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What Modelling and Reproduction Numbers are Useful in Predicting COVID-19 Spread?

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Abstract

The potent virus COVID-19 is a lower respiratory tract infection that spreads from person to person ,predominantly via aerosolized micro-droplets. The virus also transfers to humans via mucous membranes that come in contact with fingers/hands contaminated with COVID-19 [1] and through self-infection and the gastrointestinal tract [2].

Introduction

Success and Failures of Controlling Covid-19

Countries in which the leadership understood the virus, explained the gravity of a pandemic to the public, and took prompt and decisive actions managed to control the disease quickly. Whereas, those countries took a while to take actions as in the USA and United Kingdom and/or relied upon to control COVID-19 using military maneuvers (as in Indonesia and Sri Lanka, and others), such as 24-hour months-long curfews ignoring the needs and the welfare of their citizens, harmed millions of people, their employment, livelihood, food security, civil rights, and rising community deaths (mostly undiagnosed and unaccounted because of the failure to performed PCR), with little effect on controlling the disease. Because of markedly lesser number of PCR testing performed, the prevalence and the death rates reported from latter countries are markedly underestimated and unreliable.

With the hope of facilitating understanding of viral trends, epidemiologists and statisticians have been using tools such as modelling for decades. The use of such tools mushroomed during the current COVID-19 pandemic, but the outcomes, accuracy of predictions, and usefulness of the projected models have been less than anticipated. In fact, countries such as United Kingdom that relied on local modelling were misled in making the right decisions, which caused delays and prevented the implementation of effective strategic plans (https://www.imperial.ac.uk/mrc-global-infectious-disease-analysis/covid-19/); consequently, such countries failed to control the disease.

Moreover, the increases in cases local outbreaks of COVID-19secondary peaks in the community-highlight the need to adapt rapidly to emerging healthcare needs and expand testing in the community [1]. Administrations that relied on lockdowns and curfews, refused to carry out community polymerase chain reaction (PCR) testing, and restricted testing to hospitals continued to generate and report misleading statistics regarding COVID-19 incidence, prevalence, and death rates. It is unclear if theseactions are attributable to misguidance, ignorance, a lack of resources and local expertise, or political and for election maneuvers to demonstrate low case numbers and death rates, to camouflage secondary peaks, and portrait the lack of appearance of 'new' clusters of COVID infections in communities.

Growth of COVID-19

Irrespective of age, ethnicity, gender, or the country where people live, everyone is susceptible to COVID-19 [1]. The basic reproduction number, R0 (pronounced R naught), is used by statisticians as a measure for estimating the public health threat of microbial infections, especially viral diseases. When reliable data are used as input, R0 indicates the transmission potential of a communicable bacterial or viral disease, at least in theory [3,4]. However, R0 changes over time because of the changing virulence of the virus, travel patterns, weather conditions, and other circumstances. Because of the difficulty in obtaining reliable and real-time data, individual variations, and unpredictable human behavior, predictions based on modelling have been disappointing and misleading; they have provided fundamentally incorrect conclusions that have led administrators and politicians to take flawed actions that can potentially harm a country, its economy, and people [5].

Basic Interpretation of R0 values

When R0 exceeds 1, it suggests that the number of infected people is increasing exponentially the growth part of an epidemic or a pandemic. Assuming that the calculation of R0value is correct, it could provide useful information for planning and preparing for the impending spread of the disease in a given community, state, or a country in a strategic manner. When R0 is less than 1, an infected person transmits the disease to one or fewer individuals, so the disease is in the fading phase

[3,4], which could allow governments to begin removing imposed restrictions and gradually opening up markets.

There are multiple reasons for the variability of R0 values within one community or country, as published by different research groups. R0 is a calculated number, and its value is dependent on the accuracy of the data input, estimated duration of contagiousness, the likelihood of infection per contact between people, the rate of contacts, and travel patterns, etc. However, these are highly dependent on socioeconomic variables, weather, air pollution, and other biological and environmental factors.

Unreliability of relying on R0

Because of such variability and thus unreliability, unless the generated values are grossly above or below 1, R0 does not provide worthwhile information for public health planning and resource allocation, especially if one dominant model is being relied upon. From a calculation point of view, a major falsehood is the assumption that infectivity from a person to another or multiple persons remains static, but this is not the case *[6]*.

The control reproduction number (RC) is used by some to indicate the spread of a communicable disease. Sustained RC values below 1 indicate the disease is fading *[7]*. Nevertheless, the predictive value of RC is no better than that of R0 *[8]*. In a given community, district, or state, it is reasonable and more reliable to rely on real-time, community-based, RT-PCR and antibody testing data rather than using unreliable R0or RC numbers, as was done recently in the United Kingdom with disastrous clinical outcomes.

Principles of modelling:

At the start of an epidemic, estimates are somewhat slack, and many assumptions are included in all of the statistical models. Some of the intermediary estimates include the percentage of expected deaths from an epidemic and the R0. However, when an epidemic or pandemic is maturing, more reliable data begin to emerge, and these living models should be refined.

