141

Integrating spatiotemporal epidemiological models with time-to-event age-period survival models

Models of latent disease transmission processes are crucial for understanding infectious disease dynamics, to develop mitigation strategies, and to understand their impact on populations. Cross-sectional spatially referenced age-specific prevalence data can be used to estimate the force of infection, a prime example of a latent dynamic epidemiological rate that characterizes disease transmission. These data can be modeled using a time-to-event framework, estimating the force of infection on a continuous time scale. However, model estimates are sensitive to disease-associated mortality, the increase in mortality that occurs when animals are infected with a disease regardless of the source of mortality. Thus, survival is another crucial demographic process needed to understand the impact that diseases may have on populations and can also be modeled in a continuous time-to event framework when mortality data are collected. However, methods are lacking for seamlessly connecting these processes within a single modeling framework. To fill this gap, we developed an integrated hierarchical Bayesian model to jointly model cross-sectional prevalence data and known-fate mortality data, connecting continuous time disease and mortality hazard rates to correct force of infection estimates for disease associated mortality. We have developed these models to further understanding of the population impacts of chronic wasting disease, a neuro-degenerative prion disease that effects cervids. We used models to obtain age-period mortality hazard rates for white-tailed deer (Odocoileus virginianus) in south-central Wisconsin, USA using data obtained from GPS collared adult and telemetry collared juveniles from 2017-2021. We estimated the force of infection for this population, corrected for disease associated mortality, from spatially referenced cross-sectional hunter harvest surveillance data from 2002-2021. Our modeling approach provides a novel method for integrating these continuous time processes to further understanding of disease and population dynamics.