Estimating sharka dispersal function by stochastic spatiotemporal modelling

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Plant viral diseases, and especially the ones transmitted by aerial vectors, can cause considerable yield losses. A good knowledge of the distances of spread is key to the understanding of disease dynamics. Exploratory approaches aiming at characterizing the spatiotemporal distribution of diseased plants are often used to get an insight into the distances of spread. A more powerful approach is based on stochastic spatiotemporal modelling in order to estimate the dispersal function of the disease (probability density function describing the probability for an infectious plant to infect a healthy plant at distance d). In this study, we implemented a method for estimating the dispersal function of the sharka disease.

Sharka is one of the most serious diseases of stone fruit trees (*Prunus* sp.). It is caused by *Plum pox virus* (PPV, genus *Potyvirus*), transmitted by at least twenty different aphid species in a non persistent manner. Due to the inefficiency of insecticides and the very rare sources of resistance against the virus available in the host species, prophylactic disease control is based on the removal of the diseased trees in the orchards. Thus, a very good knowledge of the dispersal function of sharka is crucial for building epidemiological models and optimizing the strategies of surveillance and control.

We adapted the methodology published by Gibson (1997) based on a Markov chain Monte Carlo (MCMC) algorithm in order to estimate sharka dispersal function from the maps of 157 contiguous peach orchards reporting the exact location and the sanitary status (asymptomatic/symptomatic) of each of the trees during six consecutive years. An estimation method based on the Gibbs sampling algorithm was developed taking into account the specificities of the dataset (more than two dates of observation, annual removal of diseased trees). This estimation algorithm was validated on simulated data and was proved to be more powerful and better adapted to large datasets than the one proposed by Gibson. Moreover, the influence of latency on the estimation of the dispersal function was quantified. This methodology was then used to estimate the dispersal function of the disease from a subset of the real dataset.

The methods developed in this study are generic enough to be used and adapted for the estimation of dispersal functions of any disease transmitted in a non persistent manner, and even for diseases with similar characteristics.

References

Gibson G. J. (1997). Markov chain Monte Carlo methods for fitting spatiotemporal stochastic models in plant epidemiology. Journal of the Royal Statistical Society: Series C (Applied Statistics), 46(2): 215–233.

Keywords: dispersal function, epidemiology, Gibbs sampling, sharka.