
A Multiscale Landscape Approach to Predicting Bird and Moth Rarity Hotspots in a Threatened Pitch Pine–Scrub Oak Community

JOANNA GRAND,*‡ JOHN BUONACCORSI,† SAMUEL A. CUSHMAN,* CURTICE R. GRIFFIN,* AND MAILE C. NEEL*

*Graduate Program in Organismic and Evolutionary Biology and Department of Natural Resources Conservation, Holdsworth Natural Resources Center, University of Massachusetts, Amherst, MA 01003–9285, U.S.A.

†Department of Mathematics and Statistics, Lederle Graduate Research Tower, University of Massachusetts, Amherst, MA 01003–9305, U.S.A.

Abstract: *In the northeastern United States, pitch pine (Pinus rigida Mill.)–scrub oak (Quercus ilicifolia Wang.) communities are increasingly threatened by development and fire suppression, and prioritization of these habitats for conservation is of critical importance. As a basis for local conservation planning in a pitch pine–scrub oak community in southeastern Massachusetts, we developed logistic-regression models based on multiscale landscape and patch variables to predict hotspots of rare and declining bird and moth species. We compared predicted moth distributions with observed species-occurrence records to validate the models. We then quantified the amount of overlap between hotspots to assess the utility of rare birds and moths as indicator taxa. Species representation in hotspots and the current level of hotspot protection were also assessed. Predictive models included variables at all measured scales and resulted in average correct classification rates (optimal cut point) of 85.6% and 89.2% for bird and moth models, respectively. The majority of moth occurrence records were within 100 m of predicted habitat. Only 13% of all bird hotspots and 10% of all moth hotspots overlapped, and only a few small patches in and around Myles Standish State Forest were predicted to be hotspots for both taxa. There was no correlation between the bird and moth species-richness maps across all levels of richness ($r = -0.03$, $p = 0.62$). Species representation in hotspots was high, but most hotspots had limited or no protection. Given the lack of correspondence between bird and moth hotspots, our results suggest that use of species-richness indicators for conservation planning may be ineffective at local scales. Based on these results, we suggest that local-level conservation planning in pitch pine–scrub oak communities be based on multitaxa, multiscale approaches.*

Key Words: birds, hotspots, indicator taxa, logistic regression, moths, scale, species richness

Un Método de Paisaje Multiescala para Predecir Áreas de Rareza Crítica de Aves y Polillas en una Comunidad Amenazada de Pino–Encino

Resumen: *En el noreste de Estados Unidos, las comunidades de pino (Pinus rigida Mill.)–encino (Quercus ilicifolia Wang.) están cada vez más amenazadas por el desarrollo y la supresión de fuego y la priorización de esos hábitats es de importancia crítica. Como una base para la planeación de conservación local de una comunidad de pino–encino en el sureste de Massachusetts, desarrollamos modelos de regresión logística con base en variables a nivel de paisaje multiescala y de fragmento para predecir las áreas críticas para especies de aves y polillas raras y en declinación. Para validar los modelos comparamos las distribuciones esperadas de polillas con registros observados de la ocurrencia de especies. Posteriormente cuantificamos el traslape entre áreas críticas para evaluar la utilidad de aves y polillas raras como taxa indicadores. Los modelos predictivos incluyeron variables en todas las escalas consideradas y resultaron en tasas promedio de clasificación correcta*

‡email jgrand@metacomet.com

Paper submitted December 19, 2002; revised manuscript accepted November 4, 2003.

(punto de corte óptimo) de 85.6% y 89.2% para modelos de aves y polillas, respectivamente. La mayoría de los registros de ocurrencia de polillas estuvo dentro de 100 m del hábitat predicho. Sólo hubo traslape en 13% del total de áreas críticas para aves y en 10% del total de áreas críticas para polillas, y se predijo que sólo unos cuantos fragmentos dentro y alrededor del Bosque Estatal Myles Standish serían áreas críticas para ambos taxones. En todos los niveles de riqueza ($r = -0.03$, $p = 0.62$), no hubo correlación entre los mapas de riqueza de especies de aves y polillas. La representación de especies en áreas críticas fue alta; sin embargo, la mayoría de las áreas críticas tenía protección limitada o carecía de ella. Dada la falta de correspondencia entre las áreas críticas para aves y polillas, nuestros resultados sugieren que el uso de indicadores de riqueza de especies para la planeación de conservación puede ser inefectivo en escalas locales. Con base en estos resultados, sugerimos que la planeación de conservación a escala local en comunidades de pino-encino se base en métodos que consideren taxones y escalas múltiples.

Palabras Clave: áreas críticas, aves, escala, polillas, riqueza de especies, taxones indicadores, regresión logística

Introduction

Pitch Pine–Scrub Oak Communities

Pitch pine (*Pinus rigida* Mill.)–scrub oak (*Quercus ilicifolia* Wang.) communities, commonly called pine barrens, are priorities for conservation in the northeastern United States because they are uncommon, support an unusual number of unique and rare species, and are increasingly threatened by development and disruption of historical disturbance patterns (Motzkin et al. 1996; Finton 1998). They range from New Jersey to Maine and are essential components of the landscape in that they support species assemblages and ecological processes that differ from those on more widespread mesic uplands. In particular, these communities support a highly specialized lepidopteran fauna including several rare, barrens-restricted species (Schweitzer & Rawinski 1988; Mello et al. 1999). In addition, many species of Neotropical migratory songbirds of conservation concern breed in pine-barrens habitats. These communities have therefore become a major focus of conservation efforts in northeastern North America, and prioritization of remaining patches of pine-barrens habitat for conservation is critical.

Indicators of Species Richness

Land-prioritization decisions are often based on hotspots of species richness for groups of well-known species in the hope that these hotspots will correspond with those of other taxa (Caro & O'Doherty 1999). This indicator-taxon approach may be problematic because studies disagree on whether species-rich habitats of major taxa co-occur (e.g., Pearson & Cassola 1992; Sætersdal et al. 1993; Weaver 1995; Flather et al. 1997; Tardif & DesGranges 1998; Andelman & Fagan 2000). When concordance is low, prioritization approaches based on the species richness of one taxon will provide inadequate protection for many other organisms. Furthermore, species-richness hotspots may not include rare species that are most in need of conservation attention (Prendergast et al. 1993).

Hotspots may also fail to include a significant proportion of the total number of species present in an area and thus are typically an ineffective method of selecting representative reserves (Lombard 1995). Finally, methods commonly used to identify hotspots are also problematic. Available records of species distributions are often biased because much of these data are gathered inside protected areas and are of little use in identifying priority sites in unprotected areas (Maddock & Du Plessis 1999).

Despite these criticisms, the use of species-richness indicators as a tool for habitat prioritization remains a practical alternative to conducting logistically and financially unfeasible, exhaustive biodiversity surveys of all potential conservation lands (Carroll & Pearson 1998; Ricketts et al. 1999). Further, use of multiple, unrelated taxa might help prevent serious omissions in priority-site selection, and a focus on rare species richness (rarity hotspots) rather than total species richness would ensure that the highest conservation priorities are accounted for.

We chose to investigate the coincidence of rare bird and moth distributions for several reasons. First, birds and Lepidoptera are often used as indicator taxa because they are taxonomically and geographically well known and are phylogenetically, behaviorally, and ecologically distinct from one another. Therefore, generalizable patterns may be assumed if congruence exists (Pearson & Carroll 1999). Second, adequate survey data were available for both of these taxa in a pine-barrens community in close proximity to our study area. Third, many imperiled species of birds and moths breed in these communities and are therefore worthy of conservation attention regardless of their effectiveness as indicator taxa. Fourth, bird and butterfly hotspots may or may not co-occur, depending on factors such as spatial scale and habitat (e.g., Murphy & Wilcox 1986; Prendergast et al. 1993; Prendergast & Eversham 1997; Blair 1999; Pearson & Carroll 1999; Swengel & Swengel 1999). Although the correlation between butterfly and moth hotspots is low (Ricketts et al. 2002), we are unaware of any studies investigating the relationship between bird and moth hotspots.

Predicting Species Distributions

Because records of observed species occurrences are often biased, unreliable (Margules et al. 1994; Conroy & Noon 1996; Maddock & Du Plessis 1999), and incomplete for many taxa (Carroll & Pearson 1998; Polasky et al. 2000), predicting species distributions from species-habitat association models based on surveys using statistical sampling principles provides a reasonable alternative to reliance on questionable or limited occurrence data. We developed statistical species-habitat models with landscape and patch composition and configuration variables as predictors. This approach was justifiable given that many species, particularly birds, are strongly influenced by landscape- and patch-level variables (e.g., McGarigal & McComb 1995; Mazerolle & Villard 1999; Saab 1999; Illera 2001; Lee et al. 2002; Grand & Cushman 2003). Few researchers have attempted to assess the influence of landscape-level variables on the distribution of moths. Because many species of moths are often found in areas lacking their host plants, however, landscape characteristics may play an important role in influencing the distributions of some species (Ricketts et al. 2001; Ricketts et al. 2002). Indeed, in a community-level analysis of 10 state-listed moth species, landscape variables explained twice as much variation in the species data as plot- or patch-level variables (Grand & Mello 2004). Moreover, because it is well known that species-habitat relationships vary according to the scale at which they are investigated (Kotliar & Wiens 1990; Fielding & Hawthorn 1995; Böhning-Gaese 1997), species-habitat models must account for this scale dependence. To do so, we quantified all landscape variables included as potential predictors at a range of scales to ascertain the scale at which each species was most responsive for each variable.

