019-nCoV outbreak originating in Wuhan, China: a modelling study. Lancet. 2020. [PMID: 32014114] doi:10.1016/S0140-6736(20)30260-9
4. Imai N, Cori A, Dorigatti I, et al. Report 3: transmissibility of 2019-nCoV. 25 January 2020. Accessed at www.imperial.ac.uk/mrc-global-infectious-disease-analysis/news--wuhan-coronavirus on 25 January 2020.