Developing Habitat-based Landbird Models as Planning Tools for the Golden Gate National Recreation Area and the Point Reyes National Seashore

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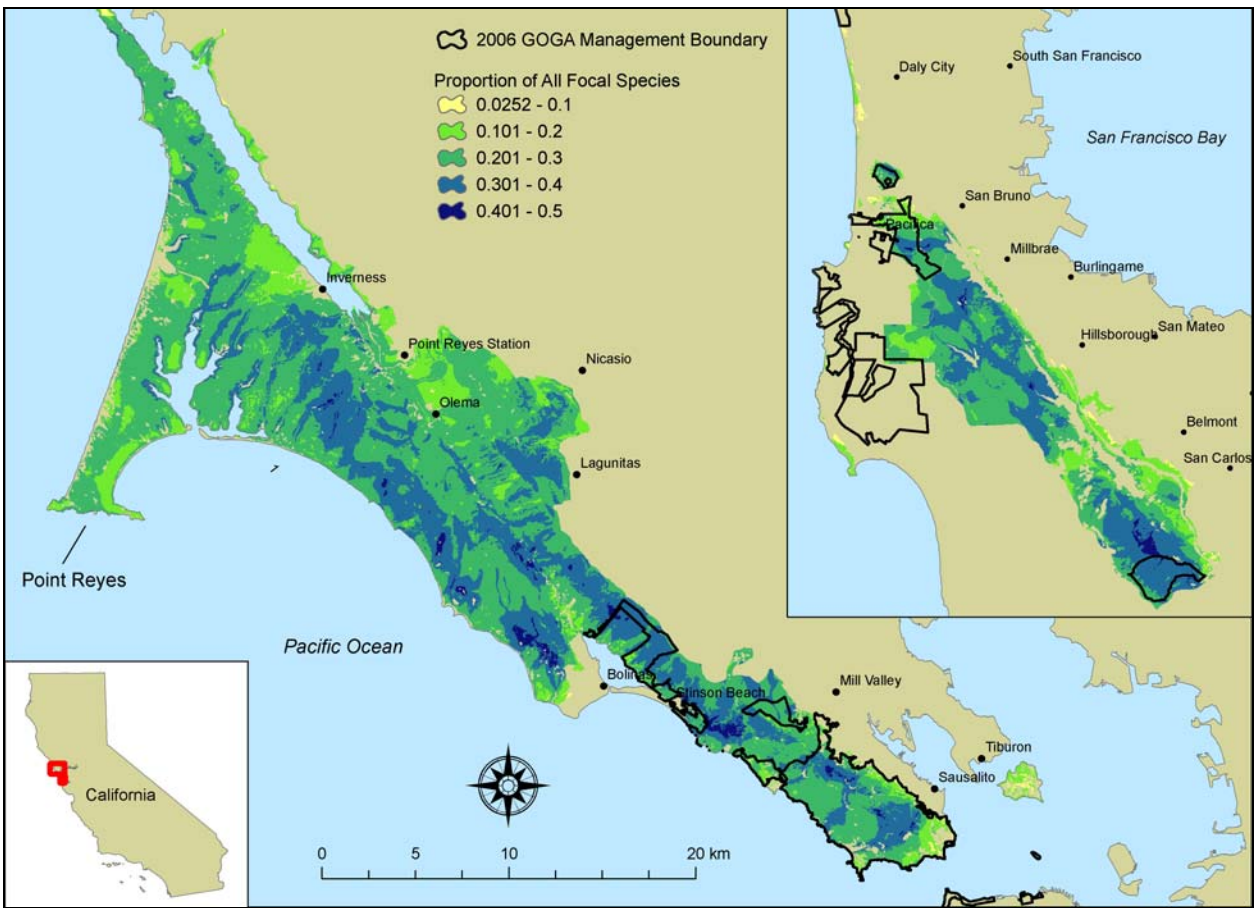

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EXECUTIVE SUMMARY

Using comprehensive avian survey data (1996-2005) and data layers derived primarily from a National Park Service vegetation map, we developed spatial models of species distribution and diversity within areas managed by the Golden Gate National Recreation Area (GOGA) and the Point Reyes National Seashore. Our objective was to assist GOGA and the Golden Gate National Parks Conservancy (GGNPC) with resource planning and management using landbirds as indicators. We used a focal species approach to select appropriate avian metrics, including the occurrence of disturbance-sensitive species, and species richness of focal species by habitat (e.g., riparian). Generalized additive models were used to represent non-linear relationships between vegetation and landscape characteristics and the distribution of avian species. Models were used to develop spatial predictions of species occurrence and diversity within the parks. Combining models for different management-sensitive species resulted in four different spatial representations of priority areas, each associated with different management goals.