Indicator Taxa and Local Conservation Planning

The purpose of our research was to examine the coincidence, level of rare species representation, and management status of bird and moth rarity hotspots on a scale relevant for local conservation planning. Many studies related to indicator taxa hotspots have been applied at relatively coarse scales—for example, entire states (Scott et al. 1993), ecoregions (Davis et al. 1999), countries (Prendergast et al. 1993), or continents (Pearson & Carroll 1998). These coarse-scale studies identify such large areas as priorities for conservation that they do not provide sufficiently detailed guidance at the local level, where most conservation decisions are made (Böhning-Gaese 1997; Prendergast & Eversham 1997; Ricketts et al. 2002). As of yet, there is little support for concordance among indicator taxa at local scales (Ricketts et al. 2002), and it remains to be seen whether this shortcut for identification of high-priority areas is a useful tool for local conservation planning. To answer this question, we focused our inves-

tigation on southeastern Massachusetts, most of which is considered of high conservation priority because it contains the largest remaining pine-barrens habitats (Mello et al. 1998) and the second largest number of state-listed rare species in the state (Barbour et al. 1998). The area is also experiencing extremely rapid human population growth, making it necessary to set realistic conservation priorities within this larger hotspot. Our study provides information that will aid local conservationists in setting practical acquisition and management priorities within our study area and in remaining pine-barrens communities throughout the northeastern United States. We also address the broader question of the utility of birds and moths as indicators of species richness at local scales.

Methods

Study Area

Our study area included 29,433 ha in southeastern Plymouth County, Massachusetts (U.S.A.). The area is bordered by the Atlantic Ocean on the east and encompasses the entire town of Plymouth, the eastern half of Carver, and all 5032 ha of Myles Standish State Forest (MSSF). A small section of northern Bourne in Barnstable County is also included.

Data Collection

We developed species-habitat models with data collected at the Camp Edwards Training Site on the Massachusetts Military Reservation (MMR) directly south of our study area. We used data from outside the study area because surveys conducted at Camp Edwards provide the most extensive sampling-based inventories of bird and moth abundance and distribution available for pine-barrens communities in Massachusetts. We believe that the models are valid for predictions of species distributions in Plymouth County because the two areas constitute the largest contiguous barrens complex in Massachusetts and therefore share the same habitat characteristics and species assemblages. Higher levels of fragmentation in the study area than at Camp Edwards may limit the applicability of the models, however.

We used bird abundance data collected from 1994–1998 by the Camp Edwards Natural Resource Office. They surveyed birds during June and July with a modified point-count transect technique within 58 plots of the U.S. Army Land Condition Trend Analysis (LCTA) plots. Observers surveyed each plot once in the morning and once in the evening by slowly walking the length of the plot along 100-m transects for 6 minutes and recording all birds seen or heard within 50 m of each side of the transect. Upon reaching the end of the plot, the observer stopped for 8 minutes and recorded all birds seen or heard within a 50-m radius. The observer then walked back to the starting

point (6-minute duration), again recording any birds detected within 50 m of each side. We used the midpoint of the transect as the point location for each plot. Observers sampled each plot for 1–4 years, with approximately 30 plots sampled per year. The complete data set on bird abundance, excluding recorded flyovers, consisted of 73 species distributed across the 58 plots. We excluded 28 of the 73 species from the analysis because they were present in <4 plots and we believed they were insufficiently sampled. Of the remaining 45 species, 10 were listed as imperiled on the Partners in Flight conservation plan for the southern New England physiographic area (Dettmers & Rosenberg 2000), and another 7 were included in the Massachusetts Audubon Society's list of species of conservation interest (Grzenda & Jones 2002). One imperiled species (Eastern Towhee) was excluded due to its presence at every site and one species (Ovenbird) that was not included in either of these lists was included in the analysis because it is extremely sensitive to landscape fragmentation (Dunn & Garrett 1997). We developed species-habitat models for these 17 species.

Personnel from the Lloyd Center for Environmental Studies collected moth abundance data at Camp Edwards from 1996–1998. Of the 547 species of macrolepidoptera identified during the course of the inventory, 17 state-listed species, most of which are endemic to pine-barrens habitat, were documented within a 24-km radius of Camp Edwards. Observers conducted daytime field counts for the coastal barrens buck moth, an active day flier, by scanning a 25-m-radius circle centered at 37 light-trap sites. Visual observation at each site lasted for 10 minutes in 1996 and for 20 minutes in 1997 and 1998. Observers counted all individuals that passed through the circle. The sites sampled and time of sample varied over the 3-year period, but all sampling was conducted during 5–31 October each year.

Observers conducted inventories of night-flying moths from late May to early November. They placed portable 15-W UV blacklight traps powered with 12-V batteries at 18 sites in 1996, 13 sites in 1997, and 7 sites in 1998. They chose sites either to represent a range of barrens habitats or to acquire baseline data in areas targeted for potential development. They used a random-design sampling schedule in 1996 and 1998. In 1997 sampling alternated between sites inside and outside a military training area that could only be accessed once each week. Mello et al. (1999) provide a more detailed description of sampling methods. Although light traps have a range of influence of approximately 3–200 m depending on moon phase, weather conditions, and trap location and efficiency (Baker 1985; Young 1997; Ricketts et al. 2001), this sampling technique was adequate for relating species presence to environmental variables because the traps were positioned to cast light primarily within the target habitat (Mello et al. 1999). Of the 17 state-listed species documented, 11 were sufficiently sampled to be included

in the analysis. Due to the high probability that one individual of a species captured at a site would have only been passing through that habitat rather than using it (M. Mello, personal communication), we considered a species present at a site only if more than one individual was recorded.

A digital land-cover map of the MMR and its immediate vicinity was developed and ground truthed by the Camp Edwards Natural Resource Office. They used photo interpretation of color infrared aerial photos taken in 1994 with a nominal resolution of 1:5000. Habitat type classification was based on the Albany Pine Bush Reserve and the Waterboro Barrens–The Nature Conservancy classification systems (Appendix 1). J. Stone (MassGIS) developed a second digital land-cover map of the study area with 1:12,000-scale, color infrared aerial photos (1993) and accounted for recent pine-barrens habitat loss due to development by inspection of 1999 aerial photos. We standardized both maps with 14 habitat types, a minimum mapping unit of 364 m², and a cell size of 10 m.

We derived 24 landscape-composition and -configuration variables from a landscape-pattern analysis of the MMR land-cover map conducted with FRAGSTATS 3.2 (McGarigal et al. 2002). The variables consisted of 15 landscape-level metrics (that characterize the mosaic of cover types), 3 class-level metrics (that characterize a focal cover type), and 6 patch-level metrics (Appendix 1). We calculated class-level metrics only for classes that were either in high abundance or were thought to be important in influencing species distributions. We derived all landscape and class metrics at five scales by generating circular windows with radii of 150, 300, 600, 900, and 1200 m around each sampling point with a geographic information system (GIS) (Environmental Systems Research Institute 1992–1999). Characterizing the landscape surrounding each point at multiple scales enabled us to select the scale at which each aspect of landscape composition and configuration was most significant for each species. Landscapes that intersected the edge of the land-cover map were truncated at the border because we did not have the fine-resolution land-cover data necessary to increase the extent of the map. In addition, overlap among landscapes surrounding adjacent sampling points prevented some landscapes from being completely independent. Patch metrics were based on contiguous areas of the single cover type in which each sampling point was located and were therefore only generated at one scale.

Logistic-Regression Models

We used SAS (SAS Institute 1999–2000) to develop logistic-regression models for each species (for species names, see Appendix 2), with landscape, class, and patch variables as predictors. To screen the large number of potential predictor variables, we initially subjected each variable to univariate tests of significance (PROC NPARIWAY

Wilcoxon; SAS Institute 1999–2000), comparing sites with and without the species under study. We eliminated all variables with p values of ≥ 0.1 . We then screened all retained variables for the scale (i.e., window size) at which they were most significant by selecting the scale with the lowest p value. We excluded all other scales of each variable from further analysis. In cases where more than one scale had the same p value, we selected the smaller scale. We then used univariate logistic regression (PROC Logistic; SAS Institute 1999–2000) to model the probability of species presence based on each of the remaining variables on both the raw and log-transformed scale. We used the Hosmer-Lemeshow goodness-of-fit test and eliminated variables with a p value of < 0.1 because this indicated a lack of fit of the logistic model (Hosmer & Lemeshow 2000). In addition, we discarded any variable that lacked adequate variability or showed a pattern of presence or absence of the species relative to the predictor that resulted in an inability to fit the logistic-regression model (due to what is known as quasi or complete separation; see Hosmer & Lemeshow 2000). For all variables that were eliminated due to lack of fit, lack of variability, or separation of data points, we assessed the next most significant scale in the same way and substituted it into the data set if it did not have the same problems.

