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From Markovian to pairwise epidemic models and the performance of moment closure approximations

Many if not all models of disease transmission on networks can be linked to the exact state-based Markovian formulation. However the large number of equations for any system of realistic size limits their applicability to small populations. As a result, most modelling work relies on simulation and pairwise models. In this paper, for a simple SIS dynamics on an arbitrary network, we formalise the link between a well known pairwise model and the exact Markovian formulation. This involves the rigorous derivation of the exact ODE model at the level of pairs in terms of the expected number of pairs and triples. The exact system is then closed using two different closures, one well established and one that has been recently proposed. A new interpretation of both closures is presented, which explains several of their previously observed properties. The closed dynamical systems are solved numerically and the results are compared to output from individual-based stochastic simulations. This is done for a range of networks with the same average degree and clustering coefficient but generated using different algorithms. It is shown that the ability of the pairwise system to accurately model an epidemic is fundamentally dependent on the underlying large-scale network structure. We show that the existing pairwise models are a good t for certain types of network but have to be used with caution as higher-order network structures may compromise their effectiveness.