Abstract:

The spread dynamics of long-distance-dispersed pathogens are influenced by the dispersal characteristics of a pathogen, anisotropy due to multiple factors, and the presence of multiple sources of inoculum. In this research, we developed a flexible class of phenomenological spatio-temporal models that extend a modeling framework used in plant pathology applications to account for the presence of multiple sources and anisotropy of biological species that can govern disease gradients and spatial spread in time. We use the cucurbit downy mildew pathosystem (caused by Pseudoperonospora cubensis) to formulate a data-driven procedure based on the 2008 to 2010 historical occurrence of the disease in the U.S. available from standardized sentinel plots deployed as part of the Cucurbit Downy Mildew ipmPIPE program. This pathosystem is characterized by annual recolonization and extinction cycles, generating annual disease invasions at the continental scale. This data-driven procedure is amenable to fitting models of disease spread from one or multiple sources of primary inoculum and can be specified to provide estimates of the parameters by regression methods conditional on a function that can accommodate anisotropy in disease occurrence data. Applying this modeling framework to the cucurbit downy mildew data sets, we found a small but consistent reduction in temporal prediction errors by incorporating anisotropy in disease spread. Further, we did not find evidence of an annually occurring, alternative source of P. cubensis in northern latitudes. However, we found a signal indicating an alternative inoculum source on the western edge of the Gulf of Mexico. This modeling framework is tractable for estimating the generalized location and velocity of a disease front from sparsely sampled data with minimal data acquisition costs. These attributes make this framework applicable anduseful for a broad range of ecological data sets where multiple sources of disease may exist and whose subsequent spread is directional.