Mathematical Analysis Of Dynamic Spread Of Pine Wilt Disease

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Abstract

Since its detection in Portugal in 1999, Bursaphelenchus xylophilus, the pinewood nematode (PWN), a causal agent of Pine Wilt Disease, represents a threat to European forestry. Significant amount of money has been spent on its monitoring and eradication.

This paper presents mathematical analysis of spread of PWN using a set of partial differential equations (PDE) with space (longitude and latitude) and time as parameters of estimated number of PWNs and consequently susceptible and infected trees. Previous work in this area used time only and studied the stability of system equilibrium under disease-free and disease-existing situations.

The set of PDEs depends on a number of parameters such as: PWN biological parameters (life cycle and number of juveniles per female PWN), parameters of PWN vector Monochamus galloprovincialis (speed and portion of PWNs transmitted by vectors), and parameters defined by humans (rate of removal of susceptible and infected trees as a defense measure).

The set of PDEs has two sets of initial boundary conditions used to calculate spread of disease in the future. The first set is initial placement of pine trees (geographical location and density) as well as areas without pine trees (e.g., lakes or fields). The second set is the location of infected area(s). This can be either an assumed high-risk entry point of disease (e.g., trading place or port) in case of preparation for eventual future outbreak or it can be actual observed disease in case of an existing outbreak.

Since the set of PDEs including initial boundary conditions cannot be solved as a closed form, it has to be discretized in space and time and solved numerically. Given life cycle of PWN and speed of vectors, calculation in steps of one day is sufficiently precise. Similarly, given usual density of pine trees (3,000 per hectare), square cells 5-10 meters wide containing 7-30 trees is sufficiently exact.

The discretized set of PDEs is solved as a set of consecutively calculated matrices. Each matrix represents one moment in discretized time spread one day apart while each matrix element represents one discretized cell of land. Each cell is characterized by the estimated number of PWNs, susceptible and infected trees as well as the number of cumulatively removed trees.

This methodology may be used in multiple ways. It can be used to evaluate risk of various assumed entry points of disease and make defense plans in advance. In case of an already existing outbreak, it can be used to draw optimal line of defense and plan removal of trees. Optimization constraints are economic loss of removal of susceptible trees as well as budgetary constraints of workforce cost. Practical usefulness of this methodology can be improved and automated if it can be connected with a database containing geographic information on forests. Then great monetary savings can be achieved while making accurate and optimal defense plans.

Keywords: Pinewood nematode, differential equations, mathematical analysis