

# Epidemics on random networks with household structure

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## Abstract

There has been a growing interest in models for epidemics among structured populations, which incorporate realistic departures from homogeneous mixing whilst maintaining mathematical tractability. Two classes of structured population epidemic models that have attracted considerable recent attention are network models (in which there is a random graph describing possible infectious contacts) and household models (in which the population is partitioned into households with different contact rates for within- and between-household infection). In this talk, based on joint work with David Sirl (Loughborough University) and Pieter Trapman (Stockholm University), I describe and analyse a model for the spread of an SIR (susceptible  $\rightarrow$  infective  $\rightarrow$  removed) epidemic that includes both of these features (see Ball et al. [1]). The analysis, which makes extensive use of branching processes, includes deriving a threshold parameter which determines whether or not an epidemic with few initial infectives can become established and lead to a major outbreak, and determining the probability and expected relative final size of a major outbreak. The model is compared and contrasted with a standard network epidemic model. Vaccination strategies are briefly considered, as is an extension of the model to include several types of individual (Ball and Sirl [2]).

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## References

- [1] Ball, F.G., Sirl, D. and Trapman, P. (2010) *Analysis of a stochastic SIR epidemic on a random network incorporating household structure*. Math. Biosci., 224, 53-73.
- [2] Ball, F.G. and Sirl, D. (2012) *An epidemic model on a population with random network and household structure, and several types of individual*. Adv. Appl. Prob., 44, 63-86.