Traditionally, population dynamics in continuous time are modeled using coupled, ordinary differential equations. Although accurate in highly scaled models, the lack of stochasticity in deterministic models can result in dynamics which do not accurately represent slower processes, especially in small-scale finite populations. To account for the shortcomings of the deterministic Ross Macdonald function, our team implemented the Gillespie algorithm. Gillespie assumes that populations of finite individuals are distributed over a finite number of states, where changes in such states occur via reactions from other states. Implementing the Gillespie in terms of the Ross MacDonald, our team identified the following two states and four reactions occurring: the infected human population I*h*, the infected vector population I*v*, transmission from infected vector to susceptible human *abIv/H(H-Ih)*, transmission from infected human to susceptible vector *acIh/H(V-Iv),* recovery of infected human γI*h*, and mortality rate of vector µI*v*. The following state change matrix represents the stochastic model, where the top row represents the infected human state and the bottom the infected vector state:

A number with black and white numbers

Description automatically generated with medium confidence