THE STATISTICS OF GENERATION TIMES IN EPIDEMIC SPREAD MODELS

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Recently, the analysis of data on past epidemics, in particular flu pandemics, has attracted great interest, because of the probable future pandemic threat posed by avian flu. The data is analyzed to yield parameter values for intervention evaluation models. Among the basic parameters, the generation time has a central role, both because of its intrinsic meaning and its relation to other basic parameters such as infectious period, latent period and contact intensity. The concept of generation time of an infectious disease has an "innocent" definition, viz. the time from the the moment one person becomes infected until that person infects another person. This concept is similar to the "generation gap" in a population, with infections replacing births.

By formulating the inference problem within a simple yet basic model, the stochastic continuous time SIR model, it is possible to derive distributional results for observations in various situations, e.g. in "isolation", in households, during large outbreaks.
In each case, it is shown that biases, usually not considered in the literature (see e.g. [1]), arise. These results lead to two further considerations, which are subject to ongoing research: 1) do further features of the observation model, such as inclusion of latent period, observation of clinical onset instead of infection, varying infectivity during the infectious period, modify the bias effects found in the basic model? 2) what consequences would the acknowledgement of these bias effects have on estimates derived from published data sets?
We will describe how the generation time is related to various basic quantities in models of epidemic spread and how the statistical properties of observed generation times are far from obvious...

Keywords: epidemic model, statistics, generation time.

REFERENCES
[1]   Fine P.E.M. (2003) The interval between succesive cases of an infectious disease. Am J Epidemiol 158, 1039-1047.