Mixing in age-structured population models of infectious diseases ☆

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ABSTRACT

Infectious diseases are controlled by reducing pathogen replication within or transmission between hosts. Models can reliably evaluate alternative strategies for curtailing transmission, but only if interpersonal mixing is represented realistically. Compartmental modelers commonly use convex combinations of contacts within and among groups of similarly aged individuals, respectively termed preferential and proportionate mixing. Recently published face-to-face conversation and time-use studies suggest that parents and children and co-workers also mix preferentially. As indirect effects arise from the off-diagonal elements of mixing matrices, these observations are exceedingly important. Accordingly, we refined the formula published by Jacquez et al. [19] to account for these newly-observed patterns and estimated age-specific fractions of contacts with each preferred group. As the ages of contemporaries need not be identical nor those of parents and children to differ by exactly the generation time, we also estimated the variances of the Gaussian distributions with which we replaced the Kronecker delta commonly used in theoretical studies. Our formulae reproduce observed patterns and can be used, given contacts, to estimate probabilities of infection on contact, infection rates, and reproduction numbers. As examples, we illustrate these calculations for influenza based on "attack rates" from a prospective household study during the 1957 pandemic and for varicella based on cumulative incidence estimated from a cross-sectional serological survey conducted from 1988–94, together with contact rates from the several face-to-face conversation and time-use studies. Susceptibility to infection on contact generally declines with age, but may be elevated among adolescents and adults with young children.

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1. Introduction

While pathogens spread via interpersonal contacts, transmission may be modeled within and between groups of similar individuals. Appropriate levels of aggregation depend on questions of interest and observations available. Given suitable expressions for heterogeneous mixing, this mean field approach yields dynamic networks whose nodes are ever changing sub-populations defined by age, location, or other strata. Recently, there has been an explosion of models in which network structure defines social contacts among individuals (see, e.g., [24]). Epidemic-control measures have been evaluated using both approaches.

Individual- and population-based models have strengths and weaknesses. Individual-based models capture the chance nature of interpersonal contacts and permit concurrent membership in multiple risk groups (e.g., households and schools or workplaces). Results are presented as frequency distributions from multiple realizations of stochastic processes, allowing policymakers to determine the risk of outcomes more extreme than desired under particular conditions. In contrast, the systems of differential equations comprising population-level models can often be analyzed for general insights. Moreover, their fewer parameters can be more easily estimated from observations. And deficiencies are easier to remedy by comparing predictions to observations and determining the cause of any discrepancies.

While existing formulae represent contacts within sub-populations (e.g., age classes) and between each such group and all others, recently published empirical studies of encounters by which respiratory diseases might be transmitted indicate that parents and children and co-workers also mix preferentially. We generalize the model of Jacquez et al. [19] to include these contacts explicitly, permitting more realistic assessments of the risks