

Modeling Risk for SOD Nationwide: What are the Effects of Model Choice on Risk Prediction?

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Abstract

Phytophthora ramorum has the potential to infect many forest types found throughout the United States. Efforts to model the potential habitat for *P. ramorum* and Sudden Oak Death (SOD) are important for disease regulation and management. Yet, spatial models using identical data can have differing results. In this paper we examine the results from five types of models generated from common input parameters, and investigate model agreement for distribution of risk for *P. ramorum*. We examine five models: (1) Rule-based, (2) Logistic regression, (3) Classification and Regression Trees, (4) Genetic Algorithm modeling, and (5) Support Vector Machines. The models differed in terms of parametric and non-parametric requirements, necessity for presence/absence data, and whether or not the explanatory variables were determined *a priori* or revealed during the model process. Nationwide input data included vegetation/host (hardwood diversity and hardwood density), topography, and climate (e.g. precipitation, frost days, temperature, and many other layers). We developed a risk map for the conterminous United States in which probabilities for SOD disease establishment were based not on one model, but on agreement between multiple models. The five models were consistent in their prediction of some SOD risk in coastal CA, OR and WA. All models predicted some risk in the northern foothills of the Sierra Nevada mountains in CA. Outside of the west coast, the combined models predicted highest risk for SOD in a east-west oriented band including eastern OK, central AR, TN, KY, northern MI, AL, GA and SC, parts of central NC, and eastern VA, DL and MD. The paper also discusses issues of input data accuracy, coverage, availability of nationwide host datasets, data scale, and model computational requirements. Although theoretical in nature, the results of this paper have practical, and applied value for managers and regulators of this disease.

Key words: spatial modeling, sudden oak death, geographic information systems

Introduction

Phytophthora ramorum has the potential to infect many forest types found throughout the United States. Efforts to model the potential habitat for *P. ramorum* and Sudden Oak Death (SOD) are important for disease regulation and management. For example, in California, researchers used an expert-knowledge driven Rule-based model to predict risk of SOD based on host, temperature and moisture data (Meentemeyer et al. 2004) which has been used to guide sampling, aerial surveys, and other statewide monitoring efforts. Rule-based models such as this one use expert input rather than statistical inference, and thus the predictor ecological variables used are known *a priori*. Other spatially referenced ecological niche models require presence data to train the model, possibly revealing ecological niches. The variety of techniques used for ecological niche

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modeling is growing (Guisan and Zimmermann 2000), and there has been a corresponding increase in the spatial modeling literature in work that compares results from different models (Guisan and Zimmermann 2000; Manel et al. 1999; Muñoz and Felicísimo 2004). These efforts show that spatially referenced models using identical data often have differing results, due in part to 1) the fact that models can be either parametric or non-parametric with varying reliance on variable distribution, 2) user-defined weightings placed on variables can differ by analyst, and 3) the different methods used for generating absence data for input to models can influence results, among other factors. In this research, we examined a collection of model types and produced a risk map for SOD nationwide based on agreement between these models. We examined five classes of models that differed in terms of parametric and non-parametric requirements, necessity for presence / absence data, and whether or not the explanatory variables were determined *a priori* or revealed during the model process. Our spatial models include the following: (1) Rule-based, (2) Logistic regression (LR), (3) Classification and Regression Trees (CART), (4) Genetic Algorithm (GA) modeling, and (5) Support Vector Machines (SVM).

