

Discussion of “Tracking reproductivity of COVID-19 epidemic in China with varying coefficient SIR model”

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The paper by Sun et al. is a thoughtful and important work for tracing the transmission of COVID-19 over the course of outbreak in China. As COVID-19 has been spreading globally as a pandemic, the lessons obtained from disease mitigation measures in China become more valuable to other countries and to future infectious diseases.

The authors adopted an epidemiological model, SIR model (Kermack and McKendrick, 1927), of infectious diseases, and made a few key modifications. First, a stochastic version of the SIR model, Poisson-vSIR model, is proposed to model the incremental numbers of infected and recovered cases by Poisson distributions, which facilitates statistical inference; more importantly, the infectious rate is allowed to vary over time and estimated by the reciprocal regression. The proposed model is applied to cases in provinces and cities of China to calculate the time-varying infection rate function. Results show that infectious rates significantly decreased after reducing the person-to-person contact and curtailing population movement, a valuable lesson for other countries facing surging COVID-19 cases and deaths. In what follows, I will discuss about the model, the preprocessing of observed data, the effective reproduction number, and the predictions of model.

The proposed Poisson-vSIR model is based on the Euler method, a numeric method for ordinary differential equations (Lapidus and Seinfeld, 1971, ODEs), discretizing cases arising from the continuous time scale to cases modelled at the discretized time scale in days. Recognizing this numeric step would help appreciate the connection between the ODEs-based SIR model and the difference equations (DEs)-based Poisson-vSIR model. In the same time, I am curious if this numeric approximation would cause some discrepancy between two models in terms of the dynamic of diseases and if higher order of numeric approximation of ODEs, like the Runge–Kutta method, would make any difference.

A key component of Poisson-vSIR model is the time-varying infection rate function, pre-specified as a parametric form possibly due to identifiability concerns. There likely exist many other parametric forms which may not be distinguishable from the current one, given the limited dataset. What interests me is the observation that the continuous infection rate function fits well for most of the provinces, even when decisions of reducing the person-to-person contact, e.g. lockdown of city or “shelter in place”, were commonly effective shortly after the announcement, and behaviors of person-to-person contact changed abruptly. Do the results of this analysis suggest the opposite, that behaviors of person-to-person contact change gradually after the abrupt lockdown? Alternatively, could it be possible that the sudden changes of infection rate is smoothed out by data preprocessing. The numbers of infected and recovered cases are subjected to underreporting bias, availability of test kits, and changes of diagnosis and report criteria, among other factors. For example, 15,152 new cases were reported of February 12 2020 in China, about 600% surge over the preceding day, largely due to the changes of criteria how cases are diagnosed and reported. Without adjusting such “outliers”, the results from the Poisson-vSIR model would be misleading. To deal with it, moving average filter was applied. While moving average will

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filter outliers, it might also smooth out the short-term exponential growth trend or some change points due to intervention policies. Additional sensitivity analysis would be of interest.

The main story of paper is built around the effective reproduction number. The authors considered two possible forms: $R_t = \tilde{\beta}(t)/\gamma(t)$, where $\tilde{\beta}(t)$ is the filtered infectious rate and $\gamma(t)$ is the removal rate; and $R_t^D = \beta(t)D$, where $\beta(t)$ is the unfiltered infectious rate and D is an average infectious duration, which can be viewed as a special case with $\gamma(t)$ remains constant over time. Authors preferred R_t^D and pointed out that $\gamma(t)$ involved in R_t is highly volatile at the early stage of COVID-19, which makes it critical to choose the proper plug-in value of average infectious duration D . Even so, the variability of such D could also make a difference in constructing confidence intervals for R_t^D . As COVID-19 comes to an end in China, it may be worthwhile revisiting the point estimation and variance of D , and updating the estimation of R_t^D accordingly. In addition, how volatile the $\beta(t)$ would be at the early stage of COVID-19 and if changes of R_t^D over time are statistically significant?

Policies of public mitigation rely on the predicted trajectory of infectious disease more than ever. For example, in order to justify the prolonged “stay at home” policy, members of the US Coronavirus Task Force explained the future outlook of COVID-19 in US based on the prediction of epidemiological models during a press briefing on March 30, 2020. To examine the promise of data-driven policy making, it would be of interest to evaluate if the observed trajectories of COVID-19 in provinces or cities of China follow the predicted ones by the proposed model closely and what lessons have been gained from predicting trajectories of infectious disease.

After fighting through the COVID-19 pandemic with blood, toil, and tears, it is the time to reflect. The tools developed by Sun et al. and lessons offered would be very valuable for a swift response to the next pandemic. More such efforts are desired.

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