We conducted multiple logistic regressions on the final variable set for each species with both stepwise and forward selection. We used both selection procedures for purposes of model validation and to obtain the model with the best predictive ability. We set the significance level to enter (SLE) the model for both stepwise and forward selection at $p = 0.1$ and to stay (SLS) in the model for the stepwise procedure at $p = 0.2$ (PROC REG selection = forward, SLE = 0.1; selection = stepwise, SLE = 0.1, SLS = 0.2; SAS Institute 1999–2000). Forward selection often resulted in the problem of quasi or complete separation. When this occurred, we eliminated the variables that caused the problem. To assess model predictive ability we used both the conservative cut point of 0.5 (Gutzwiller & Barrow 2001) and the optimal cut point (for an explanation of how optimal cut point was determined, see Appendix 3) to calculate correct classification rates, sensitivity (ability of the model to correctly predict presence), and specificity (ability of the model to correctly predict absence). We selected the model with the highest correct classification rate, except in cases where the inclusion of additional variables did not improve the classification rate by $\geq 10\%$ or increase sensitivity to $\geq 50\%$. For the final models we calculated the Cohen's Kappa statistic (K) at both cut points. Kappa is a "chance-corrected" measure of classification accuracy and indicates percent improvement over random assignment (McGarigal et al. 2000). Because there is some bias in classification rates computed from the same data used to fit the model, the logistic procedure in SAS reduces this bias by using a one-

step approximation of a cross-validation procedure, based on the leave-one-out principle, to compute the parameter estimates (SAS Institute 1999).

Mapping Predicted Probability of Occurrence

We conducted a series of FRAGSTATS moving window analyses (McGarigal et al. 2002) on the land-cover map of Plymouth County to create grids composed of cell-based values for each variable retained in the species-habitat models at the scale at which it was selected. The moving window analysis created a new grid for each variable by moving across the land-cover grid one 10-m cell at a time and calculating the value for each requested landscape or class variable within a circular window of a specified radius (scale) surrounding each cell. The creation of grids for patch variables did not require the moving window because the standard FRAGSTATS analysis calculated patch variables at every cell in the grid. For each species, we overlaid the grids for all variables included in its model in a GIS and applied the logistic function based on the variable coefficients to create a continuous probability surface across the study area for the probability of occurrence in each grid cell. The formula for the logistic function is as follows:

$$\text{probability of occurrence} = e^z / (1 + e^z),$$

where $z = (b_0 + b_1x_1 + b_2x_2 + b_3x_3 \dots)$, b_0 is the intercept, b_1 , b_2 , and b_3 are coefficients (maximum likelihood estimates), and x_1 , x_2 , and x_3 are the variable grids. The optimal cut point was then applied to the continuous probability surface to obtain a binary map on which each cell had a value of 0 for absence or 1 for presence. We considered developed land nonhabitat and excluded these cells from the analysis. We did not exclude fresh water from the analysis because it was grouped as one habitat type with wetlands; therefore, the models may erroneously include some aquatic areas as habitat.

Comparison of Predicted and Observed Occurrences

For model-validation purposes, we compared georeferenced records from the element-occurrence database of the Massachusetts Natural Heritage and Endangered Species Program (Division of Fisheries and Wildlife) to our predicted species-distribution maps. The records contained in this database were acquired mainly through opportunistic sightings of rare species rather than systematic surveys, making them useful for validation of predicted presence but not predicted absence. The database contained records for only nine of the species modeled (all moths), so only those species could be included in this part of the analysis. For each species, we overlaid all point locations in each element occurrence on the predicted presence-absence map. We calculated the percentage of points located within all grid cells predicted to contain that species. Five points had a margin of error

of 2000 m and were excluded from the analysis due to their imprecision. All other points were precise only to within a 100-m radius; therefore, we also calculated the percentage of points located within 100 m of predicted habitat.

Predicted Bird and Moth Hotspots

We calculated species richness separately for birds and moths for every grid cell by overlaying each species' predicted presence-absence map in a GIS and summing the number of species present in each cell. We selected hotspots using the criteria of Prendergast et al. (1993). We considered the richest 5% of cells in the study area to be hotspots; however, when the threshold fell within a group of cells with equal species-richness counts, these cells were excluded and the threshold was raised to cells with the next highest species counts. We then overlaid the bird and moth hotspot maps in a GIS to locate areas of overlap by selecting cells with species richness in the top 5% for both birds and moths, and we calculated the percentage of all bird and moth hotspots that overlapped.

We also conducted a correlation analysis using the grid command correlation with no offset in ArcInfo 8.2 (Environmental Systems Research Institute 1982–2002) to estimate the correlation among all paired cells in the bird and moth species-richness grids. Because spatial dependence in species-richness data may invalidate significance tests as a result of inflation of the degrees of freedom (Carroll & Pearson 1998), we used the program MODTTEST (Legendre 2000) on a random subsample of the data ($n = 400$) to conduct a significance test with a degrees-of-freedom correction (Dutilleul 1993). We then assessed the representation of rare species in hotspots by overlaying the individual species-distribution maps on the hotspot maps and identifying which species were not predicted to occur in any hotspot grid cells. We did this for all species in both bird and moth hotspots.

Finally, we assessed the current level of hotspot protection. The National Gap Analysis Program assigns currently protected areas to different categories of management status based on their level of protection from conversion of natural land cover and their ability to contribute to biodiversity conservation (Scott et al. 1993). Category 1 areas are managed to maintain a natural state, category 2 areas are allowed only limited alteration of habitat quality, category 3 areas are multiple-use lands that are subject to extractive uses (the Southern New England Gap Analysis Project [SNEGAP] subdivides this category into public (3a) and private (3b) properties), and category 4 areas are unprotected from conversion to anthropogenic habitat types. We overlaid protected areas in categories 1, 2, and 3a, which are considered by the SNEGAP to contribute significantly to biodiversity conservation, on the bird, moth, and overlapping hotspot maps and calculated the percentage of cells included in each of these management categories.

Results

Logistic-Regression Models

All bird models that retained more than one variable included variables measured at different scales (Appendix 2). In contrast, several of the moth models (Melsheimer's sack-bearer, coastal barrens buck moth, and coastal swamp metarranthis) included variables measured at only one scale. Overall, birds were associated with a wide variety of landscape and patch composition and configuration metrics. For example, 8 species were positively associated with closed-canopy mixed-woods habitat, and 10 species were positively associated with open-canopy scrub oak habitat. Moth models did not include patch variables and typically showed strong positive associations with landscapes containing large amounts of open-canopy scrub oak habitat or sparse-canopy pitch pine-scrub oak thicket and negative associations with highly connected landscapes (measured by cohesion, contagion, and area-weighted mean radius of gyration).

The average correct classification rates were 84.5% (cut point of 0.5) and 85.6% (optimal cut point) for the bird models, and 86.1% (cut point of 0.5) and 89.2% (optimal cut point) for the moth models (Appendix 3). The average Kappa statistics were 61.6% (cut point of 0.5) and 64.4% (optimal cut point) for the bird models, and 70.3% (cut point of 0.5) and 76.2% (optimal cut point) for the moth models (Appendix 3). These results suggest that the predictive ability of our models was substantial ($0.61 < K < 0.80$ r, Landis & Koch 1977).

Comparison of Predicted and Observed Occurrences

The number of occurrence records ranged from 1 to 49 per species (total $n = 91$). For all but one species (Gerhard's underwing moth), the majority of observed occurrences were located either within predicted habitat or within 100 m of predicted habitat (Fig. 1). For five species, 100% of observed occurrences were located within 100 m of predicted habitat.

Predicted Bird and Moth Hotspots

The bird species-richness analysis resulted in grid cells containing between 1 and 12 of the 17 total species. Bird hotspots comprised 617 ha, or 2% of the total study area (Fig. 2a). The moth species-richness analysis resulted in grid cells containing between 0 and 11 of the 11 total species. Moth hotspots encompassed 875 ha, or 3% of the study area (Fig. 2b). Bird and moth hotspots overlapped in 83 ha, or only 0.3% of the study area. The overlapping areas included 13% of all bird hotspots and 10% of all moth hotspots and were concentrated in small patches in and around Myles Standish State Forest (Fig. 2c). Only four grid cells, or 0.05% of overlapping cells, contained the maximum possible combined species richness

