

## RANDOM FORESTS FOR CLASSIFICATION IN ECOLOGY

D. RICHARD CUTLER,<sup>1,7</sup> THOMAS C. EDWARDS, JR.,<sup>2</sup> KAREN H. BEARD,<sup>3</sup> ADELE CUTLER,<sup>4</sup> KYLE T. HESS,<sup>4</sup>  
JACOB GIBSON,<sup>5</sup> AND JOSHUA J. LAWLER<sup>6</sup>

<sup>1</sup>Department of Mathematics and Statistics, Utah State University, Logan, Utah 84322-3900 USA

<sup>2</sup>U.S. Geological Survey, Utah Cooperative Fish and Wildlife Research Unit, Utah State University, Logan, Utah 84322-5290 USA

<sup>3</sup>Department of Wildland Resources and Ecology Center, Utah State University, Logan, Utah 84322-5230 USA

<sup>4</sup>Department of Mathematics and Statistics, Utah State University, Logan, Utah 84322-3900 USA

<sup>5</sup>Department of Wildland Resources, Utah State University, Logan, Utah 84322-5230 USA

<sup>6</sup>College of Forest Resources, University of Washington, Seattle, Washington 98195-2100 USA

**Abstract.** Classification procedures are some of the most widely used statistical methods in ecology. Random forests (RF) is a new and powerful statistical classifier that is well established in other disciplines but is relatively unknown in ecology. Advantages of RF compared to other statistical classifiers include (1) very high classification accuracy; (2) a novel method of determining variable importance; (3) ability to model complex interactions among predictor variables; (4) flexibility to perform several types of statistical data analysis, including regression, classification, survival analysis, and unsupervised learning; and (5) an algorithm for imputing missing values. We compared the accuracies of RF and four other commonly used statistical classifiers using data on invasive plant species presence in Lava Beds National Monument, California, USA, rare lichen species presence in the Pacific Northwest, USA, and nest sites for cavity nesting birds in the Uinta Mountains, Utah, USA. We observed high classification accuracy in all applications as measured by cross-validation and, in the case of the lichen data, by independent test data, when comparing RF to other common classification methods. We also observed that the variables that RF identified as most important for classifying invasive plant species coincided with expectations based on the literature.

**Key words:** additive logistic regression; classification trees; LDA; logistic regression; machine learning; partial dependence plots; random forests; species distribution models.

### INTRODUCTION

Ecological data are often high dimensional with nonlinear and complex interactions among variables, and with many missing values among measured variables. Traditional statistical methods can be challenged to provide meaningful analyses of such data. In particular, linear statistical methods, such as generalized linear models (GLMs), may be inadequate to uncover patterns and relationships revealed by more sophisticated procedures (De'ath and Fabricius 2000). Classification procedures are among the most widely used statistical methods in ecology, with applications including vegetation mapping by remote sensing (Steele 2000) and species distribution modeling (Guisan and Thuiller 2005). In recent years, classification trees (Breiman et al. 1984) have been widely used by ecologists because of their simple interpretation, high classification accuracy, and ability to characterize complex interactions among variables.

A number of highly computational statistical methods, which have potential for ecological data mining, have recently emerged from the machine-learning

literature. Random forests (hereafter RF) is one such method (Breiman 2001). RF is already widely used in bioinformatics (e.g., Cutler and Stevens 2006), but has not yet been utilized extensively by ecologists. In the few ecological applications of RF that we are aware of (see, e.g., Lawler et al. 2006 and Prasad et al. 2006), for both classification and regression RF is competitive with the best available methods and superior to most methods in common use. As the name suggests, RF combines many classification trees to produce more accurate classifications. By-products of the RF calculations include measures of variable importance and measures of similarity of data points that may be used for clustering, multidimensional scaling, graphical representation, and missing value imputation.

Potential applications of RF to ecology include (1) regression (Prasad et al. 2006); (2) survival analysis; (3) missing value imputation; (4) clustering, multidimensional scaling, and detecting general multivariate structure through unsupervised learning; and (5) classification. Descriptions of capabilities 1–4 are given in Appendix A; this article is concerned with RF as a classifier, with particular application to species distribution modeling. We highlight some features and strengths of RF compared to other commonly used classification methods.

Manuscript received 30 March 2007; revised 1 June 2007; accepted 4 June 2007. Corresponding Editor: A. M. Ellison.

<sup>7</sup> E-mail: Richard.Cutler@usu.edu

## THE RANDOM FORESTS ALGORITHM

*Classification trees*

In the standard classification situation, we have observations in two or more known classes and want to develop rules for assigning current and new observations into the classes using numerical and/or categorical predictor variables. Logistic regression and linear discriminant analysis (LDA) accomplish this by determining linear combinations of the predictor variables to classify the observations. Classification trees build the rule by recursive binary partitioning into regions that are increasingly homogeneous with respect to the class variable. The homogeneous regions are called nodes. At each step in fitting a classification tree, an optimization is carried out to select a node, a predictor variable, and a cut-off or group of codes (for numeric and categorical variables respectively) that result in the most homogeneous subgroups for the data, as measured by the Gini index (Breiman et al. 1984). The splitting process continues until further subdivision no longer reduces the Gini index. Such a classification tree is said to be fully grown, and the final regions are called terminal nodes. The lower branches of a fully grown classification tree model sampling error, so algorithms for pruning the lower branches on the basis of cross-validation error have been developed (Breiman et al. 2004). A typical pruned classification tree has three to 12 terminal nodes. Interpretation of classification trees increases in complexity as the number of terminal nodes increases.

*Random forests*

RF fits many classification trees to a data set, and then combines the predictions from all the trees. The algorithm begins with the selection of many (e.g., 500) bootstrap samples from the data. In a typical bootstrap sample, approximately 63% of the original observations occur at least once. Observations in the original data set that do not occur in a bootstrap sample are called out-of-bag observations. A classification tree is fit to each bootstrap sample, but at each node, only a small number of randomly selected variables (e.g., the square root of the number of variables) are available for the binary partitioning. The trees are fully grown and each is used to predict the out-of-bag observations. The predicted class of an observation is calculated by majority vote of the out-of-bag predictions for that observation, with ties split randomly.

Accuracies and error rates are computed for each observation using the out-of-bag predictions, and then averaged over all observations. Because the out-of-bag observations were not used in the fitting of the trees, the out-of-bag estimates are essentially cross-validated accuracy estimates. Probabilities of membership in the different classes are estimated by the proportions of out-of-bag predictions in each class.

Most statistical procedures for regression and classification measure variable importance indirectly by

selecting variables using criteria such as statistical significance and Akaike's Information Criterion. The approach taken in RF is completely different. For each tree in the forest, there is a misclassification rate for the out-of-bag observations. To assess the importance of a specific predictor variable, the values of the variable are randomly permuted for the out-of-bag observations, and then the modified out-of-bag data are passed down the tree to get new predictions. The difference between the misclassification rate for the modified and original out-of-bag data, divided by the standard error, is a measure of the importance of the variable. Additional technical details concerning the RF algorithm may be found in Appendix A.

APPLICATION OF RANDOM FORESTS  
TO ECOLOGICAL QUESTIONS

We provide examples of RF for classification for three groups of organisms commonly modeled in ecological studies: vascular plants (four invasive species), non-vascular plants (four lichen species), and vertebrates (three species of cavity-nesting birds). These examples cover a broad range of data characteristics encountered in ecology, including high to low sample sizes, and underlying probabilistic and non-probabilistic sample designs. The lichen data set also includes independent validation data, thereby providing opportunity to evaluate generalization capabilities of RF.

In all the examples that follow, we compare RF to four other classifiers commonly used in ecological studies: LDA, logistic regression, additive logistic regression (Hastie et al. 2001), and classification trees. The accuracy measures used were the overall percentage correctly classified (PCC), sensitivity (the percentage of presences correctly classified), specificity (the percentage of absences correctly classified), kappa (a measure of agreement between predicted presences and absences with actual presences and absences corrected for agreement that might be due to chance alone), and the area under the receiver operating characteristic curve (AUC). Resubstitution and 10-fold cross-validated estimates of these five accuracy measures were computed for all examples and methods. Except for the analyses pertaining to variable importance, no variable selection or "tuning" of the various classification procedures was carried out. To assess variable importance for LDA, backward elimination was carried out and the variables retained in the model ranked by *P* value. For logistic regression, backward elimination was carried out using the AIC criterion, and as with LDA, the retained variables ranked by *P* value. The variables split on in the highest nodes in classification trees were deemed to be most important for that procedure. Lists of the software used in our analyses and of available software sources for RF may be found in Appendix A.

We used predictors typically found in ecological classification applications, such as topographic variables, ancillary data (e.g., roads, trails, and habitat

TABLE 1. Accuracy measures for predictions of presence for four invasive plant species in Lava Beds National Monument, California, USA ( $N = 8251$  total observations).

