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Analysis of a General Vector Transmission Model for Infectious Disease Spread

As an extension of the framework developed by Earn and McCluskey (PNAS 2025 Vol. 122 No. 49), we consider a very general vector transmission model for the spread of an infectious disease. The human and vector populations each contain a single susceptible class and an arbitrary number of post-infection compartments, allowing for general stage structure (e.g., exposed, infectious, treated or quarantined classes). The main assumptions of the model are as follows: there is no return from infected classes to the susceptible classes in either population; each infected class can be reached from the respective susceptible class; and transmission follows a mass action incidence function with a criss-cross structure, whereby infected vectors infect susceptible humans, and infected humans infect susceptible vectors. For the resulting system of ordinary differential equations, we explicitly determine the disease-free and endemic equilibria and derive a closed-form expression for the basic reproduction number. Using techniques similar to those developed by McCluskey and Earn, we study the global stability of the disease-free equilibrium when $\mathcal{R}_0 \leq 1$ and of the endemic equilibrium when $\mathcal{R}_0 > 1$.