Models are designed to understand how people move between sectors; the rapidity and variability of susceptibility of individuals (S) to contracting the virus; ability to become infected (I); and recover (R) or die. Modelling assumes that a part of the R group has developed protective antibodies and presumably is immune to the virus and thus will not infect others. The mentioned basic SIR models assume that the population is uniformly distributed and evenly mixed (that is, infected people are equally infectious without variability until recovery or death). However, this is fundamentally flawed.

For example, despite recent unsubstantiated claims by the WHO, younger people are less susceptible to develop symptomatic COVID-19 yet are infectious. A key assumption that included in most R0calculations, that everyone has the same chance of catching the virus from an infected person is

false. Such assumptions are too rudimentary and allow significant errors in qualitative predictions. Advanced models are capable of making quantitative predictions that could be useful for officials in managing resources during an epidemic or a pandemic. Such models have the capacity to separate people into smaller groups based on age, gender, occupation, ethnicity, overall health status, exposure risks, number of contacts, and so forth, and the possibility of the inclusion of some information on social mixing. Therefore, more ethnic-group-and sector-specific outcomes can be predicted.

Mechanistic Aspects of Modelling Epidemics and Pandemics

Fundamentally, there are three types of models used for the calculation of R0: Equation-based model, Stochastic models, and Agent-based model. An equation-based model is simpler and quicker to generate. Such models are not run at high resolution, and people are put together into broad groups and are not included as individuals with varied responses. As witnessed during the springtime in 2020 with the COVID-19 pandemic, the total number of affected cases and deaths reported are heterogenous, not always accurate, and the methodologies varied much. To minimize unwanted swings in modelling R0 numbers and prevent output variability when a single input is changed, some uses sensitivity analysis and others rely on the use of multiple models. Stochastic models inject a little randomness, similar to rolling a virtual dice to see whether or not someone in the group becomes infected(for example, encounter at a meeting or during travel).

Some modelling could simulate presumed activities of people; with equation-based models, individuals are sorted into population groups. Although the use of social-subset analyses is useful and close to reality, but such models are complicated and can introduce significant errors.

Agent-based model assumes and allows room for individuals to move around and act freely. This model builds in a virtual world similar to that of equation-based models but more refine. In summary, to improve the quality of a prediction model and generate useful and practical out put, it is necessary to include information at the household level, travel patterns, work conditions, cultural and social interactions, activity during leisure time, and so forth.

Calculation of R0 Using Different Models

Different models assessing and predicting the clinical outcomes associated with COVID-19, include risk assessment, diagnostic and prognostic models. The value of predicting the outcome of any of these models, however, depends on the accuracy of the assumptions and the quality of data used. In most recently published models from industrialized counties, one or both of these parameters were improper. Therefore, the predictions are not accurate. Flawed attempts and suggestions to flattening of infectivity curves is an example. In addition to faulty assumptions, the models used have had high risks of bias, making analytical interpretation no better than inconsequential

political polls used in election campaigns *[9]*.

Another major flaw is not considering the community transmission of COVID-19 through asymptomatic carriers. The latter is a major threat for emerging outbreaks and so, controlling the disease *[10]*. Nevertheless, such is not included or captured during calculation of R0or any of the currently used models *[5]*. In addition, the variability across populations and ethnic groups (e.g., white Caucasians versus persons with brown skin (Asians), ethnic minorities, or African Americans), vulnerabilities, nutritional variability especially vitamin D status *[11]*, and individual responses, are not considered in any of the current modelling systems. Therefore, considering the mentioned hiatuses it is not surprising that the infectivity and the models describing disease spread are inaccurate.

Currently Used Prediction Models are Unreliable

Higher infection rates and virulence lead to increased disease burden and associated death rates. Despite the claim in early June 2020 by the World Health Organization, ignoring multiple sets of global data, COVID-19 is a highly contagious disease that is spread by asymptomatic and symptomatic persons to others. However, this erroneous controversy was resolved, after the fact.

Therefore, unless community PCR testing/screening is performed, as in south Korea, the USA, and many other countries, infectious disease spread by asymptomatic carriers cannot be identified and included in COVID-19 statistical reporting. For comparative understanding, as an example, the average case-fatality rate for COVID-19 and the Spanish flu a century ago, both were estimated to be approximately 2%. However, the average mortality is approximately 5 to 10 times greater than that associated with seasonal colds and influenza happens during each winter period in countries that are located in northern latitudes.

Conclusion

Because the data used are unreliable and inaccurate assumptions have been made, virtually all reported models are insensitive, not specific, and misleading, with exaggeration or under estimation of the infectiousness and potential for the spread of COVID-19. Relying on such models is likely to cause chaos, harm, wasted resources, and possibly increased deaths in any given country. Therefore, to avoid misleading clinical outcomes, epidemiologists and administrators must take a broader approach for decision making, including using multiple estimates and modelling with real-time GPS-guided

surveillance data. However, modeling must be independent and not be modified or linked to suit political agendas or support imposing or relaxing restrictions. All scientific research, publications, and country-based statistics, including modelling and publishing of morbidity and mortality data, must be devoid of personal agendas, conflicts of interest, and politics.

Conflicts of Interest

The author declares no conflicts of interest.

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