Methodology to estimate COVID-19 incidence number and R_0 coefficient

We use growth models to analyze historical data of COVID-19 outbreak. Richards' curve, which is shaped like letter S, is widely used for growth modeling. This kind of curve assumes that growth does not continue indefinitely and must stop at some point in time. Growth characterized by Richards' curve is not symmetric with respect to peak time – it is not necessary that incidence cases before and after peak time must be equal. Richards' curve is frequently used to model COVID-19 outbreak. Here is one example that uses of Richards' curve to model COVID-19 outbreaks in China Provinces.

Richards' growth model estimates four parameters: incidence cases on the first day of the epidemic in a particular country – y_o, maximum cumulative cases in country – K, maximum growth rate – μmax, and shape parameter determining the curvature – β. Estimation of these parameters gives us very useful information about the dynamics of COVID-19 in a particular country. We can extract the following information and make prediction about the peak time (this day after which infection spread starts decreasing), the total number of incidence at peak time and the ending time of epidemic in a particular country (which is the same as when "S" curve starts flattening).

In order to estimate parameters we used Levenberg-Marquardt algorithm in R programming languages using "growthrates" libraries.

The quantification of transmissibility during epidemics is essential to designing and adjusting public health responses. Transmissibility can be measured by the basic reproduction number – R_0. It is the average number of secondary infections produced by a typical case of an infection in a population where everyone is susceptible. The definition describes the state where no other individuals are infected or immunized. However, a population will rarely be entirely susceptible to an infection in the real world. Furthermore, various public health interventions decline the transmissibility. To account for this, the instantaneous effective reproduction number (R_t) is used. If $R_t > 1$, the number of new cases are expected to increase. When $R_t = 1$, the disease is endemic, and where $R_t < 1$, decline in the number of new cases are expected.

Transmission here is modeled with a Poisson process. The rate at which someone infected at a time $t - s$ generates new infections at time t, is equal to $R_t w_s$, where R_t is the instantaneous reproduction number at time t and w_s is a probability distribution describing the average infectiousness profile after infection, which depends on time since an infection of the case s only. The serial interval distribution is used as an approximation for the infectivity profile w_s.

The instantaneous reproduction number R_t can be estimated by the ratio of I_t – the number of new infections generated at time t – to the total infectiousness of infected individuals at time t, given by $\sum_{s=1}^{t} I_{t-s} w_s$, the sum of infection incidence up to time step $t - 1$, weighted by the infectivity function w_s. The incidence of cases at time step t is, on average, $E[I_t] = R_t \sum_{s=1}^{t} I_{t-s} w_s$. we assume a gamma prior distribution for R_t. Bayesian statistical inference based on this transmission model leads to a simple analytical expression of the posterior distribution of R_t.

However, the resulting R_t estimates can vary highly and hence difficult to interpret when the time step of data is small. We, therefore, calculate estimates over seven-day time windows, under the assumption that the instantaneous reproduction number is constant within that time window.

R_t is estimated in using R employing the EpiEstim package.

References:

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