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Short Communication

An approximation-based approach for periodic estimation of effective reproduction number: a tool for decision-making in the context of coronavirus disease 2019 (COVID-19) outbreak

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ABSTRACT

Objectives: The effective reproduction number (R) is a more practical epidemiological parameter than basic reproduction number (R_0) for characterization of infectious disease epidemics as it takes into account presence of immune individuals in the population which R_0 does not. Periodic assessment of R can inform public health strategies during long-standing epidemics such as the current coronavirus disease 2019 (COVID-19) situation. This is especially relevant for large and resource-poor countries such as India, which may require differential intervention strategies in different regions. However, the complexity of the calculation involved often proves to be a barrier for calculation of R. This communication proposes a simpler data collection and analytical method – involving a combination approach instead of full-fledged primary data collection – to estimate R for public health decision-making.
Study design: Literature review.
Methods: Data from available sources (time series data of new cases at population level) can be combined with some primary data (time interval between infection of index and secondary cases in family clusters) that can be collected with little resources. These data can then be fed into an approximation-based method (Wallinga and Lipsitch) for R calculation at the state/regional levels. The calculations can be repeated every fortnight using newly available data.
Results: The value of R, estimated using the proposed method, from subsequent periods can be used for assessing the status of the epidemic and values from subsequent periods can be compared for decision-making regarding implementation/modification of control measures.
Conclusions: The approximate R may be a little inaccurate but can still prove useful for rough estimation of epidemic evolution and for comparison between different periods, as the extent of error in R values across different periods is likely to be similar. Thus, the approximate R may not only be used to estimate the epidemic change in smaller geographies such as states/regions but also used for making appropriate changes to public health measures for managing a pandemic such as COVID-19.

Introduction

The current pandemic of coronavirus disease 2019 (COVID-19) presents a challenge to nations and the interconnected global community. The basic reproduction number or R_0, defined as the expected number of secondary cases generated by an index case in a fully susceptible population, is a widely used epidemiological parameter for understanding the transmission potential in a given population. However, irrespective of the type of infectious agent, the population is likely to be partially immune (especially during the later phases of the epidemic).[1] Hence, the effective reproduction number (R) is often considered a more useful metric for characterizing the epidemic spread and the effort required for epidemic containment.[1] This is especially relevant for India, where a less steep epidemic curve has been attributed (hypothetically) to cross-immunity from other infections.[2] Periodic assessment and comparison of R_0 or R does not only help in understanding the dynamics of transmission and evolution but also is immensely important for designing and/or modifying public health intervention strategies.[3] In India, similar to other resource-poor countries,

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detailed epidemiologic data on an outbreak are often scarce and decisions are often made on the basis of a line list of infected patients.[4] This often results in implementation of a single strategy (usually at the national level) that may not be relevant for all geographical or administrative units. In the current commentary, we suggest a method for local or regional level calculation of *R* (and comparison between *R* from different periods) using easily available data for devising differential intervention strategies depending on epidemic situation.

Methods

The calculation of R_0 and *R* (expressed mathematically as $R=R_0*(S/N)$, where S = number of susceptible and N = total population) in epidemiology largely follows two approaches:[5] (i) taking the average of the number of secondary cases for each index case, usually from individual contact tracing data (assuming that the index and secondary cases belong to a closed system), and (ii) a modeling-based approach which uses ordinary differential equations (ODEs). The ODE models use parameters such as disease transmissibility and progression rates (derived by model fitting on population-level data) to estimate the expected population size in different phases of the epidemic. As comprehensive data on contact tracing, usually requiring independent follow-up studies, are not often available in countries with poor surveillance systems, the modeling approach (using either Susceptible-Infectious-Recovered and Susceptible-Exposed-Infectious-Recovered models) is more widely used despite its complexity.

In the context of the current COVID-19 epidemic, this commentary proposes a relatively simpler approach for calculation of *R* based on the generation interval method of Wallinga and Lipsitch,[6] which was in turn derived from the Lotka–Euler equation.[1] *R* can be approximated using the following equation:

$$R = 1 + r*T$$

where, *r* is the rate of exponential growth (or per capita increase in the number of new cases per day) and *T* is the mean generation interval (or the time period between infection of an index case and a secondary case generated from the index case).

The value of *r* can be obtained relatively simply by fitting the number of new cases (from the time series data of new cases at population level) and assuming an exponential curve. The current growth rate (up to the second week of April 2020) in India is approximately 0.12.[7] This can be calculated for different states and regions as well. It is difficult to obtain a reliable value of *T* from population-level data. Therefore, we propose using reverse transcription polymerase chain reaction or RT-PCR positivity results of family clusters of index cases – the time interval between positive results of index and secondary cases acting as the surrogate interval between the times of infection.[8] As all family members and close contacts of the positive cases are currently being tested, the data can be obtained from nodal laboratories, treating hospitals, and quarantine facilities (as applicable). Regarding the estimation of *R*, it is recommended that the cases of foreign citizens (or individuals with recent international travel history) and those with non-domestic contact history are excluded from this exercise (as generation interval for such cases may be different from the domestic population). It is further proposed that, for tracking and periodic updates of *R*, incident cases from the previous two weeks are used, that is, for each fortnight, the growth rate will be calculated based only on the cases diagnosed during the concerned fortnight. In addition, the generation interval for each fortnight should use data from the family clusters whose index case got newly infected during that fortnight (or during a predefined lag period). This approach will allow for fortnightly updates of the *R* value and course corrections of intervention measures based on the same (if required).

Conclusion

The present manuscript describes a simpler method for estimating an approximate *R* that will allow for periodic comparison and public health decision-making. The described methodology focuses on estimating the approximate *R* instead of R_0, as *R* is more practical in a real-world scenario – regardless of the type of infection, some portion of the population will be immune to the infectious agent (COVID-19 in this case). This is more important in the Indian context as the apparent low prevalence of identified cases, compared with other high-prevalence countries, could be indicative of pre-existing immunity.[9] Experiences from previous infectious disease outbreaks suggest that the value of *R* evolves over time because of various environmental and biological factors.[10] With several public health measures already in place, the *R* for the COVID-19 outbreak is likely to change quickly as well.[11] As India continues to practice containment measures such as social distancing and lockdown, periodic comparison of *R* may facilitate tracking of the epidemic and, in turn, aid local- and regional-level decision-making on shifting of public health strategies (such as extending or reducing the period of containment, focusing on high-risk groups instead of the general population, and so on). In addition, in the future, it may prove useful to determine the population to be immunized, if and when a vaccine comes out.[10] While we admit that the value of *R* estimated by this approximation-based approach may be slightly inaccurate on its own, comparison of subsequent *R* values calculated using the same method can still inform public health decisions (as the extent of error in R values across the epidemic period is likely to be similar).[3] In addition, the approximate *R* may be influenced by underreporting (if any) of COVID-19 cases. However, unless the ratio of missed (not reported) to reported cases fluctuates widely across the epidemic period, the calculation of growth rate may not be affected by a large margin and, hence, any major impact on the *R* value is unlikely. Therefore, despite its inherent limitations, the proposed approach may prove to be a simple and efficient tool for making appropriate time-sensitive strategic changes at the regional level to better manage a pandemic such as COVID-19.

Author statements

Ethical approval

This research does not contain any data on any human subjects. No ethical approval was obtained.

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Competing interests

The author declares no competing interests.

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