News & Views

A new approach to modeling the fade-out threshold of coronavirus disease

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On 21 December of 2019, four lower respiratory tract samples were collected from patients with pneumonia of unknown cause in Wuhan, China [1]. This disease was later diagnosed as a coronavirus disease. The World Health Organization (WHO) named the coronavirus disease as COVID-19 on 11 February and declared a pandemic on 11 March 2020. The COVID-19 is a previously unknown disease with no tools available for pharmaceutical management at the early stage of its outbreak. On 23 January 2020, Wuhan was locked down and all provinces and regions across China imposed antiviral prophylaxis, quarantines, school closures, travel restrictions, and social distancing by implementing the “first-level response to major public health emergencies” during the period 23–25 January 2020. The case confirmation speed during this period improved due to development of new coronavirus nucleic acid-based detection technologies [2].

The goal of modeling the fade-out threshold is to gain insight into how to calculate the mean die-out time of the epidemic, which improves our understanding of the dynamics of the spread of the epidemic. When the infectious disease spreads in a population, a model may help to provide real-time forecasting [3,4]. Epidemic modeling is one of the essential tools for both developing strategies in preparation for the outbreak and evaluating the effectiveness of control policies during the outbreak. Furthermore, the model can also assist in decision-making by making projections regarding intervention-induced changes in the spread of disease.

Regarding the infectious disease dynamics, the basic reproduction number $R_0$ is a critical indicator. Ross [5] first proposed the concept of $R_0$ and defined it as the average number of new infections caused by a single infected individual when introduced into a wholly susceptible population over the duration of the infection of this individual. This concept has been widely used and improved since then. The $R_0$ provides an indication of whether the introduction of the disease will result in a localized burnout or signal the beginning of an epidemic that could move through all geographic scales [6]. A timely estimation on $R_0$ of the COVID-19 epidemic may prove beneficial in understanding how to control the worldwide spread of the epidemic [7].

The formula of $R_0$, the transmission rate $\beta$ is not directly observable and can be difficult to measure due to its dependence on the probability of transmission between individuals and social contact rates [8]. The transmission rate of an infectious disease is defined as the per capita rate of infection given contact, which can be expressed as the product of the number of daily contacts that a susceptible individual has with other individuals and the probability of transmission during each contact [9]. In other words, a more highly infectious disease has a higher transmission rate. However, we need to know the transmission rate if we want to predict the changes of an epidemic disease. Determining the time-dependent transmission function that exactly reproduces disease incidence data can yield useful information about disease outbreaks, including a range of potential values for the recovery rate of the disease. If the time-dependent transmission function is constructed, information regarding intervention and stopping the outbreak can be obtained.

The time-dependent transmission rate (TDTR) is used to account for intervention effects, such as raising awareness in the population about the current severity of the epidemic, implementing measures of quarantine and isolation of patients, and providing access to effective and affordable medicines. We constructed an algorithm to compute the TDTR from the well-known Susceptible-Infected-Recovered (SIR) model based on the reported data. The SIR model was first proposed in 1927 [10] in order to incorporate the possibility of switching transmission rates when the prevention strategy was changed and has been widely modified and applied since 1927 (e.g., [9,11]).

Based on the improved SIR model [9], we developed a new TDTR as follows:

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The basic reproduction number \([R_0]\) can be formulated as

\[
R_0(t) = \frac{\beta(t)}{\gamma(t) + \mu(t)}.
\]

Where \(S(t)\) represents susceptible fractions of the population at time \(t\); \(I(t)\) represents the infected fractions of the population; \(\beta(t)\) denotes the TDTR; \(\gamma(t)\) is the recovery rate; and \(\mu(t)\) refers to the fatality rate.

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Appendix A. Supplementary materials

Supplementary materials to this article can be found online at https://doi.org/10.1016/j.scib.2020.04.016.

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Conflict of interest

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