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Approximation of infection spread in multigroup SIR models through homogeneous models

In recent years there has been a tremendous increase in the complexity of epidemic models developed for the spread of infection in humans; often models include households and other types of mixing groups, as well as heterogeneities due to age, behaviour, etc. In another direction, a great number of data on infection spread have been analysed with the use of mathematical models, which often are based on homogeneous mixing, or simple variants of that. Aim of this work is starting to understand why, while definitely mixing patterns and individual behaviour are complicated, simple homogeneous models may still reproduce adequately the overall epidemic spread. Our prototype of complex models is relatively simple, namely a stochastic SIR model for a closed population divided in groups, with uniform global transmission and heterogeneous local transmission; simulations show that this type of models can be approximated adequately by a homogeneous model, as long as the number of groups is sufficiently large. Heuristic methods suggest the relations of the synthetic parameters of the homogeneous model with the original parameters. Extensions to models with differential transmission routes are being examined.