Model assessment using a subset of the data indicated strong predictive power for most models. Across the species and metrics examined, we found that landscape-level (within a 1-km radius) vegetation characteristics were generally more important predictors than local vegetation type (at the 30-m pixel level), although the latter was an essential component of each model. General vegetation classes (e.g., scrub, riparian) performed as well as or better than specific vegetation alliances in predicting species occurrence and diversity. At the local level, the presence of hardwood vegetation (primarily oak and bay trees) was a positive predictor of many species, while at the landscape level, percent riparian habitat was an important factor. Effects of anthropogenic factors such as non-native vegetation and trail density were variable and merit further study.

The spatial predictions generated by this study may be used by GOGA and GGNPC to identify priority areas for habitat conservation and potential habitat restoration and enhancement. They may also be used to determine the level and extent of possible impacts of selected planned management activities on landbirds. They are intended to be scaleable, and may be used to address management questions at a variety of different spatial scales, but should be used primarily as a filter to identify potential target areas that may be investigated more thoroughly with site visits and surveys.

INTRODUCTION

Land mangers must constantly make important decisions based on little or no scientific information. Their tasks are often complex, requiring the simultaneous consideration of multiple competing natural, cultural and recreational resource requirements. To guide and support these decisions, managers benefit from scientifically-based, appropriately scaled syntheses of available information, which may be referred to as decision support tools.

With respect to wildlife, several types of tools are available for land managers, including the California Department of Fish & Game's Wildlife Habitat Relationship (WHR) system (http://www.dfg.ca.gov/whdab/html/cwhr.html). The WHR allows the user to select general habitat types including some characteristics of those habitats (e.g., small trees) within various predefined areas with an output of predicted species occurrence lists. With appropriate geographic information system (GIS)-based habitat layers, WHR predictions can also be made spatially explicit, and can provide reasonably accurate predictions for conservation planning at the ecoregional scale (Edwards et al. 1996). For North American birds, the US Geological Survey (USGS) has developed an online tool (http://umesc-ims01.er.usgs.gov/website/new_bird/viewer.htm) that summarizes both land cover and bird survey data at a variety of spatial scales. California Partners in Flight also has a tool available online that provides site-specific bird lists (http://cain.nbii.gov/prbo/calpifmap/livemaps/). While these are all good systems, they are either most useful at broad spatial scales, or the information provided is rudimentary. WHR is based on expert opinion compiled across species' ranges, while the USGS system is based on Breeding Bird Survey routes, of which there are only two in Marin County. Thus, these systems have limited potential for extrapolation and scaling down to locally relevant planning units.

Species distribution models

When adequate survey data are available, spatial models of species habitat associations and spatial predictions of species occurrence ("species distribution models" or "habitat occupancy models") can serve as useful decision support tools for wildlife managers to identify and rank potential habitat areas, in terms of research, land management, and conservation priorities. While GIS-based, empirical species distribution models have been developed at broad spatial scales for over a decade (Lindenmayer et al. 1991, Pereira and Itami 1991, Aspinall and Veitch 1993), the recent availability of high-resolution aerial photography and satellite imagery, and resulting detailed vegetation classification maps, have improved our ability to develop fine-scale models of species occurrence for local and regional conservation purposes (Ozesmi and Mitsch 1997, Loyn et al. 2001, Gibson et al. 2004). At the landscape scale, species distribution models are generally based on habitat variables such as vegetation cover type/structure, and local topographic variation, rather than general land cover classes and broad-scale climate factors such as temperature and precipitation. Thus they can provide significant improvements in predictive power over a simple habitat suitability index or wildlife habitat relationship model, which is often based on broad-scale habitat associations that are not necessarily applicable throughout a species range. Individual species distributional models can be combined in an index of multi-species habitat value (typically overall or focal species richness).

