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Homogeneous epidemic models with nonlinear contact rate to approximate stochastic multigroup SIR models

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ABSTRACT

Despite the tremendous increase in the complexity of epidemic models developed in recent years, a great number of data on infection spread have been analysed with the use of mathematical models based on homogeneous mixing, or simple variants of that.

It seems that, while definitely mixing patterns and individual behaviour are complicated, simple homogeneous models in many cases may still adequately reproduce the overall epidemic spread.

We have examined this problem, using a relatively simple prototype of “complex” models, namely a stochastic SIR model for a closed population divided in groups, with heterogeneous within-group transmission and between-group transmission ranging from global to more localized. The simulated data were then fitted through a deterministic SIR homogeneous model with linear or nonlinear contact rates.

A critical parameter in this fit appears to be the ratio $/r/$ of between- to within-group transmission: when this is large enough, the standard homogeneous model works well, and the estimated R_0 is close to the value for the deterministic multigroup model. When $/r/$ is too small, stochastic effects dominate and deterministic models are not effective. Finally, in an intermediate region, a homogeneous SIR model with nonlinear contact rate approximate simulations better than standard bilinear model; the interpretation of its parameters may then be unclear, but a heuristic argument explains why models with nonlinear contact rate produce a better fit.