Model Descriptions

Rule-based spatial models use research data and expert input, rather than statistical inference to determine the importance of predictor variables (Meentemeyer et al. 2004). Predictor variables are given weights based on importance, and all weighted variables are summed in a geographical information system (GIS) overlay procedure to produce a mapped output. This method is straightforward and not computationally intensive. Logistic regression is a variation of ordinary regression which is used when the dependent (response) variable is a binary variable which usually represent the occurrence or non-occurrence of some outcome event, usually coded as 0 or 1, and the independent (input) variables are continuous, categorical, or both. Resulting probabilities can be mapped over space for an easily understood cartographic representation of modeled distribution. LR is a powerful parametric yet computationally non-intensive method for ecological niche modeling (Felicísimo et al. 2002; Kelly et al. 2001; Mladenoff et al. 1995). Classification trees are a non-parametric alternative to techniques such as logistic regression (De'ath and Fabricius, 2000) and Linear Discriminant Analysis (LDA) (Feldesman, 2002). The tree models are developed by recursively partitioning the response variable into increasingly homogeneous binary subsets based on critical thresholds in predictor variables. The split chosen is the one that most reduces the average impurity in the resulting bins (Breiman et al. 1984; De'ath and Fabricius 2000; Venables and Ripley 2002). The resulting “trees” are often displayed graphically, and are easy to understand as a series of if/then conditions, but they can be complex to render cartographically (Kelly and Meentemeyer 2002; Muñoz and Felicísimo 2004). Genetic Algorithm modeling is an evolutionary computing system that has excellent capabilities for delineating ecological niches and geographical distributions of species (Raxworthy et al. 2003; Stockwell 1999). The method uses genetic algorithms to predict the potential distribution of a species by generating a set of rules. Essentially, genetic algorithms apply the operational concepts similar to evolutionary biology such as mutation and crossover to evolve the solutions in order to find the best solutions. GA modeling is less susceptible to local maxima and able to handle various data formats (continuous and discrete). Finally, Support Vector Machines are a new generation of learning algorithms that can perform binary classification (pattern recognition) and real valued function approximation (regression estimation) tasks. SVM have been developed on a solid base of statistical learning theory and are designed especially to provide high flexibility for approximating class boundaries, while avoiding over-fitting phenomena. Functionally, SVM seek to find an optimal separating hyperplane with the maximal margin between the training points for presence and absence data in multidimensional space (Cristianini and Scholkopf 2002; Huang et al. 2002). SVM are able to handle non-linear and categorical data, and make no assumption on the probability density of the data, are competitive with the best available machine learning algorithms in classifying high-dimensional data sets. (Guo et al. 2005).

Model characteristics for these five models are summarized in Table 1.

Table 1—Characteristics of the five classes of models used.

Model Name	Presence/absence data required?	Parametric/Non-parametric	Important Variable selection	Output	Computational requirements
Rule-based	No	Non-parametric	<i>a priori</i>	Ranked	Low
Logistic Regression	Yes	(semi-) Parametric	Through training	Probability	Low
CART ¹	Yes	Non-parametric	Through training	P/A based on # runs	Low
GA ²	Yes	Both, depending on input models	Through training	P/A based on # runs	High
SVM ³	No (1-class) Yes (2-class)	Non-parametric	Through training	P/A based on # runs	High

¹ Classification and Regression Tree; ² Genetic Algorithm; ³ Support Vector Machines.

Methods

Predictor Ecological Variables

We developed five spatial models using common nationwide data. Physical variables included topography and climate; we used Digital Elevation Model (DEM) and DAYMET weather and climatologically modeled raster surfaces gridded at 1 km to summarize physical conditions for the pathogen. Daymet is an assortment of climate raster surfaces interpolated from ground-based meteorological stations on a daily basis over an 18 year period (1980 to 1997) (Thornton et al. 1997). The primary climate surfaces utilized in this modeling project included total annual precipitation, total annual frost days, average minimum temperature, average maximum temperature and average maximum august temperature. Topography was derived from United States Geological Survey National Elevation Dataset (U.S.G.S. 1999b).

Host/Vegetation Data

We had a considerable challenge finding a detailed vegetation map for the conterminous US with sufficient floristic and spatial detail to allow modeling. We explored the utility of several datasets. The first among these was the National Land Cover Data 1992 dataset, a 21-category classification derived primarily from Landsat Thematic Mapper (TM) imagery from 1992, containing categories for several different forest types including deciduous, conifer and mixed (Vogelmann et al. 1998; Vogelmann et al. 2001). The NLCD classification supplies high spatial resolution (30-m) but poor floristic detail, providing only three general vegetation categories relevant to our project: deciduous forest, evergreen forest, and mixed forest. Using this information, we created a 1-km gridded vegetation dataset depicting “hardwood density” based on the percent of deciduous and mixed forest found within each 1-km cell. The second dataset we investigated was the digital tree range maps for North America created by the USGS for a vegetation climate modeling study (U.S.G.S. 1999a), which provided more floristic detail, but was coarse in spatial detail. This product was based upon a series of tree range maps assembled by Elbert L. Little, Jr. in the 1970s as the “Atlas of the United States Trees” (Little 1971; Little 1976; Little 1977; U.S.G.S. 1999a). Of the 58 digital oak species maps created by USGS, we determined that 34 were potentially susceptible to SOD. These 34 oak species maps were then combined with digital maps of 12 other tree range maps of species found to either be directly susceptible to the pathogen or to be related (i.e., in the same taxonomic genus as a susceptible species). The 46 tree range