Project need and opportunity

Within the next five years, the Golden Gate National Recreation Area (GOGA) will undertake a number of large-scale planning and implementation efforts, including a new General Management Plan, the Marin Headlands and Fort Baker Transportation Plan, the Coastal Trail Corridor Enhancement Project, the Fire Management Plan, and numerous park stewardship projects. Determining possible impacts, best management practices, and habitat enhancement opportunities for special status and non-listed wildlife species will be a critical element of these planning and implementation strategies.

GOGA has a detailed vegetation map, developed in conjunction with the Point Reyes National Seashore (PORE), and classified to the alliance and association levels according to the Manual of California Vegetation (Schirokauer et al. 2003). Further, a significant amount of landbird data also exists, including species abundance and richness data within a large number of watersheds. However, surveys have not been conducted in all of the Park's watersheds, and very limited surveys have been conducted in the Park's proposed acquisitions and newly acquired lands.

Objectives

Our primary objective was to build predictive spatial models based on National Park Service (NPS) vegetation data and other GIS data layers, as well as PRBO Conservation Science (PRBO) avian survey data, to predict landbird distribution and diversity within the park. The models should assist GOGA and the Golden Gate National Parks Conservancy (GGNPC) by meeting the following objectives:

1. Identify habitat types and landscape characteristics that support the greatest diversity and abundance of avian species;
2. Identify priority areas for habitat conservation and potential habitat restoration and enhancement; and
3. Determine the level and extent of possible landbird impacts and habitat enhancement opportunities for selected planned management.

METHODS

Study area

Predictive models were developed for the area covered by the National Park Service vegetation map (Schirokauer et al. 2003), which includes PORE, GOGA (1995 legislative boundary), and a number of surrounding public and private land holdings (Figures 1, 2). Within this area, PRBO Conservation Science (PRBO) has collected extensive long-term avian survey data as part of several inventory and monitoring contracts with NPS (PORE and GOGA). We used data from 675 point count locations across 65 transects (Appendix 1).

Point count transect establishment was variable. Sometimes it was focused on an area where the NPS was interested in collecting intensive bird data (e.g., Redwood Creek), but most frequently, transect starting points were based on a randomly generated point stratified by habitat. Regardless, the end result was excellent spatial and habitat coverage (Figure 1, Table 1).

Table 1. Number of PRBO point count locations by number of years surveyed and vegetation class / habitat type.

Vegetation Class	1 year	2 years	3 years	6 years	7 years	8 years	9 years	Total
Grassland	45	79	50	6	3	2	6	191
Riparian	5	27	22	3	0	4	33	94
Conifer	101	26	45	0	8	4	0	184
Scrub	67	15	34	0	4	1	4	125
Wetland	2	7	10	2	1	0	1	23
Hardwood	37	11	3	0	0	2	5	58
Total	257	165	164	11	16	13	49	675

Field data collection

Avian surveys were conducted between 1996 and 2005 for multiple NPS efforts (e.g., Gardali and Geupel 1999a, Gardali and Geupel 1999b, Gardali et al. 1999, Holmes et al. 1999, Flannery et al. 2001, Hammond and Geupel 2001, Humple and Gardali 2005). Thus some survey points had multiple years of data collection while others had only one. At each survey point we conducted 5-minute, 50-m fixed-radius point counts, following standardized protocols (Ralph et al. 1993, Ralph et al. 1995, Gardali et al. 2006). We conducted all counts during the peak passerine breeding season (May through July). Survey stations were always at least 150 m apart but usually at least 200 m apart. Biologists familiar with the songs and calls of the species in the area and trained in distance estimation conducted all surveys. We conducted surveys from within 30 minutes after local sunrise until approximately four hours later, and did not conduct them in excessively windy or rainy conditions. For modeling purposes, we used only birds that were detected within 50 m of the observer.

