

## **Modeling spread of tick-borne disease**

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Ticks have a unique life history including a distinct set of life stages and a single bloodmeal per life stage. This makes tick-host interactions more complex from a mathematical perspective. In addition, any model of these interactions must involve a significant degree of stochasticity on the individual tick level. In an attempt to quantify these relationships, we have developed both a differential equation based population model and an individual-based model of the interactions between ticks and their hosts as well as the transmission of tick-borne disease between the two populations. The results are compared to highlight the insights gained from each approach.