Title: *Early transmissibility assessment of a novel coronavirus in Wuhan, China*

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COMMENT:

Since December 8, 2019, nearly 600 cases of respiratory illness caused by a novel coronavirus (2019–nCoV) have been diagnosed in relation to an outbreak originating in Wuhan, China **[1, 2]**. Though several cases have been linked to a local fish and live animal market, human-to-human transmission appears likely and cases have already been exported to neighboring countries **[3]**. Due to the novelty of this pathogen, rapid assessment of its associated epidemiological properties is of the essence – especially within the context of the ease with which it may be transmitted. In this Comment, we present a cumulative epidemic curve of cases that have been reported to date and assess the potential transmissibility associated with 2019–nCoV given currently available public information.

Cumulative case count data were collected from the World Health Organization Disease Outbreak News reports as well as bulletins issued by the Chinese National Health Commission and the Wuhan Municipal Health Commission **[1–4]**. Upon plotting these data over time, a reverse-L-shaped curve appeared due to reporting of large case counts from January 18–22, 2020 (Figure 1A).

This cumulative epidemic curve was then used to assess potential transmissibility via the Incidence Decay and Exponential Adjustment (IDEA) model **[5]**. The IDEA model is a simple, phenomenological method that allows for estimation of the basic reproduction number (R_0): the average number of individuals a new case is expected to infect in a fully susceptible population. When a cumulative epidemic curve of a disease is available and when the length of time between two consecutive infections in a chain of transmission (i.e. the serial interval of the pathogen) can be approximated, this model can be employed in

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otherwise data-scarce settings. Previous studies have demonstrated performance of the IDEA model to be on-par with more traditional compartmental (e.g. S–I–R) models for multiple emerging diseases, including Zika, Ebola, and Middle East Respiratory Syndrome (MERS) **[6–8]**.

The model itself can be defined by the following single equation:

$$I = \left[\frac{R_0}{(1+d)^t}\right]^t$$

Here, t is the number of serial intervals that have passed at time of model parameterization and I is incidence at serial interval t. Meanwhile, d is a discount factor that takes into account reductions in transmissibility over time due to the natural depletion of susceptible individuals in the affected population and any public interventions that may impact disease spread over time.

Because the serial interval associated with 2019–nCoV has not yet been established, we referenced mean serial interval lengths (l) from the related SARS-*Coronavirus* and MERS-*Coronavirus* [range: 6–10 days] to parameterize our model **[9, 10]**. For this range of serial interval lengths, modeled R_0 estimates varied from 2.0 to 3.3 when using data from December 8, 2019 through January 22, 2020. Estimates for d were 0 for all serial interval lengths. Model fits are shown in Figure 1A for R_0 = 3.3 (PCC = 0.98).

To ascertain the stability of our estimates thus far, we also used truncated input data (i.e. December 8, 2019 through January 18, 19, 20, and 21) to parameterize our model. Results for the estimated reproduction number range were similar to those obtained when

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using all available data, signaling relative short-term stability in our model's ability to capture the growth rate of the outbreak over the last 5 days, despite elevated case count reporting in this time frame (Figure 1B).

Because R_0 values greater than 1 indicate the possibility of sustained transmission, our analysis suggests that 2019-nCoV may exhibit epidemic potential under the assumption that currently available public information is accurate and relatively complete. Notably, our current estimates of R_0 – while preliminary and subject to change – are consistent with previous estimates associated with SARS-Coronavirus (R_0 = 2–4) **[9]**. With this in mind, timely data sharing and further epidemiological research should be pursued actively as the ongoing outbreak progresses. Pending availability of new data, repeated re-evaluation of the model presented here – as well as the transmissibility associated with 2019–nCoV more broadly – is recommended.

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Figure Legend:

Figure 1. *Cumulative epidemic curve, model fits, and early transmissibility assessment for novel coronavirus cases associated with Wuhan, China from December 8, 2019 through January 22, 2020.* In Panel A (top), reported cumulative cases are shown with pink circular markers connected by a pink dotted line and model fits for R_0 = 3.3 are shown with a blue dotted line using data from December 8, 2019 through January 22, 2020. In Panel B (bottom), reproduction number ranges as estimated by the Incidence Decay and Exponential Adjustment (IDEA) model are shown using data through January 18, 19, 20, 21, and 22 to demonstrate short-term model stability as well as transmissibility.