Accuracy metric	Classification method							
	Random forests		Classification trees		Logistic regression		LDA	
	Resub	Xval	Resub	Xval	Resub	Xval	Resub	Xval
<i>Verbascum thapsus</i> (common mullein; $n = 6047$ sites)								
PCC	95.3	<b>92.6</b>	84.2	83.2	80.6	80.0	79.4	79.2
Specificity	89.5	<b>84.5</b>	53.1	51.4	48.0	46.3	49.7	48.6
Sensitivity	97.4	<b>95.5</b>	95.5	94.7	92.5	92.3	90.2	90.3
Kappa	0.878	<b>0.809</b>	0.546	0.518	0.449	0.430	0.431	0.422
AUC	0.984	<b>0.940</b>	0.789	0.797	0.825	0.825	0.838	0.821
<i>Urtica dioica</i> (nettle; $n = 1081$ sites)								
PCC	93.9	<b>92.9</b>	91.3	90.5	88.8	88.6	87.1	87.1
Specificity	96.9	96.2	98.1	97.2	98.1	<b>97.9</b>	94.2	94.3
Sensitivity	74.6	<b>70.4</b>	45.9	45.6	27.1	26.7	40.0	39.0
Kappa	0.729	<b>0.680</b>	0.534	0.506	0.336	0.331	0.378	0.360
AUC	0.972	<b>0.945</b>	0.863	0.849	0.872	0.856	0.861	0.847
<i>Cirsium vulgare</i> (bull thistle; $n = 422$ sites)								
PCC	96.8	<b>96.5</b>	96.6	96.1	95.1	95.0	94.4	94.4
Specificity	98.8	98.7	99.6	<b>99.4</b>	99.4	<b>99.4</b>	98.0	98.1
Sensitivity	60.2	<b>56.4</b>	41.7	36.5	13.0	13.0	26.5	25.8
Kappa	0.643	<b>0.607</b>	0.540	0.474	0.209	0.195	0.297	0.296
AUC	0.938	<b>0.914</b>	0.772	0.744	0.810	0.784	0.789	0.762
<i>Marrubium vulgare</i> (white horehound; $n = 137$ sites)								
PCC	99.2	<b>99.1</b>	99.2	98.9	99.2	98.9	97.3	97.2
Specificity	99.8	<b>99.7</b>	99.9	<b>99.7</b>	99.9	<b>99.7</b>	97.7	97.7
Sensitivity	67.2	60.6	59.8	52.6	59.9	53.3	72.9	<b>67.9</b>
Kappa	0.738	<b>0.678</b>	0.716	0.621	0.706	0.627	0.463	0.434
AUC	0.988	<b>0.949</b>	0.873	0.867	0.972	0.944	0.918	0.906

Notes: LDA denotes linear discriminant analysis, PCC the percentage correctly classified, and AUC the area under the ROC curve. Resub is resubstitution accuracy estimate and Xval is the 10-fold cross-validated accuracy estimate. Sensitivity is the percentage of presences correctly classified. Specificity is the percentage of absences correctly classified. Kappa is a measure of agreement between predicted presences and absences with actual presences and absences corrected for agreement that might be due to chance alone. The largest cross-validated estimate for each classification metric for each species is in boldface type.

types), measured field variables, and down-scaled bioclimatic variables (e.g., Zimmermann et al. 2007). Tables with detailed information on the predictor variables used in each of our examples, and preliminary analyses and preprocessing of the bioclimatic and topographic predictors, may be found in Appendix B.

#### Predicting invasive species presences in Lava Beds National Monument, California, USA

**Background.**—Invasions by nonnative species are an increasing problem, especially in national parks. The U.S. National Park Service (NPS) manages its lands with an aggressive policy to control or remove invasive species and prohibit the establishment of new invaders. We used RF, classification trees, logistic regression, and LDA to predict sites of likely occurrence of four invasive plant species in Lava Beds National Monument (NM).

We obtained detection data from 2000 to 2005 for *Verbascum thapsus* (common mullein), *Urtica dioica* (nettle), *Marrubium vulgare* (white horehound), and *Cirsium vulgare* (bull thistle), and GIS layers for roads and trails within the monument. For our analyses, we imposed a 30-m grid over Lava Beds NM and a 500-m buffer outside the park ( $N = 244\,733$  total grid sites). Our data included grid sites with one or more invasive species

present ( $n = 7361$  grid sites) and sites where all four species were absent ( $n = 890$  grid sites). The predictor variables for these analyses were 28 topographic and bioclimatic variables, and three variables of distances to the nearest roads and trails.

**Results.**—For *V. thapsus*, cross-validated sensitivities for the four methods are all relatively high and similar (Table 1). However, specificities differ substantially, with RF performing substantially better than the other classifiers (Table 1). For *U. dioica* and *C. vulgare* the pattern is reversed: specificities are relatively high and similar, while sensitivities differ, with RF performing substantially better than the other classifiers (Table 1). The estimated sensitivities and specificities for *M. vulgare* are roughly the same for all four classifiers. Overall, RF had the highest PCC, kappa, and AUC values for all four invasive species. Classification trees were consistently second best in terms of PCC, suggesting some nonlinear structure that LDA and logistic regression were unable to adequately model.

Three variables in the Lava Beds NM data set concern distances to roads and trails. Because roads and trails are considered natural vectors for entry and spread of invasive species (Gelbard and Belnap 2003), we expected that distances to roads and trails would be important

predictors of presence for all four invasive species. This expectation was met for RF: for each of the four invasive species, these three variables were identified as most important to the classifications (Fig. 1). The results were similar for the other classifiers for *V. thapsus*: each of the other classifiers selected two of the vector variables among the four most important. However, there was little consistency in the variables identified as most important for the remaining three invasive species. For example, none of the distances to roads or trails variables were identified as being among the four most important for any of the other classifiers for *U. dioica*. Even though we cannot say that variables identified as “important” are right or wrong, the results for RF coincide more closely with expectations based on ecological understanding of invasions by nonnative species.

The preceding results also illustrate how the variable importance in RF differs from traditional variable selection procedures. When several variables are highly collinear but good predictors of the response, as are the distances to roads and trails in the Lava Beds NM data, stepwise and criterion-based variable selection procedures will typically retain one or two of the collinear variables, but discard the rest. In contrast, RF “spreads” the variable importance across all the variables, as we observed with the distances to roads and trails. This approach guards against the elimination of variables which are good predictors of the response, and may be ecologically important, but which are correlated with other predictor variables.

*Predicting rare lichen species presences  
in the Pacific Northwest, USA*

**Background.**—Our second application of RF involves two data sets on epiphytic macrolichens collected within the boundaries of the U.S. Forest Service’s Pacific Northwest Forest Plan, USA. The first data set (hereafter LAQ,  $n = 840$  randomly sampled sites) was collected from 1993 to 2000 and the second, independent data set (hereafter EVALUATION,  $n = 300$  randomly sampled sites) was collected in 2003 in the same region. We applied RF, classification trees, additive logistic regression, and logistic regression, to the LAQ data and used the EVALUATION data as an independent assessment of the accuracy of the predicted classifications. Design details for the EVALUATION and LAQ surveys and tables of predictor variable descriptions can be found in Appendix B and in Edwards et al. (2005, 2006). Four lichen species in the LAQ and EVALUA-

TION data sets were the subjects of our analyses: *Lobaria oregana*, *L. pulmonaria*, *Pseudocyphellaria anomala*, and *P. anthraspis*. The predictor variables were elevation, aspect, and slope, DAYMET bioclimatic variables, and four vegetation variables: percentage of broadleaf, conifer, and vegetation cover, and live tree biomass.

**Results.**—For all four species, the PCC, kappa, and AUC are highest for RF on the EVALUATION data, and RF generally outperforms the other classification procedures (Table 2). However, differences in accuracies are much smaller than we observed for the Lava Beds NM analyses, and in some cases are negligible. For *L. oregana*, sensitivity and specificity on the EVALUATION surveys for RF is better than the other classifiers, except in the case of sensitivity for additive logistic regression. It is interesting to note that the cross-validated estimates of accuracy for *L. oregana* are essentially the same for all four classifiers, while the EVALUATION estimates differ substantially, suggesting that even when both the training data and test data are collected at randomly selected sites in the same geographical region, cross-validated accuracy estimates may not reflect the true differences among classifiers. For *L. pulmonaria*, the PCC, kappa, and specificity for classification trees and RF are essentially identical, and are somewhat higher to much higher than those for additive logistic regression and logistic regression. For *P. anomala*, RF has somewhat higher EVALUATION accuracy than the other three methods, which are essentially the same. A similar pattern holds for *P. anthraspis*, except that classification trees have the largest sensitivity.

Partial dependence plots (Hastie et al. 2001; see also Appendix C) may be used to graphically characterize relationships between individual predictor variables and predicted probabilities of species presence obtained from RF. For binary classification, the y-axis on partial dependence plots is on the logit scale (details in Appendix C). In Fig. 2, there is almost a linear relationship between the logit of the probability of presence for *L. oregana* and the age of the dominant conifer. For *L. oregana*, the logit of predicted probability of presence shows a constant relationship to about 800 m and then decreases sharply. The same plot for *P. anthraspis* shows a more linear decrease between 0 and 1200 m. The logit of estimated probability of presence for *L. pulmonaria* suggests that the presence of this species are associated with sites that have more consistent precipitation over summer and winter.

FIG. 1. Variable importance plots for predictor variables from random forests (RF) classifications used for predicting presence of four invasive plant species in the Lava Beds National Monument, California, USA. The mean decrease in accuracy for a variable is the normalized difference of the classification accuracy for the out-of-bag data when the data for that variable is included as observed, and the classification accuracy for the out-of-bag data when the values of the variable in the out-of-bag data have been randomly permuted. Higher values of mean decrease in accuracy indicate variables that are more important to the classification. Variable descriptions are given in Appendix B.

