Epidemic and ecological thresholds on random and structured networks.

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Under what conditions will a virus spread in a complex population network? This question has vexed epidemiologists, mathematicians and computer scientists alike for many decades. The classical SIS (susceptible-infected-susceptible) epidemic model predicts that there is a threshold that is based on the reproductive number R_0, the number of secondary infections of the virus. Should the virus be able to reproduce itself in a fully susceptible population, $\boldsymbol{R}_0 > 1$, an endemic state will be reached where the virus persists in time, while if $\boldsymbol{R}_0 < 1$, the population will eventually reach an infection-free equilibrium where the virus is extinct. These modeling studies generally assume that the population is homogeneous and randomly mixing, so that an infected individual is equally likely to come into contact with, and infect, any susceptible present -- assumptions that have many limitations. Dietz and May generalized the basic result in the 80's for heterogeneous populations in which some individuals have more contacts than others, as for example, in scale-free networks.

We are specifically interested in understanding the way in which the detailed network structure of the population, or its "topology," might affect the persistence threshold. That is, does the exact network structure, not just its degree distribution, give extra information from which it is possible to learn more about epidemic spreading? This might be the case, for example, if the network is non-random, highly clustered, or to some degree structured, in which case the well known results for random models are no longer relevant and predictions are less easy to come by. We present some new results for these important cases.