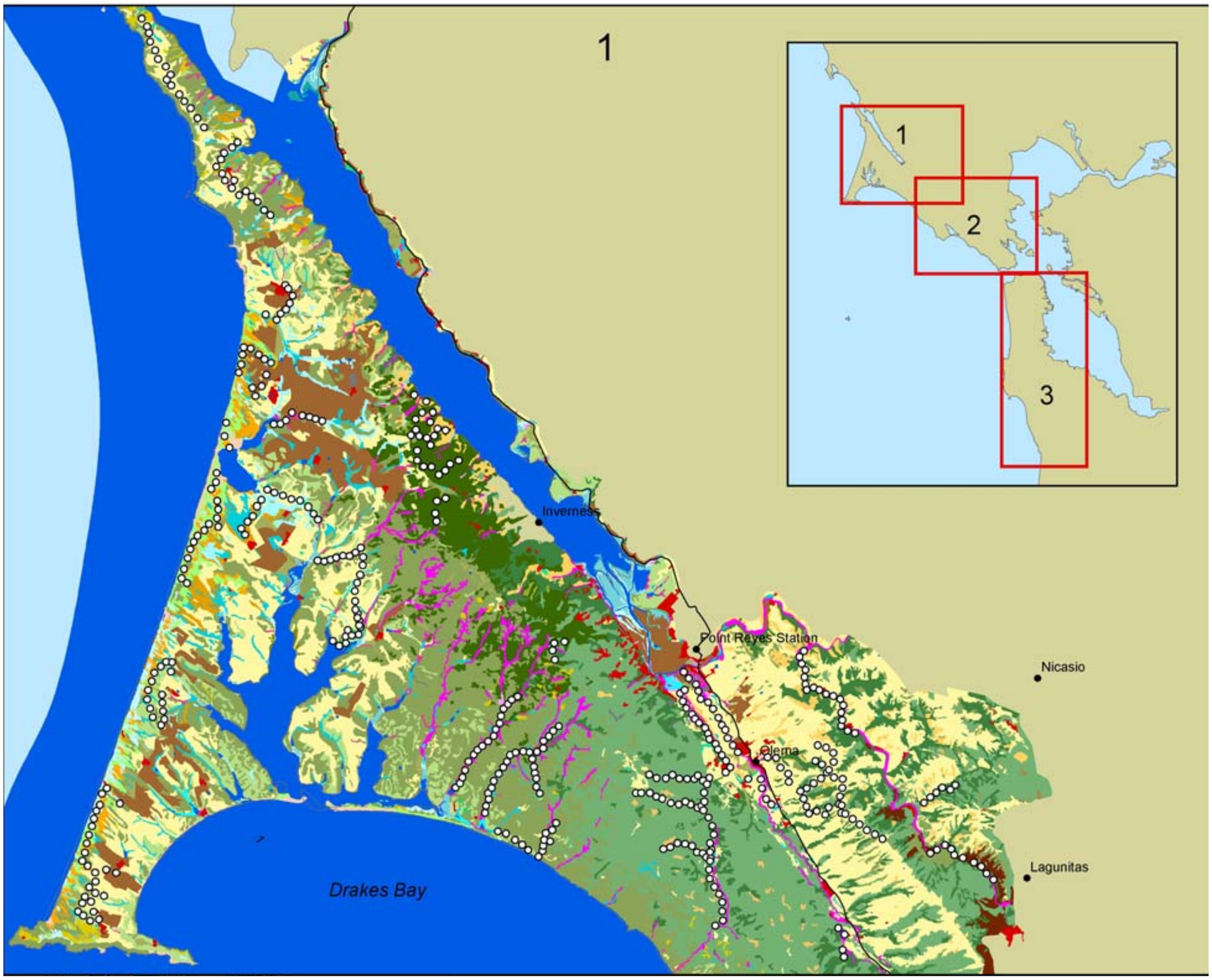


Figure 1a. NPS vegetation map (Schirokauer et al. 2003) representing the study area for development of habitat-based species distribution and diversity models. Study area covers NPS parks in Marin, San Francisco, and San Mateo counties. PRBO point count locations shown as white dots.