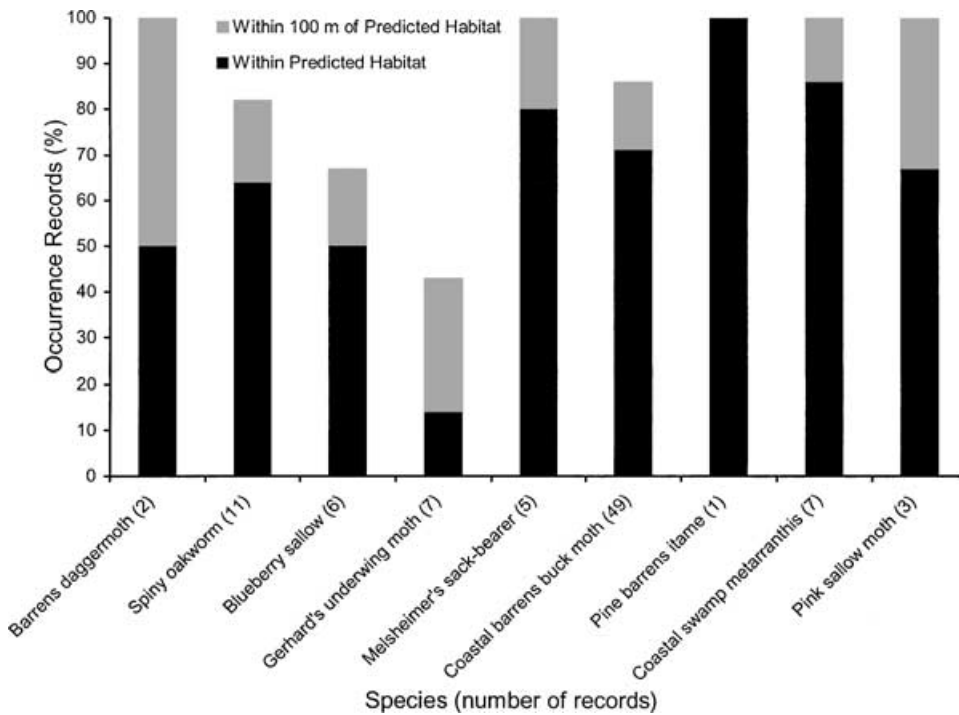


Figure 1. Percentage of moth species-occurrence records located within predicted habitat and within 100 m of predicted habitat.

(23 species). All bird and moth hotspots together covered 1409 ha, or slightly <5% of the total study area. The correlation analysis, which examined the correspondence between the bird and moth species-richness grids at all levels of richness, showed no significant association between bird and moth richness across the study area ($r = -0.03$, $p = 0.62$).

Bird hotspots contained portions of the distributional range of all bird species except the Purple Finch, which was not predicted to occur anywhere in the study area because of the failure of the model to accurately predict the presence of this species (Appendix 3). Every moth species included in the analysis was represented in moth hotspots. Likewise, all moth species were represented in bird hotspots. Two bird species (the Purple Finch and the Scarlet Tanager) were not represented in moth hotspots or overlapping hotspots.

No hotspots occurred within existing reserves that are managed to maintain a natural state (GAP management status category 1), and only 3% of bird hotspots and 2% of moth and overlapping hotspots occurred within reserves that allow limited alteration of habitat quality (GAP management status category 2). The majority of moth hotspots (71%) and overlapping hotspots (95%) occurred within Myles Standish State Forest, which is a public reserve subject to extractive uses (GAP management status category 3a) and potentially destructive recreational activities, whereas the majority of bird hotspots (63%) occurred in areas receiving no significant level of protection (Fig. 2).

Discussion

Species-Habitat Models

In general, birds and moths appeared to be associated with different landscape characteristics. The birds had diverse associations with several cover types, configurations, and scales, whereas moths associated most frequently with disjunct patches of open-canopy scrub-oak habitat. Although both bird and moth models performed well, moth models had higher predictive ability overall. These results are not surprising given that many of the moth species are pine-barrens habitat specialists (Boyd & Marucci 1998), whereas many of the birds are habitat generalists that breed throughout the northeastern United States. The success of the moth models based only on landscape variables was surprising, however, because moths are generally assumed to respond mainly to plot-level vegetation characteristics, such as abundance of host plants. Our results suggest that the surrounding landscape plays a relatively large role in habitat suitability for both moths and birds. As with all predictive models, results should be interpreted with caution because of the potential for prediction error resulting from, for example, uncertainty in species detectability (Stauffer et al. 2002) or the spatial dependence of species distributions (Guisan & Zimmermann 2000). However, due to the methods employed here for establishing species presence and to prior community-level analyses of these data assessing the role of spatial location (Grand & Cushman

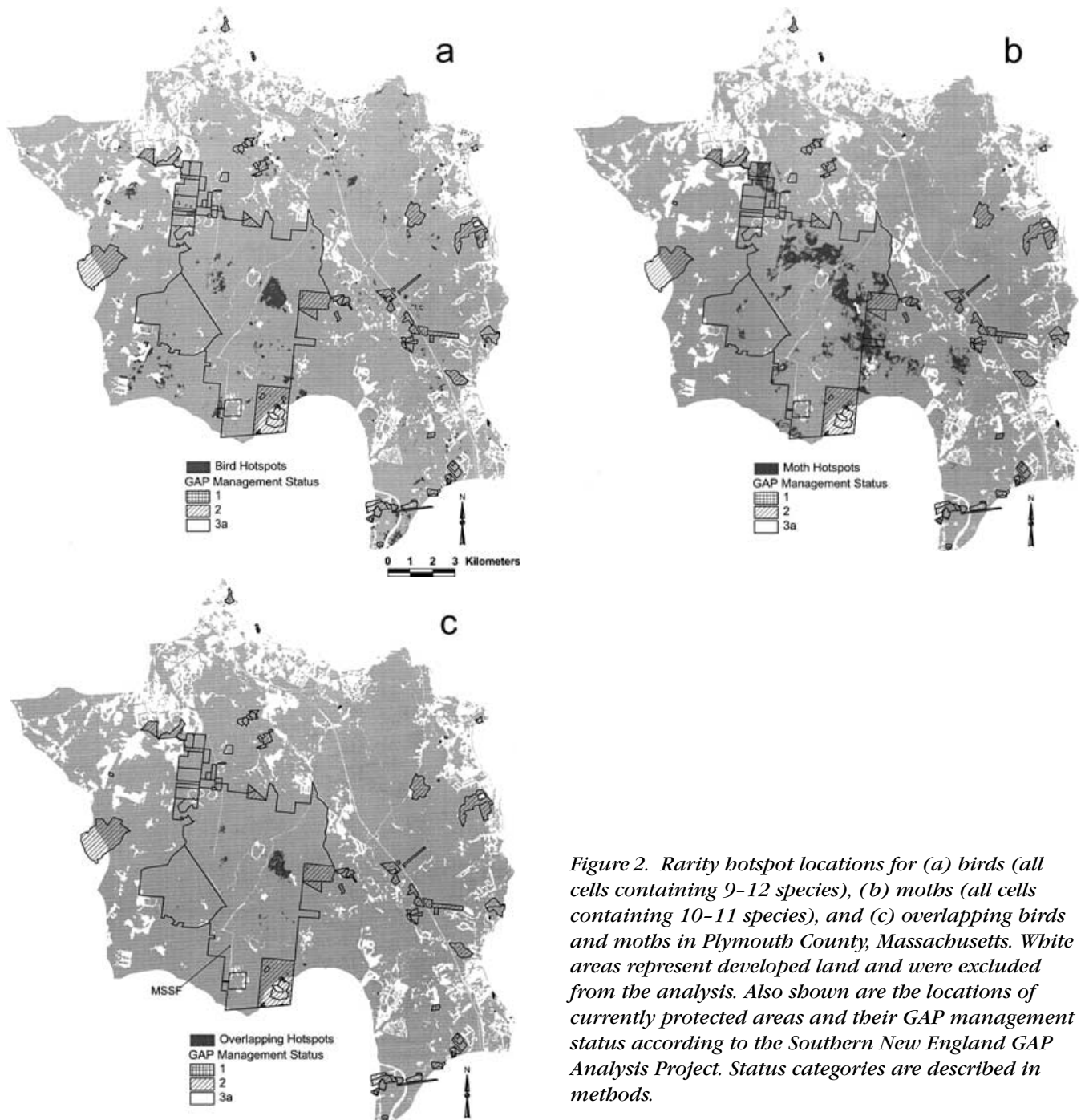


Figure 2. Rarity hotspot locations for (a) birds (all cells containing 9–12 species), (b) moths (all cells containing 10–11 species), and (c) overlapping birds and moths in Plymouth County, Massachusetts. White areas represent developed land and were excluded from the analysis. Also shown are the locations of currently protected areas and their GAP management status according to the Southern New England GAP Analysis Project. Status categories are described in methods.

2003; Grand & Mello 2004), we believe these issues did not have a major impact on our results.

Comparison of Predicted and Observed Occurrences

Although available records of observed species occurrences may be poor indicators of all potential suitable habitat because of bias in the data collection (i.e., data collected mainly in protected areas, ad hoc data collection, observer bias) and small sample size, they are valuable for purposes of model validation. The fact that a large pro-

portion of all observations of rare moth species occurred inside or within the margin of error of predicted habitat suggests that the models performed well in selecting appropriate habitat. Moreover, the models predicted additional suitable habitat that did not contain occurrence records and may provide a more conservative estimate of potential valuable habitat. These areas should be systematically surveyed to further validate model predictions.