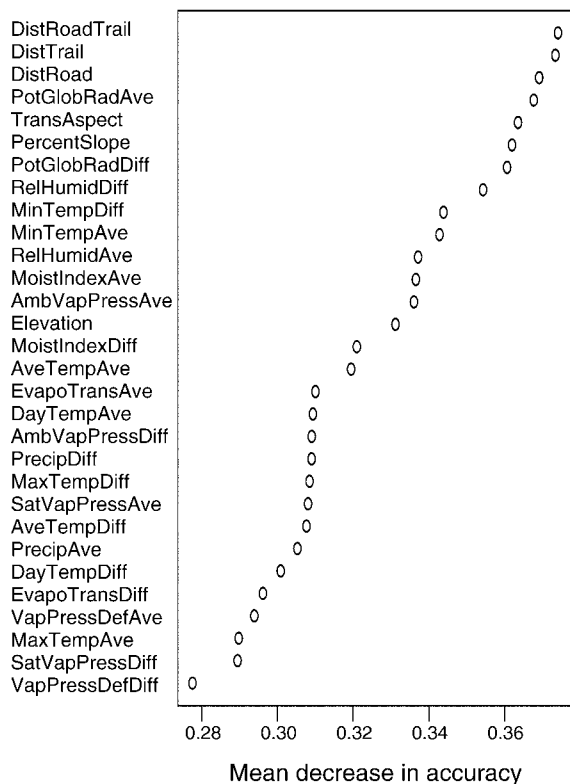
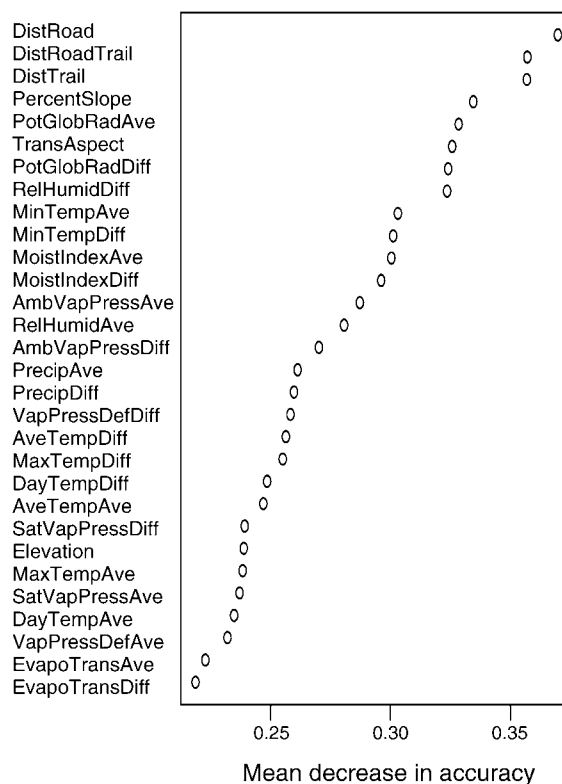
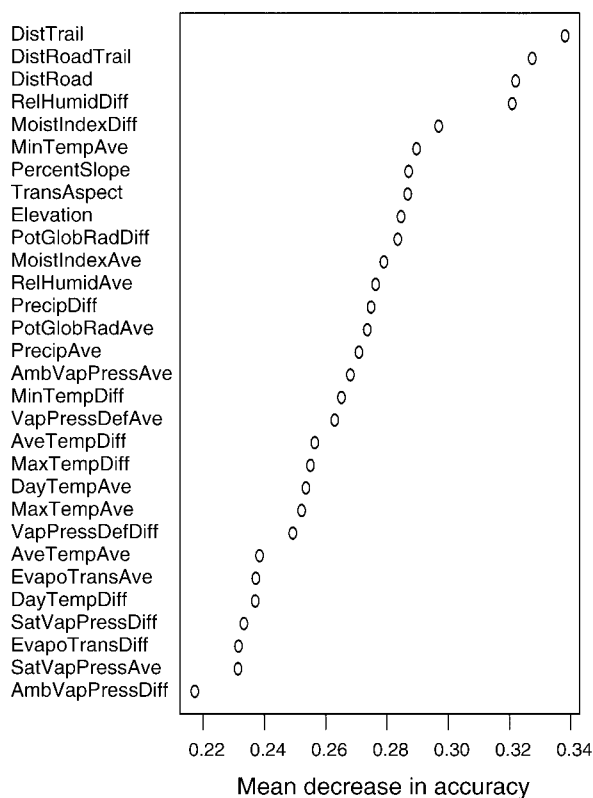
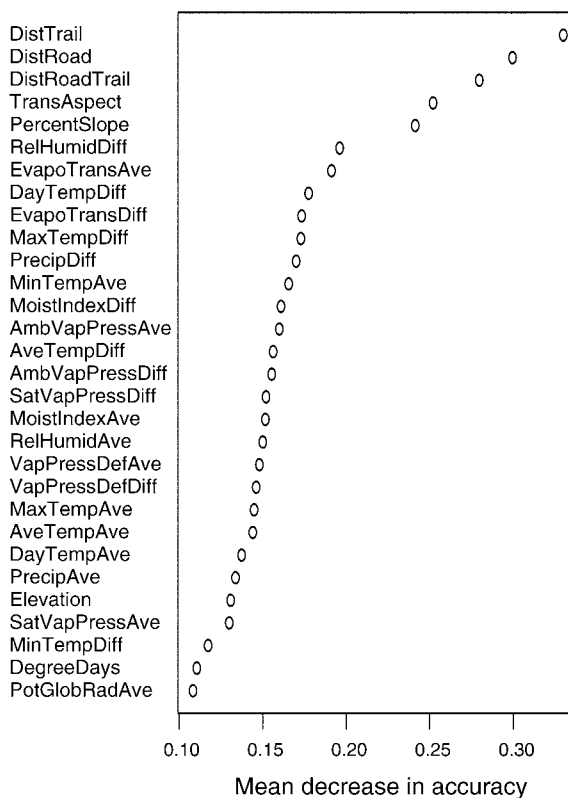
Variable importance for *Verbascum thapsus*Variable importance for *Urtica dioica*Variable importance for *Cirsium vulgare*Variable importance for *Marrubium vulgare*

TABLE 2. Accuracy measures for predictions of presence for four lichen species in the Pacific Northwest, USA.

Accuracy metric	Classification method											
	Random forests			Classification trees			Additive logistic regression			Logistic regression		
	Resub	Xval	EVAL	Resub	Xval	EVAL	Resub	Xval	EVAL	Resub	Xval	EVAL
<i>Lobaria oregana</i> ( <i>n</i> = 187 sites)												
PCC (%)	83.9	85.0	<b>82.7</b>	90.8	83.8	71.0	88.3	84.3	77.7	87.0	85.1	74.3
Specificity (%)	93.3	94.0	<b>90.0</b>	95.6	90.9	77.3	93.9	90.0	80.9	93.6	91.6	79.1
Sensitivity (%)	51.3	53.5	62.5	74.3	58.8	53.8	68.9	64.2	<b>68.8</b>	64.2	62.6	61.3
Kappa	0.489	0.523	<b>0.542</b>	0.725	0.516	0.295	0.651	0.544	0.465	0.606	0.557	0.381
AUC	0.889	0.892	<b>0.867</b>	0.910	0.817	0.753	0.946	0.897	0.818	0.924	0.904	0.806
<i>Lobaria pulmonaria</i> ( <i>n</i> = 194 sites)												
PCC (%)	84.7	84.6	<b>80.3</b>	88.8	81.3	80.0	88.3	81.2	73.0	85.9	84.6	72.7
Specificity (%)	93.5	93.2	88.5	95.5	91.0	<b>90.3</b>	94.4	87.9	75.1	93.2	92.3	76.5
Sensitivity (%)	55.2	56.2	59.0	66.5	48.9	53.0	68.0	58.8	<b>67.5</b>	61.8	59.3	62.6
Kappa	0.529	0.533	<b>0.492</b>	0.663	0.432	0.464	0.655	0.468	0.387	0.582	0.544	0.364
AUC	0.883	0.885	<b>0.869</b>	0.898	0.810	0.818	0.941	0.806	0.776	0.904	0.883	0.759
<i>Pseudocyphellaria anomala</i> ( <i>n</i> = 152 sites)												
PCC (%)	85.0	85.2	<b>86.0</b>	90.0	83.1	83.7	88.9	84.4	83.7	87.0	85.5	83.7
Specificity (%)	95.3	95.0	<b>95.0</b>	96.6	91.7	92.5	95.6	91.7	92.5	94.8	93.8	92.9
Sensitivity (%)	38.2	40.8	<b>49.2</b>	59.9	44.1	47.4	58.6	51.3	47.4	51.9	48.0	45.8
Kappa	0.398	0.418	<b>0.499</b>	0.626	0.386	0.436	0.592	0.449	0.436	0.516	0.460	0.428
AUC	0.865	0.870	<b>0.861</b>	0.865	0.794	0.794	0.944	0.865	0.829	0.905	0.878	0.854
<i>Pseudocyphellaria anthraspis</i> ( <i>n</i> = 123 sites)												
PCC (%)	88.2	87.6	<b>84.0</b>	91.7	86.1	80.0	93.2	88.1	78.7	88.1	85.4	81.3
Specificity (%)	97.1	96.6	<b>93.2</b>	95.9	93.6	86.0	97.8	95.8	86.0	95.8	94.4	89.4
Sensitivity (%)	36.6	34.9	50.0	66.7	42.3	<b>57.8</b>	66.7	43.0	51.6	43.1	32.5	51.6
Kappa	0.416	0.389	<b>0.476</b>	0.652	0.392	0.424	0.704	0.449	0.372	0.449	0.315	0.424
AUC	0.875	0.874	<b>0.816</b>	0.908	0.822	0.807	0.966	0.682	0.801	0.898	0.862	0.810

Notes: Abbreviations are: Resub, resubstitution accuracy estimates; Xval, 10-fold cross-validated accuracy estimates computed on lichen air quality data (*N* = 840 total observations); EVAL, pilot random grid survey (an evaluation data set with *N* = 300 total observations); PCC, percentage of correctly classified instances; AUC, area under the ROC curve. The largest value for each species and each metric in the EVALUATION data is in boldface type.

### Predicting cavity-nesting bird habitat in the Uinta Mountains, Utah, USA

**Background.**—In this third example, we developed species distribution models relating nest presence to forest stand characteristics in the Uinta Mountains, Utah, USA, for three species of cavity-nesting birds: *Sphyrapicus nuchalis* (Red-naped Sapsucker), *Parus gambeli* (Mountain Chickadee), and *Colaptes auratus* (Northern Flicker). Classifications were developed for each species separately, and for all three species combined. This study is an example of the application of RF to small sample sizes, to a mixture of probabilistic (randomly selected locations) and non-probabilistic (nest cavities) survey data, and shows one simple way in which RF may be used to analyze data on multiple species simultaneously.

