Estimating transmission parameters using social contact data and serological data.

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In order to restrict the damage caused by an epidemic, intervention strategies are needed to reduce the transmission of infection-specific antigens. For this purpose, the estimation of age-dependent transmission rates is required. In the past, different mixing patterns were imposed on the so-called Who-Acquires-Infection-From-Whom matrix to allow estimations from seroprevalence data (Anderson and May, 1991). These mixing assumptions, however, are rather ad hoc and result in large differences for the estimation of the basic reproduction number R_0, a basic quantity in infectious disease epidemiology. More recently, an alternative approach has come up, by assuming transmission rates for directly transmitted airborne infections are proportional to rates of conversational contacts (Wallinga et al., 2006). In this paper, we show how transmission parameters can be estimated using serological data on varicella zoster virus (VZV) and social contact data from Belgium. We elaborate on the methodology as presented by Wallinga et al. (2006), by explicitly accounting for the different sources of variability, by using a more continuous modeling approach and by exploring the proportionality assumption.
A cross-sectional survey on social contacts was conducted in Belgium from March to June 2006. Contacted persons had to record their contacts during one day including characteristics such as age, gender, location, duration and frequency of contact. Moreover, a distinction between two types of contacts was made: non-close contacts, defined as a two-way conversation of at least three words in each others proximity, and close contacts that involve any sort of physical skin-to-skin touching. The 'social contact matrix' is estimated using a bivariate smoothing approach based on thin plate regression splines. Using the mass action principle, these estimated contact rates are contrasted to seroprevalence data in order to estimate transmission parameters. A first analysis focuses on the constant proportionality assumption: transmission rates are proportional to contact rates up to a constant q. Five contact types which are likely to be responsible for VZV transmission, are considered. According to the AIC-criterion, close contacts lasting longer than 15 minutes are most capable of explaining the observed serological profile. A non-parametric bootstrap approach is applied to assess sampling variability and to account for age uncertainty. Secondly, we explore whether the proportionality factor q depends on the age of the susceptible person, the age of the infected person or both. This consideration makes logical sense, since transmission dynamics might also be influenced by age differences in susceptibility, infectivity, hygiene, etc. Age dependence is modeled using discrete structures as well as loglinear regression models. For VZV in Belgium, extending the model to age-dependent proportionality entails an improvement in fit. Concepts of model selection uncertainty are illustrated for the set of candidate models and a model averaged estimate is calculated for the basic reproduction number R_0.

References

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