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A new method for spatial analysis of irregularly spaced HLB data and biological implications

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Field data on intensity of plant diseases is very often irregularly spaced (i.e., there are varying amounts of distance between rows, ponds, voids, roads, houses, or other land areas). Typically, this type of data is gridded and the average disease intensity of the plants within the grid is used instead of the original data on each separate plant. This is done because the underlying statistical assumptions in the analysis of spatial data usually require that data be equally spaced. However, a new method of analysis, sometimes called second-generation wavelet analysis, can be used on irregularly spaced spatial data. Wavelet analysis is a method used to analyze variations in scale and position of non-stationary spatial signals (non-stationary for our data means the statistical properties can vary based on location within the orchard), and the second-generation refers to an iterative process, called a lifting scheme (1), which allows for the irregular spacing. Irregular spacing is often found in citrus groves as spacing within and between rows is often not uniform, and on a larger spatial scale, distance between blocks and plantings are not necessarily simple multiples of distances between rows and trees. In addition, there are a number of other issues such as missing trees, the presence of irregular roads, ponds, staging areas, etc., that cause citrus groves to have irregular distances between trees when viewed at the plantation or regional scale. Therefore, to test this new method, we conducted a second-generation spatial wavelet analysis on a large irregularly spaced citrus planting (Southern Gardens) in Florida where over 260,000 trees were assessed for incidence of huanglongbing (HLB) over five sampling times.

The primary result from this analysis is a wavelet coefficient for each diseased tree in the original data. This coefficient essentially represents the difference between the observed density of disease around the tree and the density predicted from neighboring diseased trees and their respective densities. The neighboring trees can simply be the nearest neighbors, or the analysis can take multiple clusters of neighbors into account. The coefficients are very useful for multiple subsequent analyses, and one of which is to identify the clustering pattern of HLB infected areas over several spatial scales. For this data, the scales ranged from 17.7 square meters (i.e., the trees at this spatial scale were completely surrounded by diseased trees on all sides) to 1,712,195 square meters. Two example maps in the figure below indicate where clustering is located within the grove at some of the A) smallest scales and B) largest scales. Interpretation of the wavelet coefficients will be presented. Results for this analysis are superior to some traditional analyses for clustering that only explore a few spatial scales. The spatial scales at which clustering is identified has often been used in plant pathology as a basis for not only theoretical understanding of epidemics, but also in identifying the most appropriate sampling methods for disease control and the scale at which management practices should be applied. For large land areas like citrus groves with highly irregular spacing and widespread diseases such as HLB, these types of applications using previous methods of analysis may lead to some incorrect interpretations.

1. Sweldens, W. 1998. The Lifting Scheme: A Construction of Second Generation Wavelets. SIAM J. Math. Anal. 29:511-546.