maps were then combined to form a “hardwood diversity index” map. It should be emphasized that the hardwood diversity index as calculated for this study was limited to a portion of the tree range maps made available by the USGS and contains only a minimal number of shrub or understory species. It is only intended to represent areas within the U.S. that potentially contain high numbers of susceptible SOD host species (both foliar and terminal hosts) with the recognition that there are many more species not included. The final vegetation layer examined was provided by the USFS Northeastern Research Station (Gottschalk et al. 2002). In this product, Forest Inventory and Analysis (FIA) plot data were used to calculate the percentage of forest basal area composed of the red and live oak groups and these points were kriged to create a continuous raster surface for the eastern United States. Percent basal area estimates were adjusted for forest density using the NLCD dataset.

Model Creation

We first developed our nationwide rule-based model using similar input data to those used in the California model. Climate variables for 6 winter months were parameterized and placed into weighted classes in accordance with the methods of Meentemeyer et al. (2002). Two different coarse-resolution vegetation maps (hardwood diversity and hardwood density) were used as a surrogate for the detailed vegetation map used in the California modeling case. The remaining models (with the exception of GA) required that presence and absence data be generated for model training. For presence data we used the database of locations ($n = 169$) of confirmed SOD existing in 12 counties in California and one in Oregon provided through the University of California, Berkeley (Kelly et al. 2004). Absence data (or in this case ‘pseudo-absence’ data, as we do not have samples of *P. ramorum* absence) were generated in the following manner. We created a zone of infestation within California consisting of the 12 infested counties, and six border counties. We then constrained the algorithms to search for and generate pseudo-absence data from locations in California outside this zone.

We began with CART modeling. Using Splus v. 6.2 © for Windows ©, we generated 100 classification trees using 100 unique pseudo-absence point distributions and the 169 SOD presence points. Each “tree” was pruned by examining a plot of deviance and tree complexity (Feldesman 2002), and the resulting tree models were implemented in ArcInfo © using Arc Macro Language (AMLs). We then developed LR equations using Splus v. 6.2 © for Windows © and implemented the results in ArcInfo. Desktop GARP (Genetic Algorithm for Rule-set Production) (Stockwell and Peters 1999) software was used for the application of the GA model. 100 model runs were performed using presence data only. Finally, we developed SVM models using Matlab © and LIBSVM software (Chuang and Lin 2001). Cross-validation was used for each of the 100 runs to optimize parameter selection. It became clear early on that the vegetation information would not be useful in the initial modeling exercises, as detailed vegetation maps are not available for every state. The initial model inputs (with the exception of the Rule-based model) were limited to climate variables.

The different predicted SOD Risk map results of the models examined in this project displayed significant levels of variation depending on the model in question and the input climate variables used. Therefore, a combination of several different model input formulas were used to create a cumulative and weighted map result. The four predictive models (excluding Rule-based) were run 100 times each with the following three collections of input predictor variables: 1) precipitation total and frost days, 2) precipitation total, frost days and average maximum temperature, and 3) precipitation total, average minimum temperature and average maximum temperature. Model results were added together along with proportional values from the Rule-based models to create a finalized SOD Risk grid. Finally, in an effort to eliminate areas of non-hardwood forest in the final risk map, we filtered the combined model results through the NLCD and red oak basal area vegetation maps

by multiplying the map by each vegetation map rescaled from 0 to 1. We did not include the USGS vegetation map in this exercise as the spatial fidelity of the product seemed problematic. The representation of hardwood diversity in the southeast US may not be accurate due to the relatively small number of tree ranges used.

All model results were normalized for visual display purposes using the following technique: the mean value was calculated and then arbitrary boundaries were set for plus or minus two standard deviations. Any values above or below were reclassified to the minimum or maximum of the 95th percentile. This grid was then rescaled from 0 to 100, and classed into five classes of risk: 0-20% low, 20-40%, 40-70% medium, 70-90%, and 90-100%. The exception to this approach was the Rule-based model, which was scaled and displayed according to Meentemeyer et al. (2004).