The stand characteristics we used consisted of numbers of trees in different size classes, numbers of conifers and snags, and stand type (pure aspen and mixed aspen/conifer), all considered habitat attributes of cavity nesting birds (see Lawler and Edwards 2002 and Appendix B). Within the spatial extent of the birds nest sites for the three species, 106 non-nest sites were randomly selected, and the same information as for the nest sites was collected.

**Results.**—For *S. nuchalis* and *P. gambeli*, RF has slightly better PCC, kappa and AUC than the other methods, while for *C. auratus* all methods have similar performance (Table 3). According to RF's variable importance measures, two stand characteristics—the numbers of trees of size class 7.5–15 cm (NumTree3to6in) and 22.5–37.5 cm (NumTree9to15in)—were two of the three most important variables for all three species. Partial plots of these variables (Fig. 3) are interesting for two reasons. First, the plots are nonlinear. For the smaller-sized trees, the probability of a nest cavity drops rapidly with increasing NumTree3to6in, and then levels off. Larger trees (NumTree9to15in) have the opposite effect: the probability of a nest cavity rapidly increases, and then levels off. The second striking feature of the partial dependence plots for cavity nesting birds is that, for these two variables, the plots look very similar for all three species, suggesting that these species may be combined and analyzed as a group. Group results are comparable to the results for the individual species (Table 3). This illustrates how RF is not limited to modeling a single species; it may be used to analyze community data, and to model several species in the same functional group simultaneously. Other approaches to analyzing community data using RF include using models for some

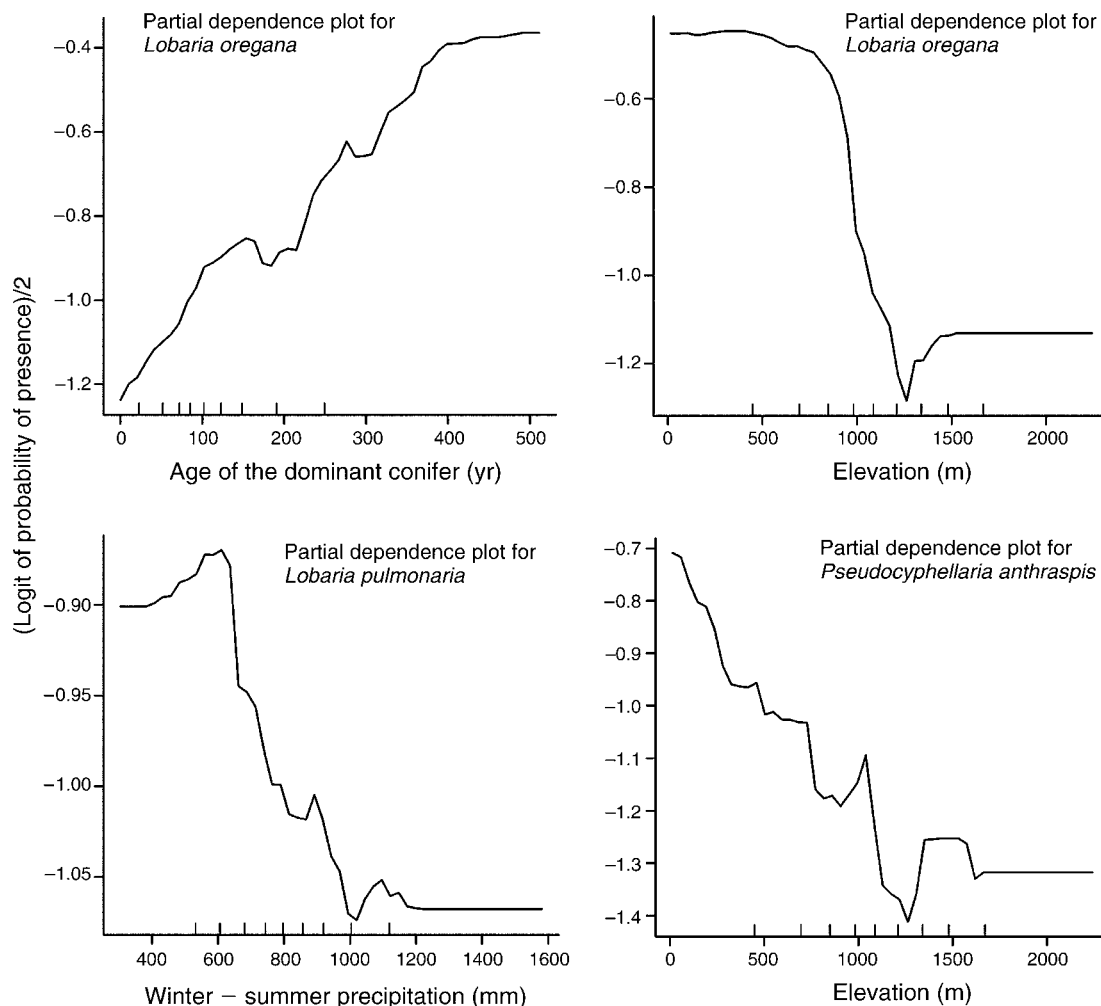


FIG. 2. Partial dependence plots for selected predictor variables for random forest predictions of the presences of three lichen species in the Pacific Northwest, USA. Partial dependence is the dependence of the probability of presence on one predictor variable after averaging out the effects of the other predictor variables in the model. "Winter - summer precipitation" is the total winter precipitation (October-March) minus the total summer precipitation (April-September). An explanation of the y-axis metric appears in Appendix C.

species to predict for much rarer, but related, species (Edwards et al. 2005) and modeling combined data with variables that identify different species.

#### DISCUSSION AND CONCLUSIONS

In three RF classification applications with presence-absence data, we observed high classification accuracy as measured by cross-validation and, in the case of the lichen data, by using an independent test set. We found a moderate superiority of RF to alternative classifiers in the lichen and bird analyses, and substantially higher accuracy for RF in the invasive species example, which involved complex ecological issues. In general, it is difficult to know in advance for which problems RF will perform substantially better than other methods, but post hoc graphical analyses can provide some insight. In

principle, RF should outperform linear methods such as LDA and logistic regression when there are strong interactions among the variables. In Fig. 4, the bivariate partial dependence plot for two variables in the bird analyses shows a nonlinear relationship of the logit of the probability of nest presence, but the effect of each of these variables is approximately the same for each value of the other variable. Thus, the effects of the two variables are approximately additive, and in this case one might expect that RF will only do slightly better than additive methods such as LDA and logistic regression, which is what we observed (Table 3). However, in the partial dependence plot for *U. dioica* in Lava Beds NM, (Fig. 4) there was a complicated interaction in the effects of the distance to the nearest road and the distance to the nearest road or trail. These

TABLE 3. Accuracy measures for nest site classification of three species of cavity nesting bird species in the Uinta Mountains, Utah, USA.

Accuracy metric	Classification method							
	Random forests		Classification trees		Logistic regression		LDA	
	Resub	Xval	Resub	Xval	Resub	Xval	Resub	Xval
<i>Sphyrapicus nuchalis</i> (Red-naped Sapsucker; $n = 42$ nest sites)								
PCC (%)	88.5	<b>87.8</b>	87.8	79.7	86.5	83.1	85.1	82.4
Specificity (%)	95.3	<b>94.3</b>	98.1	90.6	90.6	86.8	89.6	86.8
Sensitivity (%)	71.4	71.4	61.9	52.4	76.2	<b>73.8</b>	73.8	71.4
Kappa	0.702	<b>0.687</b>	0.667	0.463	0.668	0.593	0.634	0.574
AUC	0.916	<b>0.918</b>	0.848	0.761	0.929	0.879	0.909	0.868
<i>Parus gambeli</i> (Mountain Chickadee; $n = 42$ nest sites)								
PCC (%)	85.8	<b>85.1</b>	87.8	78.4	84.5	77.7	86.5	79.1
Specificity (%)	95.3	<b>93.4</b>	91.5	85.8	92.5	84.9	91.5	84.9
Sensitivity (%)	61.9	<b>64.3</b>	78.6	59.5	64.3	59.5	73.8	<b>64.3</b>
Kappa	0.621	<b>0.612</b>	0.701	0.460	0.597	0.448	0.663	0.488
AUC	0.872	<b>0.880</b>	0.896	0.756	0.890	0.800	0.881	0.803
<i>Colaptes auratus</i> (Northern Flicker; $n = 23$ nest sites)								
PCC (%)	87.6	<b>86.8</b>	89.9	82.2	90.7	86.0	89.9	85.3
Specificity (%)	97.2	<b>96.2</b>	95.3	92.5	98.1	93.4	98.1	95.3
Sensitivity (%)	43.5	43.5	65.2	34.8	56.5	<b>52.2</b>	52.2	39.1
Kappa	0.490	0.469	0.638	0.309	0.632	<b>0.489</b>	0.594	0.406
AUC	0.869	<b>0.885</b>	0.836	0.731	0.903	0.821	0.882	0.797
All species combined ( $n = 107$ nest sites)								
PCC (%)	85.9	<b>83.1</b>	85.9	75.1	83.6	77.9	82.6	77.5
Specificity (%)	86.8	<b>82.1</b>	86.8	73.6	78.3	72.6	73.6	67.0
Sensitivity (%)	85.0	84.1	85.1	76.6	88.8	83.2	91.6	<b>87.9</b>
Kappa	0.718	<b>0.662</b>	0.718	0.502	0.671	0.558	0.652	0.549
AUC	0.906	<b>0.893</b>	0.883	0.735	0.890	0.816	0.878	0.807

Notes: Abbreviations are: LDA, linear discriminant analysis; PCC, percentage of correctly classified instances; AUC, the area under the ROC curve; Resub, resubstitution accuracy estimate; Xval, 10-fold cross-validated accuracy estimate. There are 106 non-nest sites. The largest cross-validated estimate for each metric and each species is in boldface type.

