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## **Quantifying the Risk of Malaria from Prevalence Data**

This work proposes a general model for vector-borne infections that is flexible enough to comprise the dynamics of some known diseases transmitted by arthropods. From equilibrium analysis we determined the number of infected vectors as an explicit function of the model's parameters and the prevalence of infection in the hosts. From the analysis it is also possible to derive the Basic Reproduction Number and the equilibrium force of infection as a function of those parameters and variables. From the force of infection we can conclude that, depending on the disease's structure and the model's parameters, it is possible to estimate a risk quantifier for those diseases. The analysis is exemplified by the case of malaria.