Dear Editors:

We are submitting our manuscript, “Reconciling early-outbreak preliminary estimates of the basic reproductive number and its uncertainty: framework and applications to the novel coronavirus (2019-nCoV) outbreak”, for consideration for publication in Eurosurveillance. This material has not previously been published elsewhere. We have submitted a preprint to medRxiv: https://www.medrxiv.org/content/10.1101/2020.01.30.20019877v2.

The basic reproduction number (i.e., the average number of secondary cases caused by a primary case in a fully susceptible population) is a key quantity in models of disease spread. As the novel coronavirus (2019-nCoV) continues to spread in China and other parts of the world, many researchers have focused on analyzing the outbreak and estimating its basic reproductive number. Even though their analyses rely on similar data, their modeling approaches and the resulting estimates vary widely. It is crucial to compare and evaluate different estimates to accurately predict the course of an outbreak and assess the required amount of intervention.

Here, we present a novel statistical framework for comparing different estimates of the basic reproduction number. First, we show that disparate estimates of the basic reproduction number can be understood by decomposing them into three quantities: the exponential growth rate, the mean generation interval, and the generation-interval dispersion. We then use a Bayesian multilevel model to measure ``pooled'' uncertainties in these three quantities. By replacing the implicitly or explicitly assumed values of these three quantities with our pooled estimates, we can test the sensitivity of the basic reproduction number estimates with respect to their assumptions.

Our study contributes to the field by improving estimation of a central quantity in the prediction and control of epidemics. The analysis also stresses the importance of propagating all sources of uncertainty.

Sincerely,

Sang Woo Park and Jonathan Dushoff