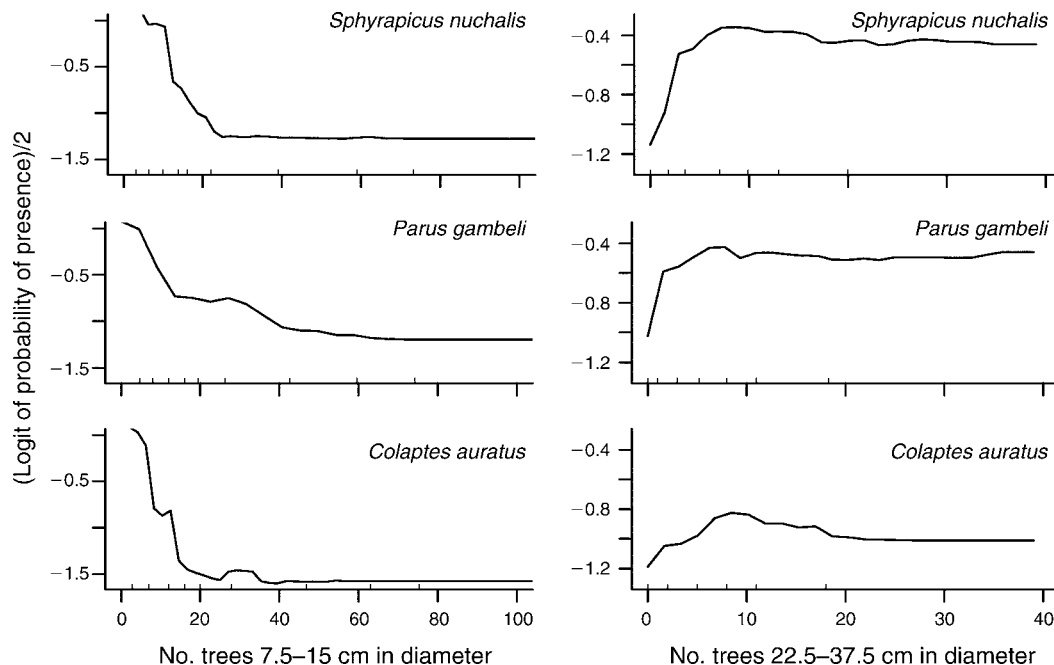


FIG. 3. Partial dependence plots for random forests classifications for three cavity-nesting bird species and two predictor variables. Data were collected in the Uinta Mountains, Utah, USA. Partial dependence is the dependence of the probability of presence on one predictor variable after averaging out the effects of the other predictor variables in the model. An explanation of the y-axis metric appears in Appendix C.



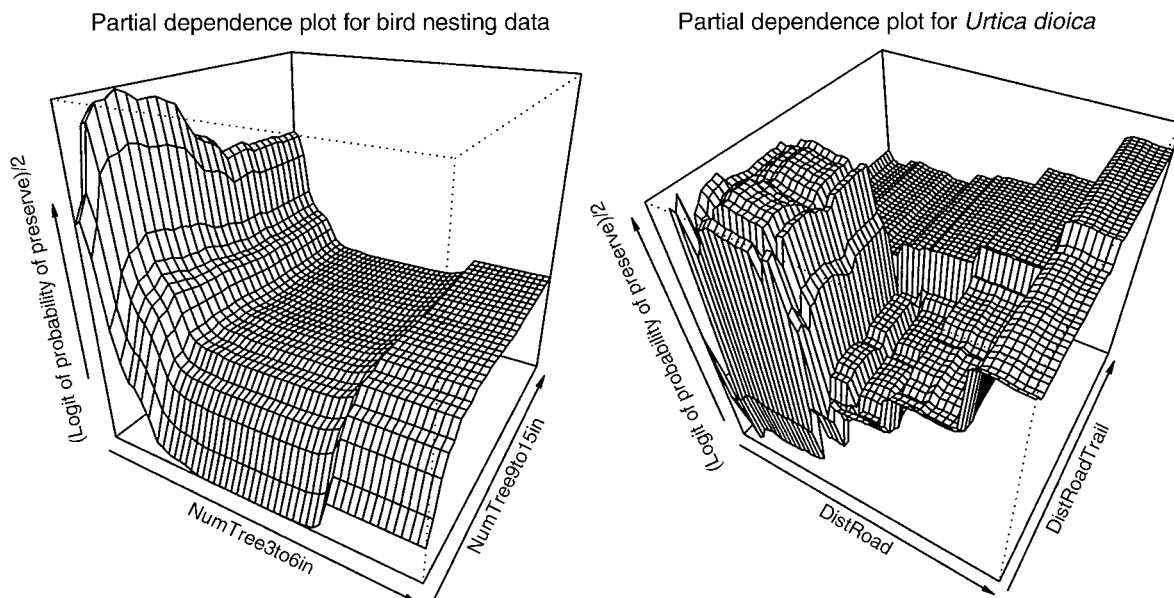


FIG. 4. Bivariate partial dependence plots for bird nesting data (107 nest sites and 106 non-nest sites) in Uinta Mountains, Utah, USA, and for *Urtica dioica* in Lava Beds National Monument, California, USA. Partial dependence is the dependence of the probability of presence on two predictor variables after averaging out the effects of the other predictor variables in the model. Variables are: NumTree3to6in, the number of trees between 7.5 cm and 15 cm dbh; NumTree9to15in, the number of trees between 22.5 cm and 37.5 cm dbh; DistRoad, distance to the nearest road (m); DistRoadTrail, distance to the nearest road or trail (m). An explanation of the y-axis metric appears in Appendix C.

kinds of interactions are the likely reason for the clear superiority of the tree-based methods, and RF in particular, in this application.

The original motivation for the development of RF was to increase the classification accuracy and stability of classification trees. In many respects RF supersedes classification trees: it is a more accurate classifier, and it is extremely stable to small perturbations of the data. For the classification situation, Breiman (2001) showed that classification accuracy can be significantly improved by aggregating the results of many classifiers that have little bias by averaging or voting, if the classifiers have low pairwise correlations. RF is an implementation of this idea using classification trees which, when fully grown, have little bias but have high variance. The restriction of the number of predictors available for each node in each tree in a RF ensures that correlations among the resultant classifications trees are small. In practical terms, RF shares the ability of classification trees to model complex interactions among predictor variables, while the averaging or voting of the predictions allows RF to better approximate the boundaries between observations in different classes.

Other classification procedures that have come from the machine learning literature in recent years include boosted trees, support vector machines (SVMs), and artificial neural networks (ANNs). All these methods, like RF, are highly accurate classifiers, and can do regression as well as classification. What sets RF apart from these other methods are two key features. The first

of these is the novel variable importance measure used in RF, which does not suffer some of the shortcomings of traditional variable selection methods, such as selecting only one or two variables among a group of equally good but highly correlated predictors. In the invasive species example presented here, we observed that the variables RF identified as most important to the classifications coincided with ecological expectations based on the published literature.

The second feature that distinguishes RF from other competitors is the array of analyses that can be carried out by RF. Most of these involve the proximities—measures of similarity among data points—automatically produced by RF (see Appendix A). Proximities may be used to impute missing data, as inputs to traditional multivariate procedures based on distances and covariance matrices, such as cluster analysis and multidimensional scaling, and to facilitate graphical representations of RF classification results (Appendix C).

As with other highly computational procedures, including boosted trees, ANNs, and SVMs, the relationships between the predictor variables and the predicted values produced by RF do not have simple representations such as a formula (e.g., logistic regression) or pictorial graph (e.g., classification trees) that characterizes the entire classification function, and this lack of simple representation can make ecological interpretation difficult. Partial dependence plots for one or two predictor variables at a time may be constructed for any “blackbox” classifier (Hastie et al. 2001:333). If the

classification function is dominated by individual variable and low order interactions, then these plots can be an effective tool for visualizing the classification results, but they are not helpful for characterizing or interpreting high-order interactions.

RF is not a tool for traditional statistical inference. It is not suitable for ANOVA or hypothesis testing. It does not compute *P* values, or regression coefficients, or confidence intervals. The variable importance measure in RF may be used to subjectively identify ecologically important variables for interpretation, but it does not automatically choose subsets of variables in the way that variable subset selection methods do. Rather, RF characterizes and exploits structure in high dimensional data for the purposes of classification and prediction.

We have focused here on RF as a classification procedure, but RF is a package of fully nonparametric statistical methods for data analysis. Quantities produced by RF may also be used as inputs into traditional multivariate statistical methods, such as cluster analysis and multidimensional scaling. Unlike many traditional statistical analysis methods, RF makes no distributional assumptions about the predictor or response variables, and can handle situations in which the number of predictor variables greatly exceeds the number of observations. With this range of capabilities, RF offers powerful alternatives to traditional parametric and semi-parametric statistical methods for the analysis of ecological data.

#### ACKNOWLEDGMENTS

Funding was provided by the U.S. Forest Service Survey and Manage Program, and the USGS National Park Monitoring Program. We thank L. Geiser and her many colleagues for primary data collection of the lichen data, D. Hays, D. Larsen, P. Latham, D. Sarr, for their help and support with the Lava Beds NM analyses, and two anonymous reviewers, for their comments that led to substantial improvements in this manuscript.

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#### APPENDIX A

Technical details and additional capabilities of random forests (*Ecological Archives* E088-173-A1).

#### APPENDIX B

Data descriptions and details of data preprocessing (*Ecological Archives* E088-173-A2).

#### APPENDIX C

Visualization techniques for random forests (*Ecological Archives* E088-173-A3).

