Infectious Diseases Quantitative Modelling to Predict and Control Epidemics

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PERSPECTIVE

Mathematical models may be used to anticipate the course of infectious illnesses, as well as the expected result of an epidemic and the creation of public health interventions. Models employ fundamental assumptions or facts, as well as mathematics, to derive parameters for various infectious illnesses, which are then used to quantify the effects of different treatments, such as mass vaccination campaigns. Modelling can help with things like deciding which actions to avoid and which to attempt, as well as predicting future development trends.

Infectious disease model is a method that has been used to explore how diseases spread, forecast the course of an outbreak, and assess control options. Bernoulli, a trained physician, created a mathematical model to support the practise of smallpox inoculation. According to this model's estimates, universal smallpox immunisation would increase life expectancy from 26 to 29 years and 9 months. Daniel Bernoulli's research precedes our knowledge of germ theory. William Hamer and Ronald Ross used the law of mass action to describe epidemic behaviour in the early twentieth century.

In the 1920s, the compartmental model initially arose. Kermack–McKendrick (1927) and Reed–Frost (1928) are two epidemic models that show the interplay of vulnerable, infected, and immune people in a society. The Kermack– McKendrick epidemic model predicted outbreak behaviour that was strikingly comparable to that of several previously observed epidemics. Simple compartmental models have lately been replaced by agent-based models (ABMs). For example, Epidemiological ABMs are often used to drive health policy (non-pharmaceutical) initiatives to stop SARS-CoV-2 from spreading. Epidemiological ABMs have been criticised for simplifying and incorrect assumptions, despite their complexity and high processing needs. Even yet, when correctly calibrated, ABMs can be useful in guiding decisions about mitigation and suppression actions.

Assumptions

The assumptions that support models are only as good as the assumptions that underpin them. If a model's predictions don't match the facts but the math is correct, the model's underlying assumptions must be altered to make it usable. Everyone in the population lives to age L and then dies, with the same number of persons in the population at each age (up to L). In developed nations, where neonatal mortality is low and a high proportion of the population lives to retirement age, this is usually justified.

Types of epidemic models

Stochastic: "Stochastic" refers to the state of being or possessing a random variable. A stochastic model is a technique for forecasting the future probability distribution function that accounts for random changes in one or more inputs across time. Chance variations in exposure risk, disease dynamics, and other sickness dynamics are used to create stochastic models. In small or large populations, stochastic methods can be utilised to determine disease distribution at the statistical agent level.

Deterministic: When dealing with large populations, such as TB, deterministic or compartmental mathematical models are commonly used. In a deterministic model, individuals in the population are split into subgroups or compartments, each reflecting a different stage of the epidemic. Because the transition rates from one class to another are formally represented as derivatives, the model is developed using differential equations. When building such models, it is important to assume that the population size in a compartment is differentiable over time and that the epidemic process is predictable. Models offer the benefit of looking at several outcomes at the same time rather than making a single forecast. Models have proven a high degree of accuracy in prior pandemics, such as SARS, Bird Flu, MERS, and Ebola.

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