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SIR epidemics on random graphs with clustering

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Abstract

In this project, we consider SIR (Susceptible \rightarrow Infectious \rightarrow Recovered) epidemics on random graphs generated by a version of the configuration model with clustering. Miller (2009) investigated SIR epidemics on graphs of this model under the assumption of homogeneous infectivity. We extend previous results by relaxing this assumption. We use a branching process approximation of the spread of the disease to provide expressions for the probability of a major outbreak and the expected final size. Furthermore, we show that for this particular model, the basic reproduction number, here defined as the rank based geometric growth rate of the epidemic, equals the perfect vaccine-associated reproduction number. Moreover, we use maximal coupling to prove that the branching process approximation is exact in the limit as the population size approaches infinity.

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