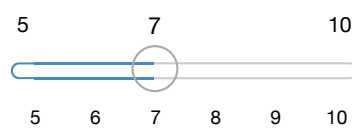# Reporting, epidemic growth, and reproduction numbers for the 2019-nCoV epidemic: understanding control
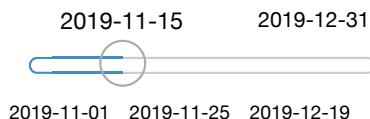
Move these sliders to see how the outbreak trajectory changes. There are many parameter combinations that create plausible epidemic curves. We regard well-calibrated curves as those that pass through the two green squares, which are case estimates generated through observation of exported case numbers before wide-scale travel restrictions came into effect.
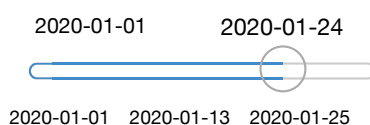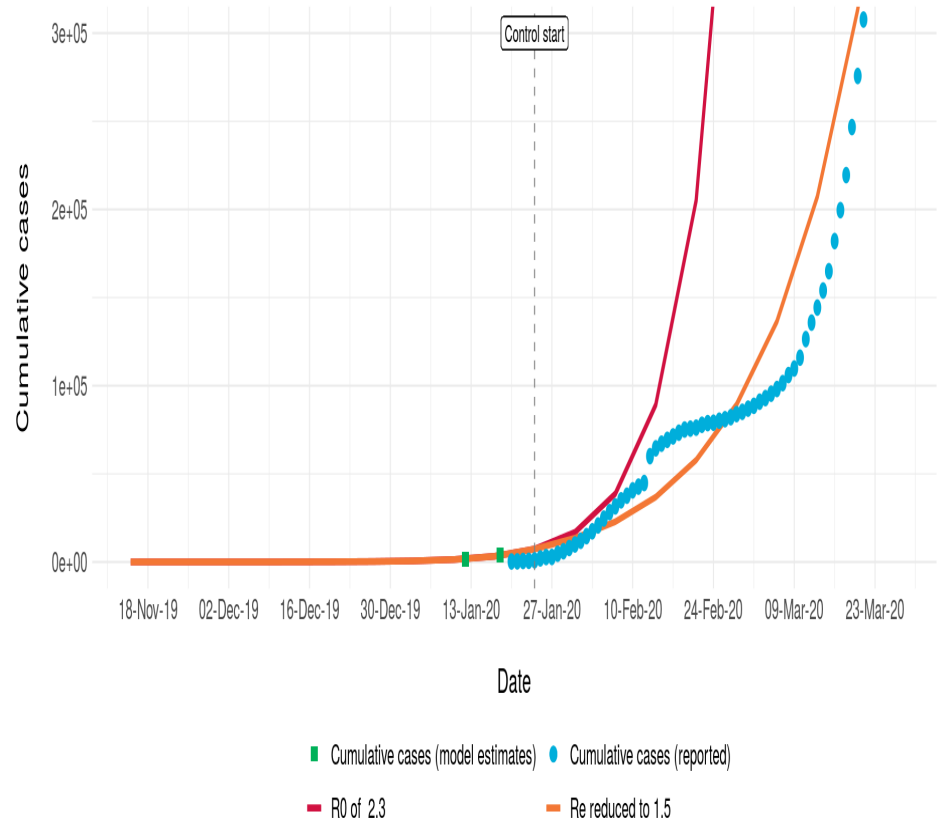
☐ Plot cases on a log scale

Serial interval (days)

5   7   10

5   6   7   8   9   10

Outbreak start date

2019-11-15   2019-12-31

2019-11-01   2019-11-25   2019-12-19

Control start date

2020-01-01   2020-01-24

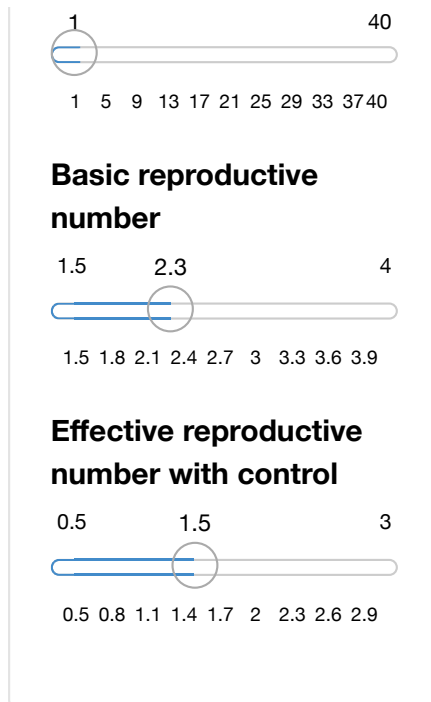2020-01-01   2020-01-13   2020-01-25

Initial number of cases

Notes

Cumulative cases (model estimates) represent outbreak size estimated using data on international case exportations [Imai et al.]. (https://www.imperial.ac.uk/mrc-global-infectious-disease-analysis/news--wuhan-coronavirus/)

Cumulative cases (reported) are based on publicly-available data [BNO News] (https://bnonews.com/index.php/2020/02/the-latest-coronavirus-cases/)

We have continued to plot virologically-confirmed cases for comparability across the time series. After 12 Feb 2020, formal case counts reported by Hubei province included both virologically-confirmed symptomatic cases and "clinically diagnosed" cases, which have symptoms of respiratory illness and radiographic evidence of pneumonia.

1		40

1 5 9 13 17 21 25 29 33 37 40

Basic reproductive number

1.5	2.3	4

1.5 1.8 2.1 2.4 2.7 3 3.3 3.6 3.9

Effective reproductive number with control

0.5	1.5	3

0.5 0.8 1.1 1.4 1.7 2 2.3 2.6 2.9

The default values for the serial interval and basic reproduction number are from an analysis of the early transmission dynamics of the outbreak in Wuhan, published by Li et al. (https://www.nejm.org/doi/full/10.1056/NEJMoa2001316?query=featured_coronavirus)

Control measures were assumed to start on January 24th, the date of quarantine of Wuhan and surrounding cities [Wu et al.]. (https://www.thelancet.com/journals/lancet/article/PIIS0140-6736(20)30260-9/fulltext)

Genomic analysis indicates that the initial human infection occurred in Nov-Dec 2019, followed by sustained human-to-human transmission [Bedford et al.]. (https://nextstrain.org/narratives/ncov/sit-rep/2020-01-30)

We provide the option of seeding the epidemic with more than one initial case, as might be seen with a point source outbreak as the initial cause of animal-to-human spill-over.

Additional model details are available at: https://annals.org/aim/article/doi/10.7326/M20-0358 (https://annals.org/aim/article/doi/10.7326/M20-0358)

Developed by Ashleigh Tuite and David Fisman, Dalla Lana School of Public Health, University of Toronto