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Assessing the average length of infection chains in an outbreak of infectious disease

Analytical expressions for the reproduction number, R0, and final size have been obtained in the past for an extremely wide variety of mathematical models for infectious disease spread. However, what has so far not been studied is the average number of infections that descend down the chains of infection begun by each of the individuals infected in an outbreak (we refer to this quantity as the "average number of descendant infections" per infectious individual, or ANDI). ANDI includes not only the number of people that an individual directly contacts and infects, but also the number of people that those go on to infect, and so on until the chain of infection dies out.

Quantification of ANDI has relevance to the anti-vaccine debate; if the individual probability of hospitalisation with a disease is p, the probability that at least one individual down an average chain of infection is hospitalised is $1 - (1-p)^{\mathrm{ANDI}}$.

Here we examine a Susceptible, Infected, Recovered (SIR) model, and obtain the analytic expression for ANDI. We compare the estimates of ANDI from this expression to those obtained using an Agent Base Monte Carlo formalism that keeps track of who infected whom. We find that ANDI is maximised for smaller R0, and that ANDI in even relatively small populations can be literally dozens of individuals.

While the model examined in this initial analysis is simple, the analytic and computational formalisms we have developed can be expanded to a wide variety of models for disease spread.