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An SIR epidemic spreading through multiple communities

Abstract

Stochastic epidemic models have evolved over recent decades from classical models which make many assumptions of homogeneity to include many aspects of heterogeneity. Many of these models still submit to significant analysis, including asymptotic (large population limit) results such as threshold theorems determining whether a large outbreak is possible and provable approximations for the probability and size of such an outbreak. In this spirit, we present and analyse a stochastic model for the spread of an SIR (susceptible-infective-removed) epidemic in a population of communities in which links between communities are much weaker than those within communities. Our analysis is asymptotic as the size of the communities to to infinity, with either a fixed or growing number of communities. We present threshold results and central limit type results for the size of large outbreaks.

This is joint work with Frank Ball (University of Nottingham) and Pieter Trapman (Stockholms Universitet).