Cross-Taxon Congruence

The association between bird and moth hotspots was weak. The majority of hotspots for each taxon would remain unprotected if species-rich areas for only the other of these taxa were used to select areas for conservation. The lack of correlation between bird and moth species richness supports Ricketts et al.'s (2002) hypothesis that species-richness patterns of different taxa are unlikely to correspond at local scales. Thus, the use of indicators of high species richness at scales relevant to local conservation planning may be ineffective. If representation of every species is the goal, protection of only bird hotspots would suffice. However, this approach would exclude 90% of high richness areas for moths. Given that only 5% of the total study area would be required to capture the current diversity present in all bird and moth hotspots, prioritizing the richest areas of both taxa may provide the basis for a more comprehensive conservation strategy in this landscape than would either taxon alone. However, at the fine scale that we have defined them (10-m cells), hotspots alone would not represent large enough areas to maintain populations of all species over the long term and should therefore only be used to guide efforts to establish larger reserves.

Conservation Implications

Crucial conservation decisions, such as establishing reserves within a local area or identifying critical habitats within established reserves, are made at scales much smaller than typically investigated in habitat-prioritization studies (Ricketts et al. 2002). We used a local area in Massachusetts in critical need of conservation planning as a case study to test the utility of species-richness indicators as a fine-scale conservation planning tool. The extent and resolution of our study are appropriate for local land managers seeking guidance on how to prioritize remaining habitat fragments for conservation.

Our results suggest that the current reserve system in our study area may be inadequate for the long-term protection of bird and moth rarity hotspots. The results also have important implications for managers of Myles Standish State Forest. This reserve is the most extensive in the study area and contains the largest aggregations of cells with the highest levels of combined bird and moth species richness (Fig. 2c). Although this land is afforded a higher level of protection from development than the surrounding landscape, its primary purpose includes recreation as well as conservation, and it is therefore under threat from recreational users such as off-road vehicle drivers seeking greater access to sensitive habitats (McCaffrey 2001). Our results could be used to direct harmful recreational activities away from these rarity hotspots and initiate monitoring programs to more thoroughly assess indicators of habitat quality for rare species, such as reproductive suc-

cess. Furthermore, unprotected hotspots should be given high priority in the evaluation of potential sites for addition to the existing reserve system. Hotspot characteristics could also be used to guide management of land not currently supporting high species diversity. For example, the majority of birds and moths examined were positively associated with open-canopy scrub-oak habitat, whereas most of the landscape is composed of later-successional closed-canopy forest. Therefore, managing for early-successional stages might increase the overall diversity of the study area.

Although the applicability of our results may be limited to pine-barrens communities, this study demonstrates the potential ineffectiveness of single-taxon, single-scale prioritization schemes for local-level conservation planning. Although pine-barrens communities are most often considered valuable habitat for Lepidoptera, they also provide habitat for many birds of conservation concern. Based on these results, prioritization based on only one of these taxa would do little to protect the most species-rich areas of the other. Because the success of species-richness indicators may vary with location, geographical scale, and taxa, this potentially valuable conservation tool should be applied with caution. Moreover, predictions of suitable habitat are heavily dependent on the scale at which environmental variables are measured, suggesting that single-scale models may have limited utility for conservation planning. Given the lack of correspondence between species-rich areas of different taxa at local scales and the scale-dependence of habitat associations, we suggest that conservation planners use multitaxa, multiscale assessments to develop more comprehensive conservation strategies.

Acknowledgments

We thank M. Ciaranca and D. Cray at the Camp Edwards Natural Resource Office, M. Mello at the Lloyd Center for Environmental Studies, J. Stone at MassGIS, and the Natural Heritage & Endangered Species Program of the Massachusetts Division of Fisheries & Wildlife for providing the necessary data. We also thank K. McGarigal for his helpful guidance throughout the study and two anonymous reviewers for their constructive comments. Funding for this study was provided by the Nuttall Ornithological Club (J.G.), the Robert & Patricia Switzer Foundation (J.G.), the Graduate School at the University of Massachusetts Amherst (J.G.), the U.S. Department of Education Graduate Assistance in Areas of National Need Program (S.A.C.), and the D.H. Smith Conservation Research Fellows Program (M.C.N.). The sentence should read "Funding for this study was provided by the Nuttall Ornithological Club (J.G.), The Robert & Patricia Switzer Foundation (J.G.), the Graduate School at the University

of Massachusetts Amherst (J.G.), the U.S. Department of Education Graduate Assistance in Areas of National Need Program (S.A.C.), and the D.H. Smith Conservation Research Fellows Program (M.C.N.).

Literature Cited

- Andelman, S. J., and W. F. Fagan. 2000. Umbrellas and flagships: efficient conservation surrogates or expensive mistakes? *Proceedings of the National Academy of Sciences of the United States of America* **97**:5954–5959.
- Baker, R. R. 1985. Moths: population estimates, light-traps and migration. Pages 188–211 in L. M. Cook, editor. *Case studies in population biology*. Manchester University Press, Manchester, United Kingdom.
- Barbour, H. T., T. Simmons, P. Swain, and H. Woolsey. 1998. Our irreplaceable heritage: protecting biodiversity in Massachusetts. *Natural Heritage and Endangered Species Program, Massachusetts Division of Fisheries and Wildlife and The Massachusetts Chapter of the Nature Conservancy*, Westborough, Boston.
- Blair, R. B. 1999. Birds and butterflies along an urban gradient: surrogate taxa for assessing biodiversity? *Ecological Applications* **9**:164–170.
- Böhning-Gaese, K. 1997. Determinants of avian species richness at different spatial scales. *Journal of Biogeography* **24**:49–60.
- Boyd, H. P., and P. E. Marucci. 1998. Arthropods of the pine barrens. Pages 505–525 in R. T. T. Forman, editor. *Pine barrens: ecosystem and landscape*. Rutgers University Press, New Brunswick, New Jersey.
- Caro, T. M., and G. O'Doherty. 1999. On the use of surrogate species in conservation biology. *Conservation Biology* **13**:805–814.
- Carroll, S. S., and D. L. Pearson. 1998. Spatial modeling of butterfly species richness using tiger beetles (Cicindelidae) as a bioindicator taxon. *Ecological Applications* **8**:531–543.
- Conroy, M. J., and B. R. Noon. 1996. Mapping of species richness for conservation of biological diversity: conceptual and methodological issues. *Ecological Applications* **6**:763–773.
- Davis, F. W., D. M. Stoms, and S. Andelman. 1999. Systematic reserve selection in the USA: an example from the Columbia Plateau ecoregion. *Parks* **9**:31–41.
- Dettmers, R., and K. V. Rosenberg. 2000. Partners in Flight bird conservation plan, physiographic area 9: southern New England. *American Bird Conservancy, The Plains, Virginia*.
- Dunn, J. L., and K. L. Garrett. 1997. *A field guide to warblers of North America*. Houghton Mifflin, New York.
- Dutilleul, P. 1993. Modifying the t-test for assessing the correlation between two spatial processes. *Biometrics* **49**:305–314.
- Environmental Systems Research Institute (ESRI). 1982–2002. ArcGIS. 8.2. ESRI, Redlands, California.
- Environmental Systems Research Institute (ESRI). 1992–1999. ArcView GIS. 3.2. ESRI, Redlands, California.
- Fielding, A. H., and P. F. Haworth. 1995. Testing the generality of bird-habitat models. *Conservation Biology* **9**:1466–1481.
- Finton, A. D. 1998. Succession and plant community development in pitch pine-scrub oak barrens of the glaciated northeast United States. M.S. thesis. University of Massachusetts, Amherst.
- Flather, C. H., K. R. Wilson, D. J. Dean, and W. C. McComb. 1997. Identifying gaps in conservation networks: of indicators and uncertainty in geographic-based analyses. *Ecological Applications* **7**:531–542.
- Grand, J., and S. A. Cushman. 2003. A multi-scale analysis of species-environment relationships: breeding birds in a pitch pine-scrub oak (*Pinus rigida-Quercus ilicifolia*) community. *Biological Conservation* **112**:307–317.
- Grand, J., and M. Mello. 2004. A multi-scale analysis of species-environment relationships: rare moths in a pitch-pine scrub oak (*Pinus rigida-Quercus ilicifolia*) community. *Biological Conservation* (in press).
- Grzenda, M., and A. Jones. 2002. Avian species of conservation interest in MA. *Massachusetts Audubon Society, Lincoln*. Available from http://www.massaudubon.org/Birds_&Beyond/IBA/bird_data/cons-int_ma.html (accessed May 2002).
- Guisan, A., and N. E. Zimmermann. 2000. Predictive habitat distribution models in ecology. *Ecological Modelling* **135**:147–186.
- Gutzwiller, K. J., and W. C. J. Barrow. 2001. Bird-landscape relations in the Chihuahuan Desert: coping with uncertainties about predictive models. *Ecological Applications* **11**:1517–1532.
- Hosmer, D. W., Jr., and S. Lemeshow. 2000. *Applied logistic regression*. Wiley, New York.
- Illera, J. C. 2001. Habitat selection by the Canary Islands stonechat (*Saxicola dacotiae*) (Meade-Waldo, 1889) in Fuerteventura Island: a two-tier habitat approach with implications for its conservation. *Biological Conservation* **97**:339–345.
- Kotliar, N. B., and J. A. Wiens. 1990. Multiple scales of patchiness and patch structure: a hierarchical framework for the study of heterogeneity. *Oikos* **59**:253–260.
- Landis, J. R., and G. C. Koch. 1977. The measurement of observer agreement for categorical data. *Biometrics* **33**:159–174.
- Lee, M., L. Fahrig, K. Freemark, and D. J. Currie. 2002. Importance of patch scale vs landscape scale on selected forest birds. *Oikos* **96**:110–118.
- Legendre, P. 2000. Modified t-test for a Pearson correlation coefficient. University of Montreal, Montreal. Available from <http://www.fas.umontreal.ca/biol/legendre> (accessed September 2003).
- Lombard, A. T. 1995. The problems with multi-species conservation: do hotspots, ideal reserves and existing reserves coincide? *South African Journal of Zoology* **30**:145–163.
- Maddock, A., and M. A. Du Plessis. 1999. Can species data only be appropriately used to conserve biodiversity? *Biodiversity and Conservation* **8**:603–615.
- Margules, C. R., M. P. Austin, D. Mollison, and F. Smith. 1994. Biological models for monitoring species decline: construction and use of databases. *Philosophical Transactions of the Royal Society of London Series B* **344**:69–75.
- Mazerolle, M. J., and M. A. Villard. 1999. Patch characteristics and landscape context as predictors of species presence and abundance: a review. *Ecoscience* **6**:117–124.
- McCaffrey, J. 2001. ORV abuse rampant in state parks system. *The Massachusetts Sierran* **8**:1.
- McGarigal, K., and W. C. McComb. 1995. Relationship between landscape structure and breeding birds in the Oregon Coast Range. *Ecological Monographs* **65**:235–260.
- McGarigal, K., S. A. Cushman, and S. Stafford. 2000. *Multivariate statistics for wildlife ecology research*. Springer-Verlag, New York.
- McGarigal, K., S. A. Cushman, M. C. Neel, and E. Ene. 2002. FRAGSTATS: spatial pattern analysis program for categorical maps. Version 3.2. University of Massachusetts, Amherst. Available from <http://www.umass.edu/landeco/research/fragstats/fragstats.html> (accessed May 2002).
- Mello, M. J., R. J. Nagel, and T. Ruehli. 1998. Inventory of state-listed Lepidoptera at the Camp Edwards Training Site, year II. Final report to the Army National Guard, Camp Edwards Training Site. The Lloyd Center for Environmental Studies, Dartmouth, Massachusetts.
- Mello, M. J., M. Aliberti, S. Galusha, K. Gerber, F. Hohn, A. Lawrence, D. Luers, R. J. Nagel, T. Ruehli, and B. Stephenson. 1999. Inventory of state-listed Lepidoptera and other insects at the Massachusetts Military Reservation 1996–1998. Final report to the Massachusetts Army National Guard, Camp Edwards Training Site. The Lloyd Center for Environmental Studies, Dartmouth, Massachusetts.
- Motzkin, G., D. Foster, A. Allen, J. Harrod, and R. Boone. 1996. Controlling site to evaluate history: vegetation patterns of a New England sand plain. *Ecological Monographs* **66**:345–365.
- Murphy, D. D., and B. A. Wilcox. 1986. Butterfly diversity in natural habitat fragments: a test of the validity of vertebrate based management. Pages 287–292 in J. Verner, M. L. Morrison, and C. J. Ralph, editors. *Wildlife 2000: modeling habitat relationships of terrestrial vertebrates*. University of Wisconsin Press, Madison.