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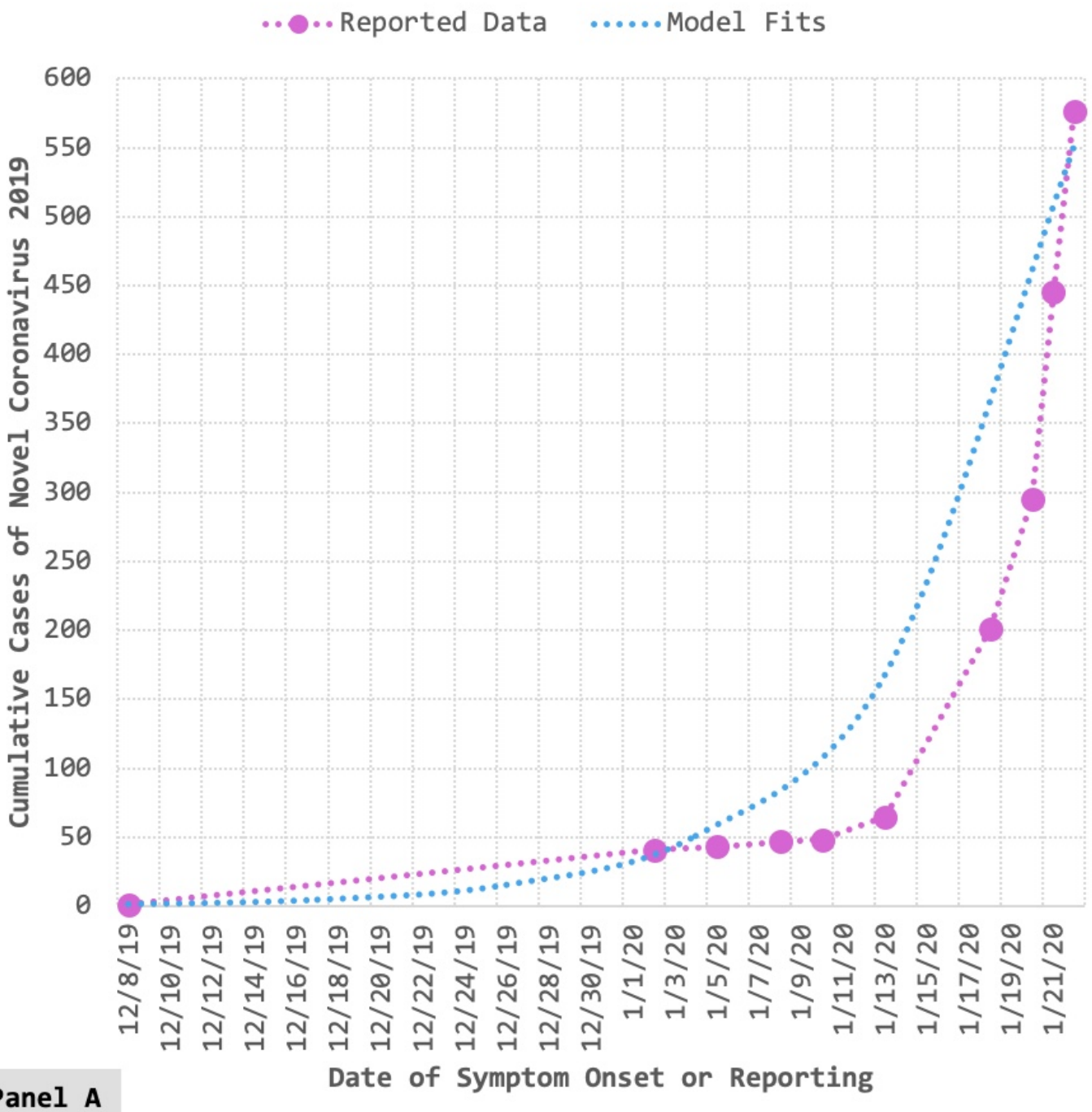
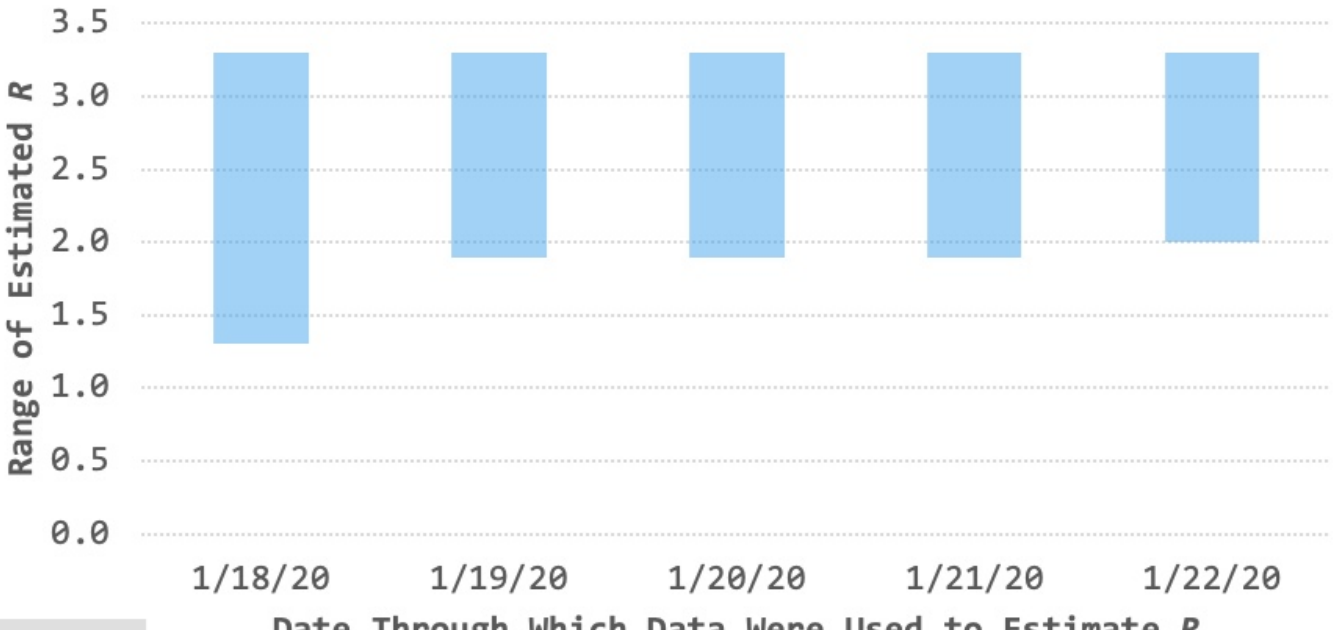


Panel A



Panel B

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