10.7 Estimating the spatial distribution of Huanglongbing from a sample

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The ability to accurately estimate the spatial distribution of plant disease is crucial for effective disease management. Resource constraints mean sampling cannot be done at every host location and so estimates must be made about disease incidence at unsampled locations. A key focus in plant pathology has been in the development of methods to estimate the mean incidence of disease in a given host population. Although much progress has been made in this area, these approaches provide no spatial information on disease incidence. Information on the spatial distribution of plant disease is essential in understanding disease epidemiology and facilitates the implementation of disease control policies. In plant pathology common solutions to this disease mapping problem have been taken from the field of geostatistics. Interpolation techniques (e.g. kriging) are employed to generate continuous statistical models from disease observations at point samples. However, these approaches do not incorporate the epidemiological processes and host heterogeneities which shape disease distribution. We use an iterative optimization approach which utilizes information on the underlying host distribution and on the spatial complexities in pathogen dispersal and infection to accurately map the probability of disease at unsampled host locations. The approach is pathogen generic but is especially relevant for diseases such as HLB which exhibit strong spatial dependencies. An example using observed data of HLB incidence in citrus plantations in Florida is presented.