Results

The results from each of five models are shown in Figure 1. The rule-based model shows a high risk for SOD spread across the southeast from eastern TX to VA, with declining risk to the north. The model also shows high risk in the northwest and risk in the northern foothills of the Sierra Nevada mountains in CA. While this model is a replica of that provided by the Meentemeyer et al. (2004) model, this is a different result and likely due to qualitative differences in input data and spatial resolution. The LR results show a broadly similar pattern to the Rule-based model, with less risk on the west coast and less overall risk in the southeast: the model constrains the highest risk to the deep southern states of LA, AL, and MS. The LR formula determined that precipitation total, average minimum temperature and average maximum temperature were important in risk prediction. CART and GA results are similar, with a band of highest risk occurring throughout the middle southeast from OK in the west to VA and NC in the east. This is likely due to the importance both models placed on latitudinally controlled temperature variables. Both models found precipitation total, frost days and average maximum temperature to be the most important predictors. The SVM result is coarser than the others; the algorithm required resampling of the input data to a coarser spatial resolution (~12-km) due to computational limitations. The SVM algorithm predicted risk as a result of precipitation total, frost days and average maximum temperature.

The final risk map – a combination of the results from five models – is shown in Figure 2. The five models were consistent in their prediction of some SOD risk in coastal CA, OR and WA, although LR and GA show less risk than do the other models. All models predicted some risk in the northern foothills of the Sierra Nevada mountains in CA. Outside of the west coast, the combined models predicted highest risk for SOD in a east-west oriented band including hardwood forested areas of OK, AR, TN, KY, northern portions of MI, AL, GA and SC, parts of central NC, eastern VA, DL and MD. This area includes portions of several ecoregions, including the Piedmont ecoregion of NC, SC, GA, AL and MI, a transitional area between the mostly mountainous ecoregions of the Appalachians to the northwest and the relatively flat coastal plain to the southeast. Much of this region has reverted to successional pine and hardwood woodlands, with an increasing conversion to an urban and suburban land cover (ECOMAP 1993; Omernik 1987; Omernik 1995). There is also predicted risk for SOD in hardwood forests of the Southwestern Appalachians in TN and in the primarily oak-hickory forests of the Interior Plateau in KY and TN. Eastern OK and central AR shows high risk in the oak-hickory-pine forests of the Ouachita Mountains, and in the red oak, white oak, and hickory dominated forests of the Boston Mountains, and in the predominantly oak forests of the Southern Ozarks (ECOMAP 1993; Omernik 1987; Omernik 1995). Coastal MD and DL, part of the Middle Atlantic Coastal Plain, are climactically susceptible and have forests at risk in riparian areas.

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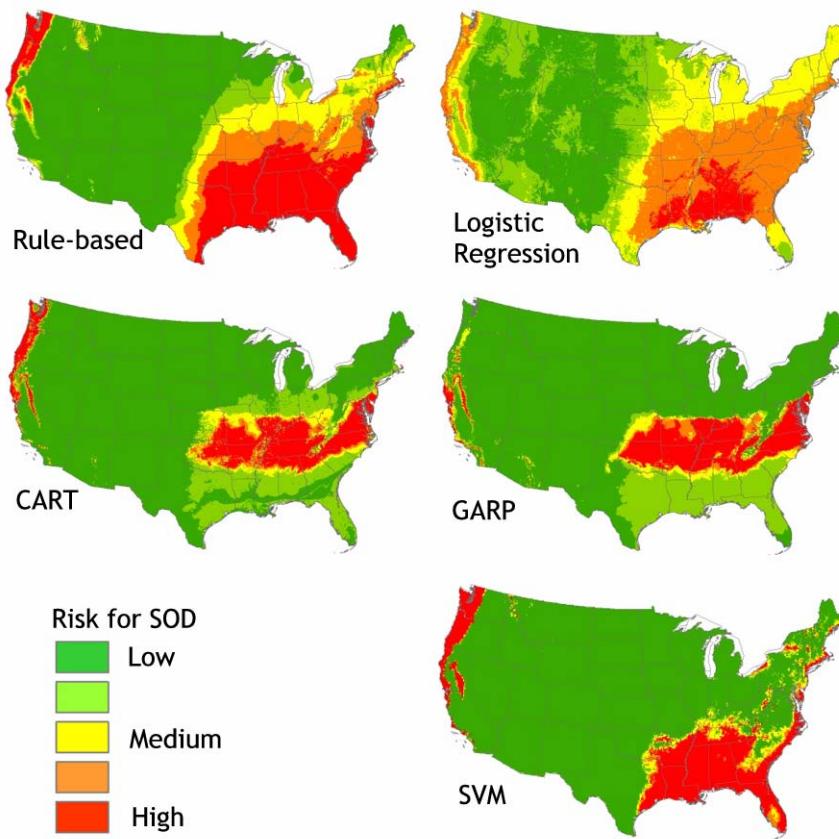


Figure 1—Risk for Sudden Oak Death in the conterminous United States: results from five spatially referenced models.