D. Richard Cutler, Thomas C. Edwards, Jr., Karen H. Beard, Adele Cutler, Kyle T. Hess, Jacob Gibson, and Joshua J. Lawler. 2007. Random forests for classification in ecology. *Ecology* 88:2783–2792.

Appendix A. Technical details and additional capabilities of random forests.

## TECHNICAL DETAILS

### *The Gini Index*

For the  $K$  class classification problem the Gini index is defined to be  $G = \sum_k p_k(1 - p_k)$ , where  $p_k$  is the proportion of observations at the node in the  $k^{\text{th}}$  class. The index is minimized when one of the  $p_k$  takes the value 1 and all the others have the value 0. In this case the node is said to be pure and no further partitioning of the observations in that node will take place. The Gini index takes its maximum value when all the  $p_k$  take on the value  $1/K$ , so the observations at the node are spread equally among the  $K$  classes. The Gini index for an entire classification tree is a weighted sum of the values of the Gini index at the terminal nodes, with the weights being the numbers of observations at the nodes. Thus, in the selection of the next node to split on, nodes which have large numbers of observations but for which only small improvements in the  $p_k$ s can be realized may be offset against nodes that have small numbers of observations but for which large improvements in the  $p_k$ s are possible.

### *The Number of Variables Available for Splitting at Each Node*

The parameter `mtry` controls the number of variables available for splitting at each node in a tree in a random forest. The default values of `mtry` are (the integer value of) the square root of the number of variables for classification, and the number of variables divided by three for regression. The smaller value of `mtry` for classification is to ensure that the fitted classification trees in the random forest have small pairwise correlations, a characteristic that is not needed for regression trees in a random forest. In principle, for both applications, if there is strong predictive capability in a few variables then a smaller value of `mtry` is appropriate, and if the data contains a lot of variables that are weakly predictive of the response variable larger values of `mtry` are appropriate. In practice, RF results are quite insensitive to the values of `mtry` that are selected. To illustrate this point, for *Verbascum thapsus* in the Lava Beds NM invasive plants data, we ran RF five times at the default settings (`mtry` = 5) and obtained out-of-bag PCC values of 95.3%, 95.2%, 95.2%, 95.3%, 95.4%. Next, we ran RF once for each of the following values of `mtry`: 3, 4, 6, 7, 10, and 15. The out-of-bag PCC values for these six cases were 95.2%, 95.3%, 95.3%, 95.2%, 95.3%, and 95.3%. So, in this example, decreasing `mtry` to three and increasing it to half the total number of predictor variables had no effect on the correct classification rates. The other metrics we used—sensitivity, specificity, kappa, and AUC—exhibited the same kind of stability to changes in the value of `mtry`.

The R implementation of RF (Liaw and Wiener 2002) contains a function called `tuneRF` which will automatically select the optimal value of `mtry` with respect to out-of-bag correct classification rates. We have not used this function, in part because the performance of RF is insensitive to the chosen value of `mtry`, and in part because there is no research as yet to assess the effects of choosing RF parameters such as `mtry` to optimize out-of-bag error rates on the generalization error rates for RF.

### *The Number of Trees in the Random Forest*

Another parameter that may be controlled in RF is the number of bootstrap samples selected from the raw data, which determines the number of trees in the random forest (`ntree`). The default value of `ntree` is 500. Very small values of `ntree` can result in poor classification performance, but `ntree` = 50 is adequate in most applications. Larger values of `ntree` result in more stable classifications and variable

importance measures, but in our experience, the differences in stability are very small for large ranges of possible values of `ntree`. For example, we ran RF with `ntree` = 50 five times for *V. thapsus* using the Lava Beds NM data and obtained out-of-bag PCC values of 95.2%, 94.9%, 95.0%, 95.2%, and 95.2%. These numbers show slightly more variability than the five values listed in the previous section for the default `ntree` = 500, but the difference is very modest.

## ADDITIONAL APPLICATIONS OF RANDOM FORESTS IN ECOLOGICAL STUDIES

In this section we describe RF's capabilities for types of statistical analyses other than classification.

### *Regression and Survival Analysis*

RF may be used to analyze data with a numerical response variable without making any distributional assumptions about the response or predictor variables, or the nature of the relationship between the response and predictor variables. Regression trees are fit to bootstrap samples of the data and the numerical predictions of the out-of-bag response variable values are averaged. Regression functions for regression trees are piecewise constant, or "stepped." The same is true with regression functions from RF, but the steps are smaller and more numerous, allowing for better approximations of continuous functions. Prasad et al. (2006) is an application of RF to the prediction of abundance and basal area of four tree species in the southeastern United States. When the response variable is a survival or failure time, with or without censoring, RF may be used to compute fully non-parametric survival curves for each distinct combination of predictor variable values in the data set. The approach is similar to Cox's proportional hazards model, but does not require the proportional hazards assumption that results in all the survival curves having the same general shape. Details of survival forests may be found in Breiman and Cutler (2005).

### *Proximities, Clustering, and Imputation of Missing Values*

The proximity, or similarity, between any two points in a dataset is defined as the proportion of times the two points occur at the same terminal node. Two types of proximities may be obtained from RF. Out-of-bag proximities, which use only out-of-bag observations in the calculations, are the default proximities. Alternatively, proximities may be computed using all the observations. At this time proximities are the subject of intense research and the relative merits of the two kinds of proximities have yet to be resolved. Calculation of proximities is very computationally intensive. For the Lava Beds NM data ( $n = 8251$ ) the memory required to compute the proximities exceeded the memory available in the Microsoft Windows version of R (4Gb). The FORTRAN implementation of RF (Breiman and Cutler 2005) has an option that permits the storage of a user-specified fixed number of largest proximities for each observation and this greatly reduces the amount of memory required.

Proximities may be used for cluster analysis and for graphical representation of the data by multidimensional scaling (MDS) (Breiman and Cutler 2005). See [Appendix C](#) for an example of an MDS plot for the classification of the nest and non-nest sites in the cavity nesting birds' data. Proximities also may be used to impute missing values. Missing numerical observations are initially imputed using the median for the variable. Proximities are computed, and the missing values are replaced by weighted averages of values on the variable using the proximities as weights. The process may be iterated as many times as desired (the default is five times). For categorical explanatory variables, the imputed value is taken from the observation that has the largest proximity to the observation with a missing value.

As a sample application of imputation in RF, in three separate experiments using the LAQ data, we randomly selected and replaced 5%, 10%, and 50% of the values on the variable Elevation with missing values. We then imputed the missing values using RF with the number of iterations ranging from 1 to 25. The results for all the combinations of percentages of observations replaced by missing values and numbers of iterations of the RF imputation procedure were qualitatively extremely similar: the means of the original and imputed values were about the same (1069 vs. 1074, for one typical case); the correlations between the true and imputed values ranged from 0.964 to 0.967; and the imputed values were less dispersed than the

true values, with standard deviations of about 335 for the imputed values compared to about 460 for the true values. This kind of contraction, or shrinkage, is typical of regression-based imputation procedures. When a large percentage of the values in a dataset have been imputed, Breiman and Cutler (2005) warn that, in subsequent classifications using the imputed data, the out-of-bag estimates of correct classification rates may overestimate the true generalization correct classification rate.

### *Detecting Multivariate Structure by Unsupervised Learning*

Proximities may be used as inputs to traditional clustering algorithms to detect groups in multivariate data, but not all multivariate structure takes the form of clustering. RF uses a form of unsupervised learning (Hastie et al. 2001) to detect general multivariate structure without making assumptions on the existence of clusters within the data. The general approach is as follows: The original data is labeled class 1. The same data but with the values for each variable independently permuted constitute class 2. If there is no multivariate structure among the variables, RF should misclassify about 50% of the time. Misclassification rates substantially lower than 50% are indicative of multivariate structure that may be investigated using other RF tools, including variable importance, proximities, MDS plots, and clustering using proximities.

### SOFTWARE USED IN ANALYSES

Stepwise discriminant analysis and preliminary data analyses and manipulations were carried out in SAS version 9.1.3 for Windows (SAS Institute, Cary NC). All other classifications and calculations of accuracy measures were carried out in R version 2.4.0 (R Development Core Team 2006). Logistic regression is part of the core distribution of R. LDA is included in the MASS package (Venables and Ripley 2002). Classification trees are fit in R using the `rpart` package (Therneau and Atkinson 2006). The R implementation of RF, `randomForest`, is due to Liaw and Wiener (2002).

### SOURCES OF RANDOM FORESTS SOFTWARE

Three sources of software for RF currently exist. These are:

1. FORTRAN code is available from the RF website. (<http://www.math.usu.edu/~adele/forests>).
2. Liaw and Wiener (2002) have implemented an earlier version of the FORTRAN code for RF in the R statistical package.
3. Salford Systems ([www.Salford-Systems.com](http://www.Salford-Systems.com)) markets a professional implementation of RF with an easy-to-use interface.

The use of trade, product, or firm names in this publication is for descriptive purposes only and does not imply endorsement by the U.S. Government.

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Appendix B. Data descriptions and details of data preprocessing.

This appendix contains tables giving descriptions of all the variables used in our three example analyses, and also information on the preprocessing of the data.

# INVASIVE PLANTS IN LAVA BEDS NATIONAL MONUMENT, CALIFORNIA, USA

## Data Sources

Lava Beds National Monument (NM) personnel provided us with data on detections and treatment in 2000–2005 for *Verbasum thapsus* (common mullein), *Urtica dioica* (nettle), *Marrubium vulgare* (white horehound), and *Cirsium vulgare* (bull thistle), as well as GIS layers for roads and trails in Lava Beds NM. For data analysis purposes, we imposed a 30-m grid over Lava Beds NM and a 500 m buffer outside the park. There were a total of 244,733 grid points in the park and buffer. Values of all the topographic and bioclimatic predictor variables were obtained for all points on the grid and minimum distances to roads and trails for all points on the grid were computed in a GIS and merged with the other predictor variables. Table B1 contains a list of names and descriptions of variables used in our analyses of the Lava Beds NM invasive plant data. Topographic variables (Elevation, Aspect, and PercentSlope) were obtained from the National Elevation Dataset (NED) (Gesch et al. 2002). Bioclimatic variables were obtained from the DAYMET 1 km grid daily weather surfaces (Thornton et al. 1997) by interpolation. Daily values for each variable were aggregated to create monthly variables. Thus for each bioclimatic predictor in Table B1 (except DegreeDays) there were originally 12 monthly values.

