Gillespie implementation of SIR epidemic without vital dynamics

(source: https://en.wikipedia.org/wiki/Gillespie_algorithm)

The SIR model is a classic biological description of how certain diseases permeate through a fixed-size population. In its simplest form there are N members of the population, whereby each member may be in one of three states – susceptible, infected, or recovered – at any instant in time, and each such member transitions irreversibly through these states according to the directed graph below. We can denote the number of susceptible members as n_S, the number of infected members as n_I, and the number of recovered members as n_R. Therefore we may also conclude that $N = n_S + n_I + n_R$ for any point in time.

Further, a given susceptible member will transition to the infected state by coming into contact with any of the n_I infected members, and so infection occurs with rate αn_I (dimensions of inverse time). A given member of the infected state recovers without dependence on any of the three states, which is specified by rate β (also with dimensions of inverse time). Given this basic scheme, it possible to construct the following non-linear system.

$$\frac{dn_S}{dt} = -\frac{\alpha n_S}{V} n_I \tag{1}$$

$$\frac{dn_I}{dt} = \left(\frac{\alpha n_S}{V} - \beta\right) n_I \tag{2}$$

$$\frac{dn_R}{dt} = \beta n_I \tag{3}$$

This system has no analytical solution. However, with the Gillespie algorithm, it can be simulated many times, and a regression technique such as least-squares may be applied to fit a polynomial over all of the trajectories. As the number of trajectories increases, such polynomial regression will

asymptotically behave like an analytic solution. In addition to estimating the solution to an intractable problem like the SIR epidemic, the stochastic nature of each trajectory allows one to compute statistics other than $\mathrm{E}[n|t]$.