- Ozanne, C. M. P., C. Hambler, A. Foggo, and M. R. Speight. 1997. The significance of edge effects in the management of forests for invertebrate biodiversity. Pages 534–550 in N. E. Stork, J. Adis, and R. K. Didham, editors. *Canopy arthropods*. Chapman & Hall, London.
- Paton, P. W. C. 1994. The effect of edge on avian nest success: how strong is the evidence? *Conservation Biology* **8**:17–26.
- Pearson, D. L., and S. S. Carroll. 1998. Global patterns of species richness: spatial models for conservation planning using bioindicator and precipitation data. *Conservation Biology* **12**:809–821.
- Pearson, D. L., and S. S. Carroll. 1999. The influence of spatial scale on cross-taxon congruence patterns and prediction accuracy of species richness. *Journal of Biogeography* **26**:1079–1090.
- Pearson, D. L., and F. Cassola. 1992. World-wide species richness patterns of tiger beetles (Coleoptera: Cicindelidae): indicator taxon for biodiversity and conservation studies. *Conservation Biology* **6**:376–391.
- Polasky, S., J. D. Camm, A. R. Solow, B. Csuti, D. White, and R. Ding. 2000. Choosing reserve networks with incomplete species information. *Biological Conservation* **94**:1–10.
- Prendergast, J. R., and B. C. Eversham. 1997. Species richness covariance in higher taxa: empirical tests of the biodiversity indicator concept. *Ecography* **20**:210–216.
- Prendergast, J. R., R. M. Quinn, J. H. Lawton, B. C. Eversham, and D. W. Gibbons. 1993. Rare species, the coincidence of diversity hotspots and conservation strategies. *Nature* **365**:335–337.
- Ricketts, T. H., E. Dinerstein, D. M. Olson, and C. Loucks. 1999. Who's where in North America? *BioScience* **49**:369–381.
- Ricketts, T. H., G. C. Daily, P. R. Ehrlich, and J. P. Fay. 2001. Country-side biogeography of moths in a fragmented landscape: biodiversity in native and agricultural habitats. *Conservation Biology* **15**:378–388.
- Ricketts, T. H., G. C. Daily, and P. R. Ehrlich. 2002. Does butterfly diversity predict moth diversity? Testing a popular indicator taxon at local scales. *Biological Conservation* **103**:361–370.
- SAS Institute. 1999. SAS onlinedoc. Version 8. SAS Institute, Cary, North Carolina. Available from: <http://v8doc.sas.com> (accessed September 2003).
- SAS Institute. 1999–2000. SAS. Release 8.01. SAS Institute, Cary, North Carolina.
- Saab, V. 1999. Importance of spatial scale to habitat use by breeding birds in riparian forests: a hierarchical analysis. *Ecological Applications* **9**:135–151.
- Sætersdal, M., J. M. Line, and H. J. B. Birks. 1993. How to maximize biological diversity in nature-reserve selection: vascular plants and breeding birds in deciduous woodlands, western Norway. *Biological Conservation* **66**:131–138.
- Schweitzer, D. F., and T. J. Rawinski. 1988. Northeastern pitch pine/scrub oak barrens. Eastern Heritage Task Force, The Nature Conservancy, Boston.
- Scott, J. M., et al. 1993. Gap analysis: a geographic approach to protection of biological diversity. *Wildlife Monographs* **123**.
- Stauffer, H. B., C. J. Ralph, and S. L. Miller. 2002. Incorporating detection uncertainty into presence-absence surveys for Marbled Murrelet. Pages 357–365 in J. M. Scott, P. J. Heglund, M. L. Morrison, J. B. Haufler, M. G. Raphael, W. A. Wall, and F. B. Samson, editors. *Predicting species occurrences: issues of accuracy and scale*. Island Press, Washington, D.C.
- Swengel, S. R., and A. B. Swengel. 1999. Correlations in abundance of grassland songbirds and prairie butterflies. *Biological Conservation* **90**:1–11.
- Tardif, B., and J. L. DesGranges. 1998. Correspondence between bird and plant hotspots of the St. Lawrence River and influence of scale on their location. *Biological Conservation* **84**:53–63.
- Weaver, J. C. 1995. Indicator species and scale of observation. *Conservation Biology* **9**:939–942.
- Young, M. 1997. *The natural history of moths*. T & A.D. Poyser, London.

Appendix 1. Habitat-type classification system and landscape, class, and patch variables^a measured with FRAGSTATS.