TABLE B1: Names and descriptions of predictor variables used in analyses of invasive plant data from Lava Beds National Monument, California, USA.

Variable type	Variable name	Variable description	Units
Bioclimatic	DegreeDays	Degree days	°C days
	EvapoTrans	Monthly potential evapotranspiration	mm
	MoistIndex	Monthly moisture index	cm
	Precip	Monthly precipitation	cm
	RelHumid	Monthly relative humidity	%
	PotGlobRad	Monthly potential global radiation	kJ
	AveTemp	Monthly average temperature	°C
	MinTemp	Monthly minimum temperature	°C
	MaxTemp	Monthly maximum temperature	°C
	DayTemp	Monthly average daytime temperature	°C
	AmbVapPress	Monthly average ambient vapor pressure	Pa
	SatVapPress	Monthly average saturated vapor pressure	Pa
	VapPressDef	Monthly average vapor pressure deficit	Pa
Topographic	PercentSlope	Percent slope	%
	Aspect	Aspect	°

	Elevation	Elevation	m
Distances to Roads or Trails	DistRoad	Distance to the nearest road	m
	DistTrail	Distance to the nearest trail	m
	DistRoadTrail	Distance to the nearest road or trail	m

### *Preliminary Data Analyses and Processing*

All preliminary data summaries and statistical analyses were carried out in SAS version 9.1.3 (SAS Institute, Cary, North Carolina). The variable aspect is measured on a circular scale. Values of aspect near 0° and 360° both represent directions close to due north, yet are at opposites ends of the aspect scale. The usual remedy for this problem is to apply a trigonometric transformation to the raw aspect values. The transformation we used is given by the formula  $Transformed\ Aspect = [1 - \cos(2\pi Aspect/360)]/2$ . This formula is similar (but not identical) to that used by Roberts and Cooper (1989). The transformed aspect values lie in the interval from 0 to 1. Values near 0 represent aspects close to due north, while values near 1 represent aspects close to due south. East and west are treated identically with transformed aspect values of 0.5.

Preliminary analyses showed that correlations among the monthly values for each of the 12 sets of bioclimatic predictor variables (excluding DegreeDays) were extremely high. Principal components analyses of the correlation matrices of the 12 sets of bioclimatic variables showed that, in each case, the first principal component was approximately an average of the 12 monthly measurements, and the second principal component was a contrast of values for the 6 “summer” months (April–September) to the 6 “winter” months (October–December and January–March). For each set of 12 monthly variables, these two principal components explained over 95% of the variability, and in most cases the first two principal components explained over 99% of the variability in the sets of variables. Accordingly, for each set of monthly bioclimatic predictors, we defined two new variables:

1. the *average* of the 12 monthly variables, and
2. the *difference* between the sum of the April–September monthly values and the October–December and January–March monthly values, divided by 12.

We use the suffix “Ave” to indicate the average of the 12 monthly values of each bioclimatic predictor and “Diff” to indicate the Summer–Winter difference. For example, PrecipAve is the average precipitation over all 12 months and PrecipDiff is the normalized difference between summer and winter precipitations, as described above. In all our classification analyses we used only the pair of derived variables for each bioclimatic predictor, not the 12 monthly values. Thus there were 12 pairs of bioclimatic predictors, DegreeDays, three topographic variables (using transformed Aspect instead of raw Aspect), and three variables containing distances to roads and trails, for a total of 31 predictor variables.

## LICHENS IN THE PACIFIC NORTHWEST, USA

### *Data Sources*

The lichen data sets were collected in seven national forests and adjoining BLM lands in Oregon and southern Washington USA, between 1993 and 2003. The Current Vegetation Survey (CVS) is a randomly started 5.4 km grid that covers all public lands in the Pacific Northwest. On all public lands except designated wilderness areas and national parks, the primary grid has been intensified with 3 additional grids spaced at 2.7 km from the primary grid. The primary purpose of the CVS grid is to generate estimates of forest resources (Max et al. 1996). The Lichen Air Quality (LAQ) data were collected as part of a study to evaluate air quality in the Pacific Northwest (Geiser 2004). The data used in our analyses is from 840 sites on the primary CVS grid. The pilot random grid surveys (EVALUATION) were conducted by the Survey



and Manage Program as part of the Northwest Forest Plan, the conservation plan for the northern spotted owl (*Strix occidentalis caurina*). The EVALUATION surveys were conducted in three areas in the Pacific Northwest: Gifford-Pinchot National Forest in southern Washington, the Oregon Coast Range, and the Umpqua Basin, also in Oregon. At each location, a stratified random sample of 100 sites from the intensified CVS grid was drawn. The stratification criteria were Reserve Status (Reserve, Non-reserve) and Stand Age Class (< 80 years and 80+ years). The allocations of the sampled sites to the strata were (at each location): 60 to Reserve/80+, 20 to Reserve/< 80, and 10 to each of the Non-reserve strata. These allocations reflected the information priorities of the Survey and Manage program at the time of the surveys.

The four lichen species used in our analyses—*Lobaria oregana*, *Lobaria pulmonaria*, *Pseudocyphellaria anomala*, and *Pseudocyphellaria anthraspis*—were the four most common species observed in the LAQ surveys that were also searched for in the EVALUATION surveys. All four species are large, foliose, broadly distributed cyanolichens that can be found on tree trunks, live branches, and leaf litter of conifers in the Pacific Northwest. All achieve their largest biomass in riparian and late seral forests. Eye-level habitat and large size makes them relatively easy to find and identify. All sites in both surveys were surveyed by field botanists trained in the recognition and differentiation of regional epiphytic macrolichens, and specimens were obtained at all sites for later laboratory identification.

Table B2 contains the names and descriptions of the predictor variables used in our analyses. Topographic variables were obtained from the NED (Gesch et al. 2002). Aspect was transformed according to the formula  $Transformed\ Aspect = [1 - \cos(2\pi(Aspect - 30^\circ)/360)]/2$ , following Roberts and Cooper (1989). Daily values of the DAYMET bioclimatic predictors (Thornton et al. 1997) were aggregated to monthly values. Correlations among the monthly bioclimatic predictors were very high and principal components analyses suggested that considerable dimension reduction could be carried out without loss of information. For the variables EvapoTrans, MoistIndex, Precip, RelHumid, and PotGlobRad, the 12 monthly values for each observation were replaced by an average of the 12 values, denoted with the suffix “Ave” on the variable name, and a difference of the average values for the six “summer” months (April–September) and the six winter months (January–March, October–December), denoted with the suffix “Diff.”. For the temperature and vapor pressure measurements, further dimension reduction was possible for the LAQ and EVALUATION data. The 24 vapor pressure measurements at each site were replaced with just two values: an average of all 24 values and a summer-to-winter difference. Similarly, the 48 temperature measurements were replaced by just two values, again an average and a summer-to-winter difference. In all our classification analyses we used only the derived bioclimatic variables. The total number of predictor variables used in our analyses was 24.

TABLE B2: Names and descriptions of predictor variables used in analyses of lichen data from the Pacific Northwest, USA.

Variable type	Variable name	Variable description	Units
Bioclimatic	EvapoTrans	Monthly potential evapotranspiration	mm
	MoistIndex	Monthly moisture index	cm
	Precip	Monthly precipitation	cm
	RelHumid	Monthly relative humidity	%
	PotGlobRad	Monthly potential global radiation	kJ
	AveTemp	Monthly average temperature	°C
	MinTemp	Monthly minimum temperature	°C
	MaxTemp	Monthly maximum temperature	°C
	DayTemp	Monthly average daytime temperature	°C
	AmbVapPress	Monthly average ambient vapor pressure	Pa
	SatVapPress	Monthly average saturated vapor pressure	Pa

Topographic	PercentSlope	Percent slope	%
	Aspect	Aspect	°
	Elevation	Elevation	m
Stratification	ReserveStatus	Reserve Status (Reserve, Non-reserve)	
	StandAgeClass	Stand Age Class (< 80 years, 80+ years)	
Vegetation	AgeDomConif	Age of the dominant conifer	Years
	PctVegCov	Percent vegetation cover	%
	PctConifCov	Percent conifer cover	%
	PctBrdLfCov	Percent broadleaf cover	%
	ForBiomass	Live tree (> 1inch DBH) biomass, Above ground, dry weight.	tons/acre

### CAVITY NESTING BIRDS IN THE UINTA MOUNTAINS, UTAH, USA

#### *Data Source*

Data was collected on nest sites for three cavity nesting birds in the Uinta Mountains, Utah, USA. The species *Sphyrapicus nuchalis* (Red-naped Sapsucker)( $n = 42$ ), *Parus gambeli* (Mountain Chickadee)( $n = 42$ ), and *Colaptes auratus* (Northern Flicker)( $n = 23$ ). Within the spatial extent of the birds nest sites for the three species, 106 non-nest sites were randomly selected, and the same information as for the nest sites was collected. The plot size for the data collection was 0.04 ha. The variables used in our analyses are given below.

TABLE B3: Stand characteristics for nest and non-nest sites for three cavity nesting bird species. Data collected in the Uintah Mountains, Utah, USA.