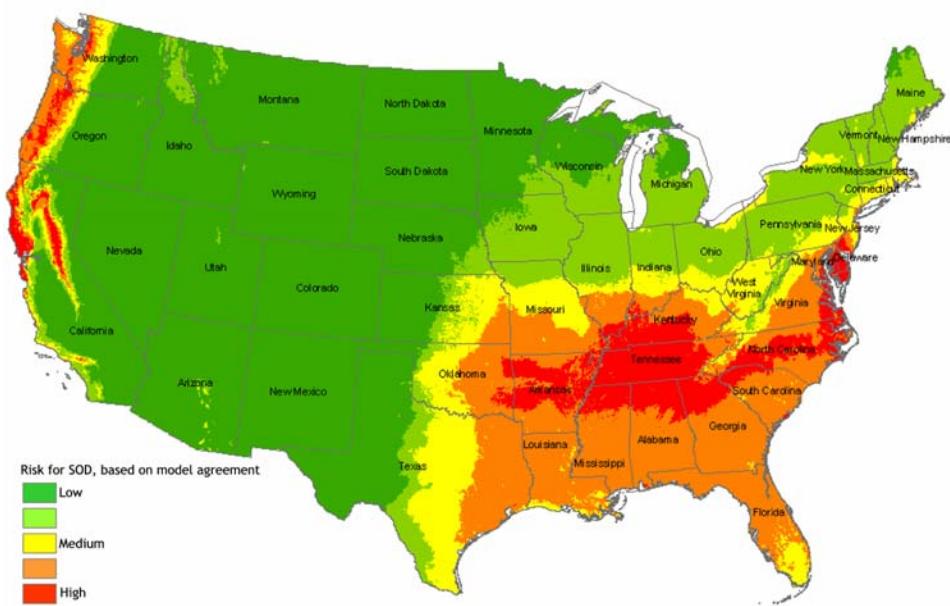


Figure 2—Risk for Sudden Oak Death in the conterminous United States based on agreement between five spatially referenced models.

Discussion and Conclusions

Because there are no wildland cases of SOD outside of California and Oregon, none of these models can be assessed for accuracy. This is an unfortunate but not uncommon situation when modeling invasive species (Muñoz and Felicísimo 2004). Several of the models allow for some form of cross-fold validation tools for assessing accuracy, but these tools can be problematic due to the small number of training samples and their concentrated distribution (Graham et al. 2004). The generation of pseudo-absence data must also be examined. We do not have reliable negatives for *P. ramorum*, so we used a common method for generation of pseudo absence data, constraining the pool of possible absence points to be taken from outside the zone of infestation in California. Experiments with pseudo-absence data generated within the zone of infestation resulted in models that over-predicted the risk of the disease. One-class SVM are able to model species distributions without absence data (Guo et al. 2005), and this method might be of use in this case. We only examined two-class SVMs in this paper, for consistency. Finally, the host data available for the entire United States was the largest limiting factor in our modeling exercise; all nationwide vegetation layers we used had significant drawbacks. For example, the NLCD data was the most spatially comprehensive layer, with compete coverage at a high spatial resolution; however, specific floristic detail was absent, and the vegetation classes were much too broad to be of use in the modeling exercise. The USGS layer had sufficient floristic detail, but was tremendously course in resolution. Finally, the FIA product only covered the east coast area, and thus could not be used in the models that required training. A similar west coast product is not available. Computationally, the Rule-based, Logistic regression and CART were the least computationally demanding of the algorithms. GARP and SVM require more CPU time. This work examined common ecological niches for *P. ramorum*, but an investigation of the human component to disease establishment and spread should also be considered. The locations of nurseries might be an additional important component to this research. Attempts at finding similar climate datasets for European locations of *P. ramorum* was not successful prior to completion of this paper but should be considered. Although theoretical in nature, the results of this paper have practical, applied value for managers and regulators of this disease.

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