<i>Class and variable</i>	<i>Description</i>
Habitat type (class)	
scrub oak (SO)	areas of predominantly scrub oak, usually within a larger pitch pine–scrub oak thicket; few scattered pitch pines present as overstory; includes heathlands dominated by ericaceous shrubs
scrub oak frost pocket (SOFP)	depressions of predominantly scrub oak with few scattered pitch pines present as overstory
immature pitch pine (IPP)	areas of small pitch pine (0–6 meters tall) within pitch pine barrens or thickets
pitch pine–scrub oak forest (PPSOF)	areas of predominantly pitch pine (6–18 meters tall), with a canopy closure of approximately 60% or more and a scrub oak understory; includes mixed stands with at least approximately 20% pitch pine present
pitch pine–scrub oak thicket (PPSOT)	areas with a sparse canopy of pitch pine (6–18 meters tall) and dense understory of scrub oak; 10–60% canopy
hardwoods (HW)	areas of predominately hardwood trees, sometimes with a small percentage of pitch pine
immature hardwoods (IHW)	areas of predominately immature hardwood trees
mixed woods (MW)	areas of mixed hardwoods and conifers; includes stands of predominately conifers other than pitch pine
native grassland (G1)	areas dominated by native grasses in “natural” state; includes grassy areas within power lines and right-of-ways
cultural grassland (G2)	disturbed areas dominated by grasses and other herbaceous vegetation; includes abandoned fields, pastures, and previously cleared areas
power line (PL)	power lines and other right-of-ways that are maintained and wide enough to delineate on aerial photos
developed land/nonvegetated (DL/NV)	land built on, paved, or cleared and in the process of being developed; includes maintained lawns and greens (golf courses); also disturbed or sandy areas that lack vegetation
agricultural land (AL)	farmland that is being used intensively for crops; includes orchards and cranberry bogs
water/wetlands (W)	all wetlands large enough to delineate on aerial photos; includes permanent open water; forested, shrub, and emergent wetlands; and vernal pools
Landscape-level variables^b	
patch density (PD)	number of patches per unit area
edge density (ED)	edge length per unit area
largest patch index (LPI)	percentage of total landscape area comprised by the largest patch
mean patch area (area)	average area of all patches within the landscape
area-weighted mean radius of gyration (gyrate AM)	correlation length—a measure of landscape connectedness
mean radius of gyration (gyrate)	a measure of patch extent affected by both patch size and patch compaction
mean shape index (shape)	a measure of patch shape complexity
disjunct core area density ^c (DCAD)	sum of disjunct core areas contained within each patch, divided by landscape area
mean core area index ^c (CAI)	average core area of patches as a percentage of patch area
contrast weighted edge density (CWED)	sum of lengths of all edge segments weighted by amount of contrast across patches
contagion	aggregation of patch types; amount of dispersion and interspersion of types
cohesion	physical connectedness of patch types
patch richness density (PRD)	number of different patch types divided by total landscape area
Simpson's diversity index (SIDI)	probability that any pixels selected at random would be different types
Simpson's evenness index (SIEI)	distribution of area among patch types
Class-level variables^d	
percentage of landscape (PLAND)	percentage of the landscape in specified class
patch density (PD)	patch density of specified class within the landscape
mean patch area (area)	average area of all patches of specified class within the landscape
Patch-level variables^e	
patch area (area)	area of patch
radius of gyration (gyrate)	patch radius of gyration
perimeter-area ratio (PARATIO)	ratio of patch perimeter to area; a simple measure of patch shape complexity
fractal dimension (FRACT)	reflects shape complexity across a range of spatial scales
core area ^c (core)	area in the patch greater than the specified depth-of-edge distance from the perimeter
edge contrast (EDGECON)	user-specified amount of contrast between patch edge and surrounding landscape

^aVariable descriptions from McGarigal et al. (2002).^bIncludes all habitat types within a specified radius surrounding each sampling point.^cEdge depth was set at 50 m for birds and 30 m for moths based on the range of edge effects for different taxa presented in Paton (1994) and Ozanne et al. (1997).^dIncludes only the specified focal habitat type within the landscape. Calculated for the following habitat types: DL/NV, G2, MW, PL (moths only), PPSOF, PPSOT, SO, SOFP, W^eIncludes only the patch within which the sampling point was located.

Appendix 2. Logistic-regression model parameters and associated statistics for bird and moth species models.

Species	Variable ^a	Scale	ML est. ^b	SE of ML est.	p	Odds ratio ^c
Whip-poor-will (<i>Caprimulgus vociferous</i>)	intercept		-12.55	6.05		
	PLAND-SOFP	300	1.44	0.52	0.005	4.22
	PD-MW	150	0.14	0.07	0.03	1.15
	PRD	1200	2.84	1.86	0.13	17.15
Purple Finch (<i>Carpodacus purpureus</i>)	intercept		-0.00001	0.85		
	PLAND-MW	900	-0.08	0.03	0.02	0.93
Black-billed Cuckoo (<i>Coccyzus erythrophthalmus</i>)	intercept		204.40	98.52		
	PLAND-SO ^d	150	0.49	0.23	0.03	1.63
	PD-DL	150	0.07	0.06	0.26	1.07
	PD-MW	600	-3.32	1.53	0.03	0.04
	contagion ^d	600	-45.72	21.80	0.04	<0.001
Eastern Wood-Pewee (<i>Contopus virens</i>)	SIEI	600	-18.57	11.85	0.12	<0.001
	intercept		-0.53	0.90		
	PLAND-DL	900	-0.10	0.05	0.04	0.91
	PD-SO	300	-0.34	0.16	0.03	0.72
Northern Bobwhite (<i>Colinus virginianus</i>)	PD-MW	1200	1.54	0.85	0.07	4.67
	intercept		-10.01	5.77		
	PLAND-G2	900	0.16	0.17	0.37	1.17
	CWED	150	-0.03	0.01	0.02	0.97
Prairie Warbler (<i>Dendroica discolor</i>)	FRACT	patch	8.60	5.05	0.09	>999.99
	intercept		-19.44	7.45		
	PLAND-MW	300	-0.05	0.02	0.02	0.96
Chestnut-sided Warbler (<i>Dendroica pennsylvanica</i>)	PLAND-DL	300	0.12	0.06	0.06	1.13
	area-SO	600	0.28	0.12	0.02	1.33
	area-PPSOT	1200	0.06	0.04	0.10	1.06
	shape	900	10.13	3.90	0.009	>999.99
	intercept		61.89	43.25		
	PLAND-PPSOF	300	0.31	0.21	0.13	1.37
Gray Catbird (<i>Dumetella carolinensis</i>)	area-MW	150	2.02	1.46	0.17	7.56
	area-SO ^d	150	4.12	2.93	0.16	61.50
	shape	1200	-40.40	27.29	0.14	<0.001
	intercept		-474.50	239.20		
	ED	1200	1.68	0.79	0.03	5.37
	core	patch	-0.06	0.03	0.05	0.94
Baltimore Oriole (<i>Icterus galbula</i>)	LPI	900	1.24	0.63	0.05	3.44
	PLAND-SO	600	1.91	1.03	0.06	6.74
	shape	150	232.10	120.30	0.05	>999.99
	PD-DL	150	2.90	1.63	0.07	18.16
	area ^d	patch	6.22	3.52	0.08	502.40
	area	150	19.75	10.13	0.05	>999.99
	gyrate	150	-1.18	0.63	0.06	0.31
	intercept		-0.34	1.18		
	PD-DL	150	-0.15	0.08	0.06	0.87
	PD-MW	600	3.26	1.24	0.009	25.94
Black-and-white Warbler (<i>Mniotilta varia</i>)	intercept		-12.09	7.53		
	PLAND-SO ^d	1200	1.16	0.51	0.02	3.19
	PD-PPSOT	900	-1.57	0.87	0.07	0.21
	area-MW	900	0.06	0.03	0.02	1.07
	CWED	150	-0.05	0.02	0.009	0.95
	CAI	600	-0.37	0.15	0.02	0.69
	SIDI	900	31.18	13.84	0.02	>999.99
Great Crested Flycatcher (<i>Myiarchus crinitus</i>)	intercept		-6.28	1.78		
	PD-MW	900	2.24	0.81	0.006	9.41
Hairy Woodpecker (<i>Picoides villosus</i>)	intercept		-2.43	2.06		
	PLAND-PPSOT	150	0.23	0.11	0.03	1.26
	PD-SO	300	-2.27	1.53	0.14	0.10
	area-SOFP	1200	-12.56	8.05	0.12	<0.001
	PRD	300	0.65	0.36	0.07	1.19
Scarlet Tanager (<i>Piranga olivacea</i>)	DCAD	600	-1.08	0.51	0.03	0.34
	intercept		-13.07	6.16		
	PLAND-MW	1200	0.28	0.12	0.02	1.32
	PLAND-SO	1200	0.22	0.10	0.03	1.25
Ovenbird (<i>Seiurus aurocapillus</i>)	PD-PPSOT ^d	900	-0.87	0.37	0.02	0.42
	DCAD	150	-0.39	0.24	0.11	0.68
	intercept		-224.30	94.73		
	PD-MW ^d	150	0.70	0.22	0.001	2.01
	PD-SO	900	-2.43	1.44	0.09	0.09
	PD-PPSOF	300	0.30	0.19	0.12	1.35
	cohesion	300	2.18	0.97	0.02	8.87
gyrate AM	600	-0.07	0.03	0.01	0.94	
contagion	600	0.43	0.16	0.007	1.54	

continued

Appendix 2. (continued).

