Evaluating uncertainties associated with early estimates of the basic reproduction number during the novel coronavirus (2019-nCoV) outbreak

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Abstract

1 Introduction

Since the end of December 2019, a novel coronavirus (2019-nCoV) continues to spread in China and in other parts of the world. As of January 27th, 2020, the World Health Organization has confirmed 2798 cases, including 37 confirmed cases in 11 different countries, outside China (World Health Organization (WHO), 2020b). Although the virus is suspected to have originated from animal reservoirs, a recent case from Viet Nam demonstrated its ability to transmit between humans (World Health Organization (WHO), 2020a), posing a greater threat for a wider spread.

Many researchers have been rushing to publish their analysis of the outbreak (Imai et al., 2020; Riou and Althaus, 2020; Read et al., 2020; Zhao et al., 2020; Majumder and Mandl, 2020; Liu et al., 2020) and, in particular, their estimates of the basic reproductive number $\mathcal{R}_0$ (i.e., the average number of secondary cases generated by a primary case in a fully susceptible population). The basic reproductive number is of particular interest because it allows prediction about the final size of an epidemic. While their efforts are valuable, their analyses rely on several assumptions that could immediately affect their estimates of $\mathcal{R}_0$ and the associated uncertainties.

Here, we present a simple framework for evaluating uncertainties associated with parameter estimates across a wide range of models. Our results indicate that most published estimates of $\mathcal{R}_0$ are likely to be overly confident. We also lay down several principles that needs to be taken into consideration.

Early estimates of $\mathcal{R}_0$

Early in an outbreak, $\mathcal{R}_0$ cannot be estimated directly. Instead, estimates of $\mathcal{R}_0$ are often inferred from the exponential growth rate r can be estimated reliably from incidence data. Given estimates of the exponential growth rate r and the distribution $g(\tau)$ of generation intervals (i.e., the time between when a person become infected and that person infects another person), the basic reproduction number can be estimated via the Euler-Lotka equation:

$$1/\mathcal{R}_0 = \int \exp(-r\tau)g(\tau)d\tau. \tag{1}$$

Therefore, early estimates of $\mathcal{R}_0$ must necessarily depend on the assumptions about r and $g(\tau)$.

We use the gamma approximation framework to demonstrate how assumptions about r and $g(\tau)$ affects $\mathcal{R}_0$. Assuming that generation intervals follow a gamma distribution with the mean $\bar{G}$ and the squared coefficient of variation κ, we have

$$\mathcal{R}_0 = \left(1 + \kappa r \bar{G}\right)^{1/\kappa}. \tag{2}$$

This equation demonstrates that generation-interval distributions with a larger mean (higher $\bar{G}$) or less variability (lower κ) will give a higher estimate of $\mathcal{R}_0$. Likewise, strong assumptions about $\bar{G}$ and κ will give estimates of $\mathcal{R}_0$ with narrow confidence intervals.

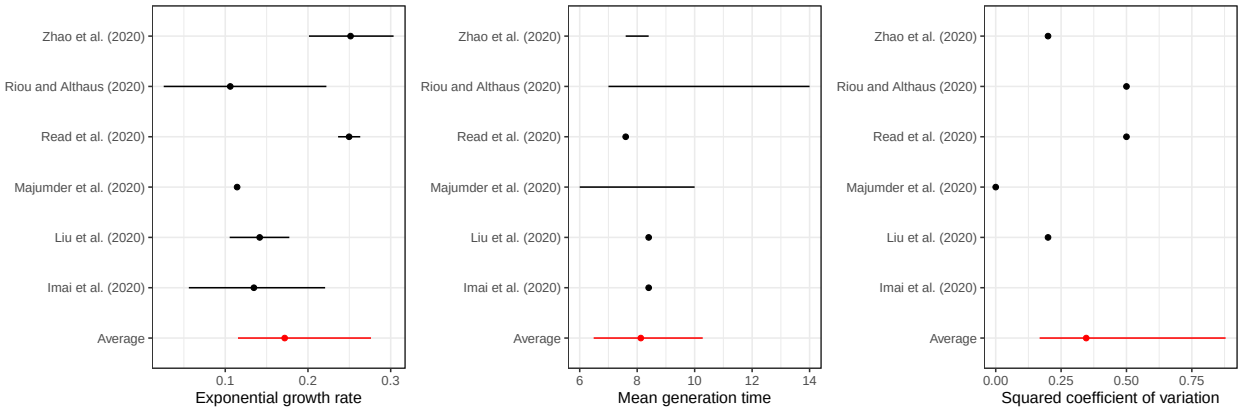

Figure 1: Early estimates of $\mathcal{R}_0$ and associated assumptions about r and $g(\tau)$.

Figure 1 clearly demonstrates the lack of uncertainties in the underlying parameters of the current $\mathcal{R}_0$ estimates. In particular, no studies properly propagate uncertainties associated with the amount of variability in generation intervals, which can have large effects on the estimates of $\mathcal{R}_0$ For example, when the relative mean generation interval is long ($r\bar{G} \approx 2$ based on the estimates by Zhao et al. (2020)), varying κ from 0 to 1 reduces the estimate of $\mathcal{R}_0$ by more than a two fold.

$$\begin{aligned} \mathcal{R}_i &\sim \text{distrib}(\theta_i) \\ \bar{G}_i &\sim \text{distrib}(\theta_i) \\ \kappa &\sim \text{distrib}(\theta_i) \end{aligned} \tag{3}$$

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