

TRANSMISSION GRAPHS AND NEXT-GENERATION MATRICES FOR COMPLEX TICK-BORNE DISEASE SYSTEMS

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Next-generation matrices are simple models that describe generational growth in infected. While they cannot predict dynamics of infection or prevalence of infection, they enable the calculation of the basic reproduction number (R_0), the type reproduction number (T) and composite elasticities that quantify contributions to R_0 from specific hosts, vectors or transmission routes. They can also be directly compared with differential equation models but have fewer parameters. Existing work on next-generation matrices for tick-borne disease systems consider a single tick vector and a single competent, vertebrate host. We present solutions to the more complex, but more representative problem where multiple tick species (M vector species) and multiple vertebrate hosts (N competent, vertebrate host species) contribute to the spread and maintenance of a tick-borne pathogen. The simplest case we consider is when a generalist tick parasitizes two or more vertebrate hosts competent for the pathogen of concern, i.e. $M=1$, $N>1$, and we provide a solution for when $M>1$ and $N>1$. We illustrate the utility of the proposed matrices by applying the approach to pathogens circulating in small mammals in Kielder Forest, UK and in birds in Southeastern Virginia.