Species	Variable ^a	Scale	ML est. ^b	SE of ML est.	p	Odds ratio ^c
Field Sparrow (<i>Spizella pusilla</i>)	intercept		-0.93	0.73		
	area-G2	1200	0.14	0.08	0.07	1.15
	area-SO	600	0.19	0.08	0.02	1.20
Brown Thrasher (<i>Toxostoma rufum</i>)	area-MW	600	-0.08	0.03	0.01	0.92
	intercept		-3.51	0.86		
	PLAND-SO	900	0.20	0.06	0.0006	1.22
Eastern Kingbird (<i>Tyrannus tyrannus</i>)	area-DL	300	0.50	0.27	0.06	1.65
	intercept		1.61	0.93		
	PD-SO	150	0.10	0.06	0.09	1.11
Barrens daggermoth (<i>Acronicta albarufa</i>)	PD-G2	900	3.64	2.09	0.08	38.10
	area-MW	600	-0.07	0.03	0.008	0.93
	CAI ^d	150	-0.56	0.32	0.08	0.57
	intercept		14.65	5.87		
Spiny oakworm (<i>Anisota stigma</i>)	contagion	150	-0.14	0.06	0.02	0.87
	area-MW	1200	-0.05	0.02	0.03	0.95
	area-G2	1200	-1.06	5.18	0.84	0.35
	intercept		-7.87	3.77		
Blueberry sallow (<i>Apbaretra dentata</i>)	PLAND-MW	150	0.11	0.06	0.07	1.12
	area-MW ^d	150	-2.86	1.55	0.06	0.06
	area-SO ^d	900	1.54	0.73	0.03	4.67
	intercept		1375.40	632.10		
Straight lined mallow moth (<i>Bagisara rectifascia</i>)	CWED	900	-0.40	0.22	0.07	0.67
	cohesion	1200	-13.68	6.28	0.03	<0.001
	intercept		-13.74	4.53		
Gerhard's underwing moth (<i>Catocala berodias gerhardi</i>)	PRD	1200	5.83	1.98	0.003	341.63
	PLAND-PPSOT	150	0.07	0.04	0.05	1.07
	intercept		4.73	3.04		
	PLAND-PPSOF	900	-0.17	0.08	0.03	0.84
Melsheimer's sack-bearer (<i>Cicinnus melsheimeri</i>)	area-SOFP ^d	600	1.90	0.84	0.02	6.70
	area-PPSOT	1200	0.42	0.19	0.03	1.52
	intercept		-8.06	3.94		
	PRD	300	0.37	0.24	0.12	1.44
Coastal plain euchlaena (<i>Euchlaena madusaria</i>)	PLAND-SOFP	300	1.68	0.76	0.03	5.35
	intercept		12.88	4.89		
	gyrate AM	1200	-0.02	0.01	0.01	0.98
Coastal barrens buck moth (<i>Hemileuca maia maia</i>)	PLAND-MW	900	-0.08	0.03	0.01	0.92
	intercept		-22.23	9.94		
	gyrate	900	0.12	0.06	0.03	1.13
Pine barrens itame (<i>Itame</i> sp. 1 nr. <i>inextricata</i>)	PLAND-PPSOT	900	0.53	0.26	0.04	1.69
	intercept		83.99	30.30		
	shape	150	-14.37	6.59	0.03	<0.001
	gyrate AM ^d	1200	-11.00	4.18	0.009	<0.001
Coastal swamp metarranthis (<i>Metarranthis pilosaria</i>)	PLAND-SO	600	0.12	0.04	0.005	1.13
	intercept		2.10	2.45		
	gyrate	150	-0.08	0.05	0.09	0.93
Pink sallow moth (<i>Psectraglaea carnosa</i>)	PLAND-SO	150	0.03	0.01	0.03	1.03
	intercept		-7.32	2.34		
	DCAD	900	0.82	0.29	0.005	2.27

^aVariable names followed by habitat-type abbreviation are class level; all others are landscape or patch level, as designated in scale column. Variables are defined in Appendix 1.

^bMaximum-likelihood estimate.

^cChange in probability of presence given one unit change in the independent variable (Hosmer & Lemeshow 2000).

^dVariable was log transformed.

Appendix 3. Classification tables^a and Cohen's Kappa (K) statistics for bird and moth logistic regression models.

Species	Cut point ^b	Correct ^c		Incorrect ^d		Total correct (%)	Sensitivity ^e (%)	Specificity ^f (%)	False ^g		K ^h
		present	absent	present	absent				+	- (%)	
Purple Finch	0.50	0	51	2	5	87.9	0.0	96.2	100.0	8.9	0.38
	0.62	0	53	0	5	91.4	0.0	100.0	—	8.6	0.48
Whip-poor-will	0.50	1	49	3	5	86.2	16.7	94.2	75.0	9.3	0.43
	0.30	4	49	3	2	91.4	66.7	94.2	42.9	3.9	0.63
Black-billed Cuckoo	0.50	4	47	3	4	87.9	50.0	94.0	42.9	7.8	0.59
	0.34	5	47	3	3	89.7	62.5	94.0	37.5	6.0	0.64
Eastern Wood-Pewee	0.50	21	20	9	8	70.7	72.4	69.0	30.0	28.6	0.55
Northern Bobwhite	0.50	4	38	3	13	72.4	23.5	92.7	42.9	25.5	0.47
	0.53	4	39	2	13	74.1	23.5	95.1	33.3	25.0	0.49
Prairie Warbler	0.50	19	27	8	4	79.3	82.6	77.1	29.6	12.9	0.65
	0.27	21	26	9	2	81.0	91.3	74.3	30.0	7.1	0.68
Chestnut-sided Warbler	0.50	5	50	1	2	94.8	71.4	98.0	16.7	3.8	0.78
Gray Catbird	0.50	37	11	4	6	82.8	86.0	73.3	9.8	35.3	0.64
	0.04	39	10	5	4	84.5	90.7	66.7	11.4	28.6	0.66
Baltimore Oriole	0.50	51	3	3	1	93.1	98.1	50.0	5.6	25.0	0.67
	0.13	52	2	4	0	93.1	100.0	33.3	7.1	0.0	0.64
Black-and-white Warbler	0.50	23	25	3	7	82.8	76.7	89.3	11.5	21.9	0.71
Great Crested Flycatcher	0.50	2	53	0	3	94.8	40.0	100.0	0.0	5.4	0.68
Hairy Woodpecker	0.50	7	44	3	4	87.9	63.6	93.6	30.0	8.3	0.67
Scarlet Tanager	0.50	7	44	3	4	87.9	63.6	93.6	30.0	8.3	0.67
	0.31	8	43	4	3	87.9	72.7	91.5	33.3	6.5	0.68
Ovenbird	0.50	31	16	7	4	81.0	88.6	69.6	18.4	20.0	0.67
	0.27	33	14	9	2	81.0	94.3	60.9	21.4	12.5	0.66
Field Sparrow	0.50	8	39	3	8	81.0	50.0	92.9	27.3	17.0	0.60
	0.40	11	37	5	5	82.8	68.8	88.1	31.3	11.9	0.65
Brown Thrasher	0.50	9	40	4	5	84.5	64.3	90.9	30.8	11.1	0.65
	0.38	11	39	5	3	86.2	78.6	88.6	31.3	7.1	0.69
Eastern Kingbird	0.50	16	31	5	6	81.0	72.7	86.1	23.8	16.2	0.66
Barrens daggermoth	0.50	22	12	3	1	89.5	95.7	80.0	12.0	7.7	0.80
Spiny oakworm	0.50	18	14	4	2	84.2	90.0	77.8	18.2	12.5	0.73
Blueberry sallow	0.76	17	17	1	3	89.5	85.0	94.4	5.6	15.0	0.81
	0.50	26	7	2	3	86.8	89.7	77.8	7.1	30.0	0.70
Straight-lined mallow moth	0.50	10	24	2	2	89.5	83.3	92.3	16.7	7.7	0.78
	0.61	10	25	1	2	92.1	83.3	96.2	9.1	7.4	0.83
Gerhard's underwing moth	0.50	16	17	3	2	86.8	88.9	85.0	15.8	10.5	0.77
	0.74	16	19	1	2	92.1	88.9	95.0	5.9	9.5	0.85
Melsheimer's sack-bearer	0.50	4	30	1	3	89.5	57.1	96.8	20.0	9.1	0.69
Coastal plain euchaena	0.42	5	30	1	2	92.1	71.4	96.8	16.7	6.3	0.76
	0.50	10	22	3	3	84.2	76.9	88.0	23.1	12.0	0.70
Coastal barrens buck moth	0.62	10	24	1	3	89.5	76.9	96.0	9.1	11.1	0.79
	0.50	12	21	2	2	89.2	85.7	91.3	14.3	8.7	0.79
Pine barrens itame	0.36	13	21	2	1	91.9	92.9	91.3	13.3	4.5	0.84
	0.50	10	23	2	3	86.8	76.9	92.0	16.7	11.5	0.74
Coastal swamp metarranthis	0.43	11	23	2	2	89.5	84.6	92.0	15.4	8.0	0.79
	0.50	1	29	2	6	78.9	14.3	93.5	66.7	17.1	0.43
Pink sallow moth	0.33	3	29	2	4	84.2	42.9	93.5	40.0	12.1	0.56
	0.50	5	26	2	5	81.6	50.0	92.9	28.6	16.1	0.60
	0.40	6	26	2	4	84.2	60.0	92.9	25.0	13.3	0.65

^a Prior probability is sample proportion of occupied sites.
^b Cut point = 0.5 (first row), cut point = optimal (second row). Optimal cut point is that associated with the highest total correct classification rate. In the event that more than one cut point resulted in the same correct classification rate, the one with the highest sensitivity was selected. When there were several cut points with the same correct classification rate and sensitivity, the mean of those cut points was selected. When only one cut point is reported, optimal = 0.5.
^c Number of sites correctly classified as present and absent.
^d Number of sites incorrectly classified as present and absent.
^e Proportion of sites with species present that were classified correctly.
^f Proportion of sites with species absent that were classified correctly.
^g Formulas for calculating false positive and false negative rates are available in the SAS online documentation (SAS Institute 1999).
^h Kappa ranges from 0 to 1; 0 indicates no improvement over chance, 1 indicates perfect assignment (McGarigal et al. 2000)

