CORRESPONDENCE

Influenza—Insights From Mathematical Modelling

by Dr. med. Rafael Mikolajczyk, Ralf Krumkamp,
Dr. med. Reinhard Bornemann, Amana Ahmad, Markus Schwehm,
Dr. rer. nat. Hans-Peter Duerr in volume 47/2009

Basic Reproduction Number

The basic reproduction number according to the formula

$$R_0 = K \times \frac{\beta}{\alpha} = \frac{\log \frac{S_0}{S_\infty}}{K - S_\infty}$$

(K=population size, beta=transmission rate, alpha=recovery rate, S_0 =susceptible at the onset of the epidemic, S_∞ =susceptible at the end of the epidemic) of an infection leading to immunity depends on the size of the exposed population and on the number of people with immunity. Students in school years 8/9 would currently comprehend that infections with a basic reproduction number of 2 and a duration of illness of 10 days would infect an entire urban population of 160 000 within 23 days. But epidemics progress through large populations without infecting every single person. In a school class of 30, which means 30 contacts per student—including the occasional missing student—the resultant basic reproduction number is 1.5, whereas R_0 for 100 persons is 2.0 and for 1000 persons, 3.0. Not every infected person therefore equally qualifies for spreading an epidemic with discrete compartments. An elderly person living by themselves will not acquire flu from external contacts, nor will they prolong a chain of infection if they contract influenza. Doctors who look after an average of 1000 patients, however, are effective index patients if they contract flu. Epidemiological models assume that the transmission rate of a causative strain is identical across an entire population. The differences in the observable spread result precisely from this assumption..

DOI: 10.3238/arztebl.2010.0276a

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Dr. med. Martin P. Wedig
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In Reply:

The equation cited by Dr Wedig comes from the Kermack-McKendrick model developed in 1927 (1). The model explained why medieval epidemics did not result in the complete extinction of mankind. However,

the equation is not suitable for calculating the basic reproduction number using a constant transmission rate in groups of varying sizes while assuming that the number of contacts increases with the population. Still, someone living in a city with a population of 1 million does not have 1000 times more contacts than someone living in a village. Rather, what the Kermack-McKendrick model was able to come up with was an estimated transmission rate derived from the actual dynamics of an epidemic.

The statement that the number of contacts differs individually by age, profession, and personal behavior, etc, is correct. But even relatively simple epidemiological models take into consideration different contact rates among the groups—for example, age groups. Until quite recently, such “who mixes with whom” matrices were based on simplified assumptions and estimates. As late as in 2008, several European countries published empirical contact rates that were suitable for mathematical modeling (2).

The simple enumeration of contacts does, however, not take into consideration several aspects of possible heterogeneity—among others, viral particle shedding by infected persons and/or the duration of the corresponding exposure of susceptible persons need to be considered. If the duration of a contact is taken as a proxy for exposure (3), the high numbers of contacts that doctors encounter, for example, might play a lesser part in the spread of an epidemic—because of their short duration—than household contacts, which are more intense and whose duration is longer. These considerations will yield increasingly sophisticated models in the future.

DOI: 10.3238/arztebl.2010.0276b

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Conflict of interest statement

The authors of both contributions declare that no conflict of interest exists according to the guidelines of the International Committee of Medical Journal Editors.