Reconciling early-outbreak estimates of the basic reproductive number and its uncertainty: framework and applications to the novel coronavirus (2019-nCoV) outbreak

Sang Woo Park1,\* Benjamin M. Bolker2,3,4 David Champredon5 David J.D. Earn3,4

Michael Li2 Joshua S. Weitz6, 7 Bryan T. Grenfell1,8,9 Jonathan Dushoff2,3,4,\*

1. Department of Ecology and Evolutionary Biology, Princeton University, Princeton, NJ,

USA

1. Department of Biology, McMaster University, Hamilton, ON, Canada
2. Department of Mathematics and Statistics, McMaster University, Hamilton, ON, Canada
3. M.G.DeGroote Institute for Infectious Disease Research, McMaster University,

Hamilton, ON, Canada

1. Department of Pathology and Laboratory Medicine, University of Western Ontario,

London, Ontario, Canada

1. School of Biological Sciences, Georgia Institute of Technology, Atlanta, GA, USA
2. School of Physics, Georgia Institute of Technology, Atlanta, GA, USA
3. Division of International Epidemiology and Population Studies, Fogarty International

Center, National Institutes of Health, Bethesda, MD, USA

1. Woodrow Wilson School of Public and International Affairs, Princeton University,

Princeton, NJ, USA

\*Corresponding authors: swp2@princeton.edu and dushoff@mcmaster.ca

# Abstract

## Background

A novel coronavirus (2019-nCoV) has recently emerged as a global threat. As the epidemic progresses, many disease modelers have focused on estimating the basic reproductive number , the average number of secondary cases caused by a primary case in an otherwise susceptible population. The modeling approaches and resulting estimates of vary widely, despite relying on similar data sources.

## Aim

We aimed to develop a framework for comparing and combining different estimates of across a wide range of models.

## Methods

We reviewed 7 model-based analyses of the 2019-nCoV outbreak that were published online between January 23–26, 2020. We decompose their estimates into three key quantities: the exponential growth rate *r*, the mean generation interval , and the generation-interval dispersion *κ*. We use a Bayesian multilevel model to construct pooled estimates and measure uncertainties associated with these quantities.

## Results

We find that most early estimates of rely on strong assumptions, especially about the generation-interval dispersion. Estimates that rely on narrow generation-interval distributions are overly sensitive to estimates of the exponential growth rate.

## Conclusion

Our results emphasize the importance of propagating uncertainties in all components of , especially the shape of the generation-interval distribution in efforts to estimate at the outset of an epidemic.

**Keywords**

Basic reproductive number, 2019-nCoV, novel coronavirus, Bayesian multilevel model

# Funding

BMB and DJDE were supported by Natural Sciences and Engineering Research Council (NSERC). ML was supported by Canadian Institutes of Health Research (CIHR). The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

**Declaration of interests**

We declare no competing interests.

**Acknowledgements**

We thank Daihai He for providing helpful comments on the manuscript.

# Contribution

SWP and JD developed the statistical framework. SWP reviewed the published literature. SWP performed the analysis. SWP, BMB, and JD created the figures. SWP and JD wrote the first draft. All authors contributed to the writing and approval of the final report.