<b>Variable name</b>	<b>Variable description</b>
NumTree<1in	Number of trees less than 2.5 cm diameter at breast height
NumTree1to3in	Number of trees 2.5 cm to 7.5 cm diameter at breast height
NumTree3to6in	Number of trees 7.5 cm to 15 cm diameter at breast height
NumTree6to9in	Number of trees 15 cm to 22.5 cm diameter at breast height
NumTree9to15in	Number of trees 22.5 cm to 37.5 cm diameter at breast height
NumTree>15in	Number of trees greater than 37.5 cm diameter at breast height
NumSnags	Number of snags
NumDownSnags	Number of downed snags
NumConifer	Number of conifers
PctShrubCover	Percent shrub cover
StandType	Stand Type (0 = pure aspen; 1 = mixed aspen conifer)

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**D. Richard Cutler, Thomas C. Edwards, Jr., Karen H. Beard, Adele Cutler, Kyle T. Hess, Jacob Gibson, and Joshua J. Lawler. 2007. Random forests for classification in ecology. *Ecology* 88:2783–2792.**

Appendix C. Visualization techniques for random forests.

This appendix contains some technical details concerning partial dependence plots and information about additional visualization techniques for random forests.

#### MULTIDIMENSIONAL SCALING PLOTS FOR CLASSIFICATION RESULTS

With regard to the data for the cavity nesting birds in the Uinta Mountains, Utah, USA, a natural question to ask is whether there are any differences on the measured stand characteristics among the nest sites for the three bird species. An RF classification of the nest sites produced correct classification rates at the chance level (i.e., very low), and we sought to understand why this was the case through graphical summaries. RF produces measures of similarity of data points called proximities (see [Appendix A](#)). The matrix of proximities is symmetric with all entries taking values between 0 and 1. The value ( $1 - \text{proximity}$  between points  $j$  and  $k$ ) is a measure of the distance between these points. A bivariate, metric, multidimensional scaling (MDS) plot is a scatter plot of the values of the data points on the first two principal components of the distance matrix (the matrix of  $1 - \text{proximities}$ ). Using the RF classification for the combined data on the cavity nesting birds, we constructed an MDS plot (Fig. C1). Note that the nest sites for the three species are completely intermingled, showing that it is not possible to separate the nest sites for the different species on the basis of the measured stand characteristics. The nest sites for all the species are fairly well separated from the non-nest sites, which explains why the classification accuracies for nest sites versus non-nest sites were high. Plots of pairs of measured stand characteristics—including the two stand characteristics that RF identifies as most important to the classification—do not show such a clear separation of the nest and non-nest sites.

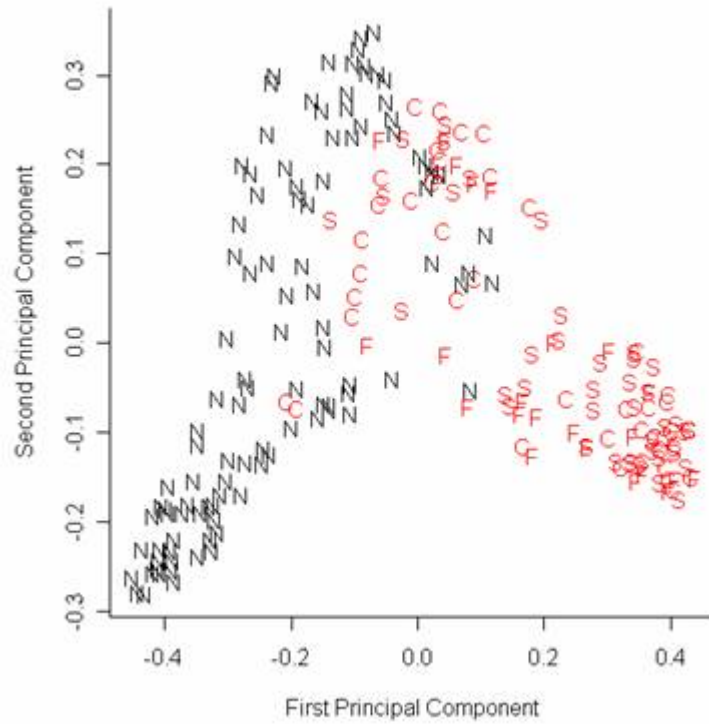


FIG. C1. Random forest-based multi-dimensional scaling plot of non-nest vs. nest sites for three species of cavity nesting birds in the Uinta Mountain, Utah, USA. Non-nest sites are labeled "N". Nest sites are coded "S" for *Sphyrapicus nuchalis*, "C" for *Parus gambeli*, and "F" for *Colaptes auratus*.

## PARTIAL DEPENDENCE PLOTS

Partial dependence plots (Hastie et al. 2001; Friedman 2001) are tools for visualizing the effects of small numbers of variables on the predictions of “blackbox” classification and regression tools, including RF, boosted trees, support vector machines, and artificial neural networks. In general, a regression or classification function,  $f$ , will depend on many predictor variables. We may write  $f(X) = f(X_1, X_2, X_3, \dots, X_s)$ , where  $X = (X_1, X_2, \dots, X_s)$  are the predictor variables. The partial dependence of the function  $f$  on the variable  $X_j$  is the expectation of  $f$  with respect to all the variables except  $X_j$ . That is, if  $X_{(-j)}$  denotes all the variables except  $X_j$ , the partial dependence of  $f$  on  $X_j$  is given by  $f_j(X_j) = E_{X_{(-j)}} [f(X)]$ . In practice we estimate this expectation by fixing the values of  $X_j$ , and averaging the prediction function over all the combinations of observed values of the other predictors in the data set. This process requires prediction from the entire dataset for each value of  $X_j$  in the training data. In the R implementation of partial dependence plots for RF (Liaw and Wiener 2002), instead of using the values of the variable  $X_j$  in the training data set, the partialPlot function uses an equally spaced grid of values over the range of  $X_j$  in the training data, and the user gets to specify how many points are in the grid. This feature can be very helpful with large data sets where the number of values of  $X_j$  may be large.

The partial dependence for two variable, say  $X_j$  and  $X_l$ , is defined as the conditional expectation the function  $f(X)$  with respect to all variables except  $X_j$  and  $X_l$ . Partial dependence plots for two predictor variables are perspective (three-dimensional) plots (see Fig. 4 in the main article). Even with moderate

sample sizes (5,000–10,000), such as the Lava Beds NM invasive plants data, bivariate partial dependence plots can be very computationally intensive.

In classification problems with, say,  $K$  classes, there is a separate response function for each class. Letting  $p_k(X)$  be the probability of membership in the  $k^{\text{th}}$  class given the predictors.

$X = (X_1, X_2, X_3, \dots, X_s)$ , the  $k^{\text{th}}$  response function is given by

$$f_k(X) = \log p_k(X) - \sum_j \log p_j(X) / K$$

(Hastie et al. 2001, Liaw and Wiener 2002). For the case when  $K = 2$ , if  $p$  denotes the probability of “success” (i.e., presence, in species distribution models), the above expression reduces to

$$f(X) = 0.5 \log(p(X)/(1 - p(X))) = 0.5 \text{logit}(p(X)).$$

Thus, the scale on the vertical axis of Figs. 2–4 is a half of the logit of probability of presence.

### REAL-TIME 3D GRAPHICS WITH `rgl`

Bivariate partial dependence plots are an excellent way to visualize interactions between two predictor variables, but choosing exactly the correct viewing angle to see the interaction can be quite an art. The `rgl` real-time 3D graphics driver in R (Adler and Murdoch 2007) allows one to take a 3D plot and spin it in three dimensions using the computer mouse. In a matter of seconds one can view a three-dimensional plot from literally hundreds of angles, and finding the “best” perspective to view the interaction between two variables is quick and easy. Figure C2 is a screen snapshot of an `rgl` 3D plot for the cavity nesting birds data, using the same variables as in Fig. 4 of the main article.

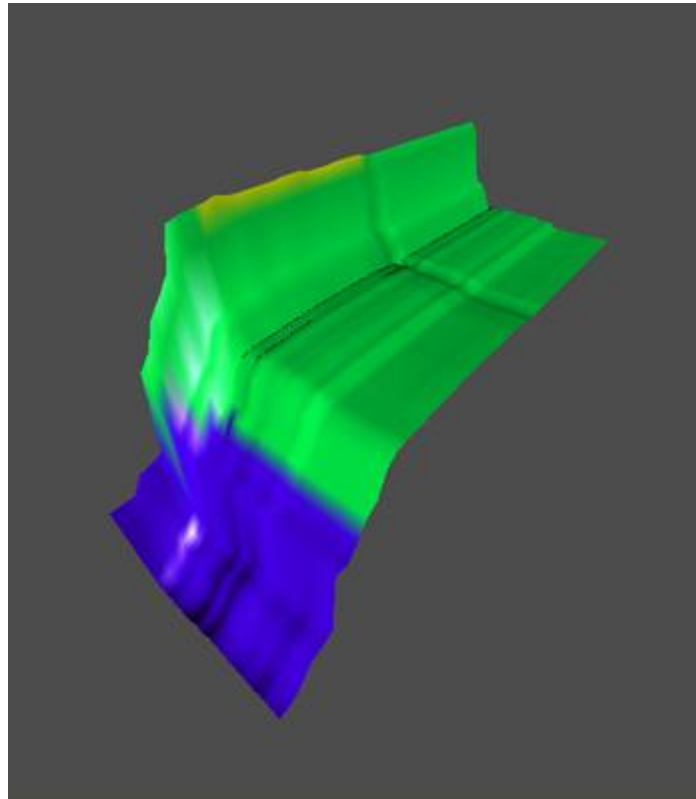


FIG. C2. Screen snapshot of 3D `rgl` partial dependence plot for variables `NumTree3to6in` and `NumTree9to15in`. Nest site data for three species of cavity nesting birds collected in the Uinta Mountains, Utah, USA.

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