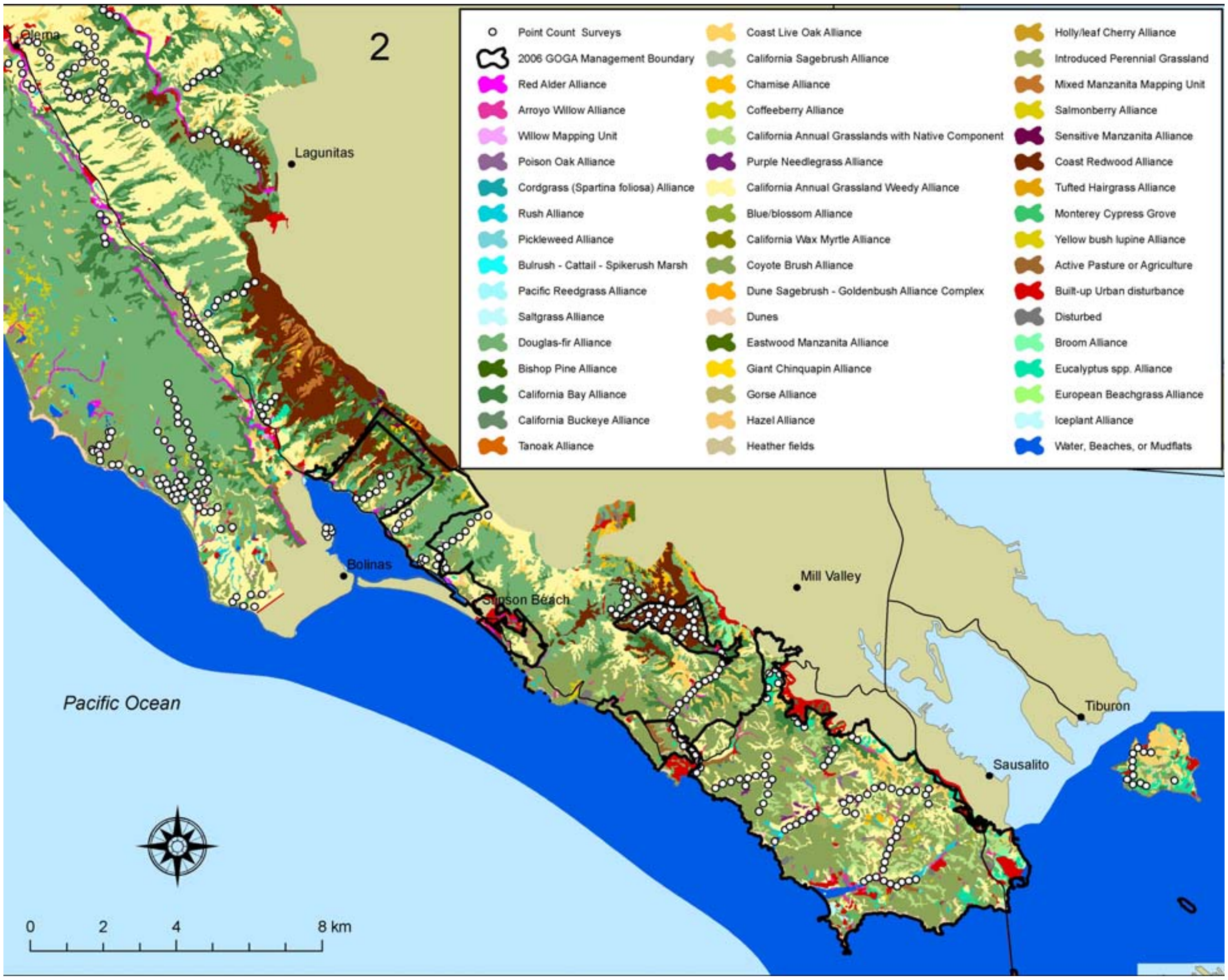


Figure 1b. NPS vegetation map (Schirokauer et al. 2003) representing the study area for development of habitat-based species distribution and diversity models. Study area covers NPS parks in Marin, San Francisco, and San Mateo counties. PRBO point count locations shown as white dots.

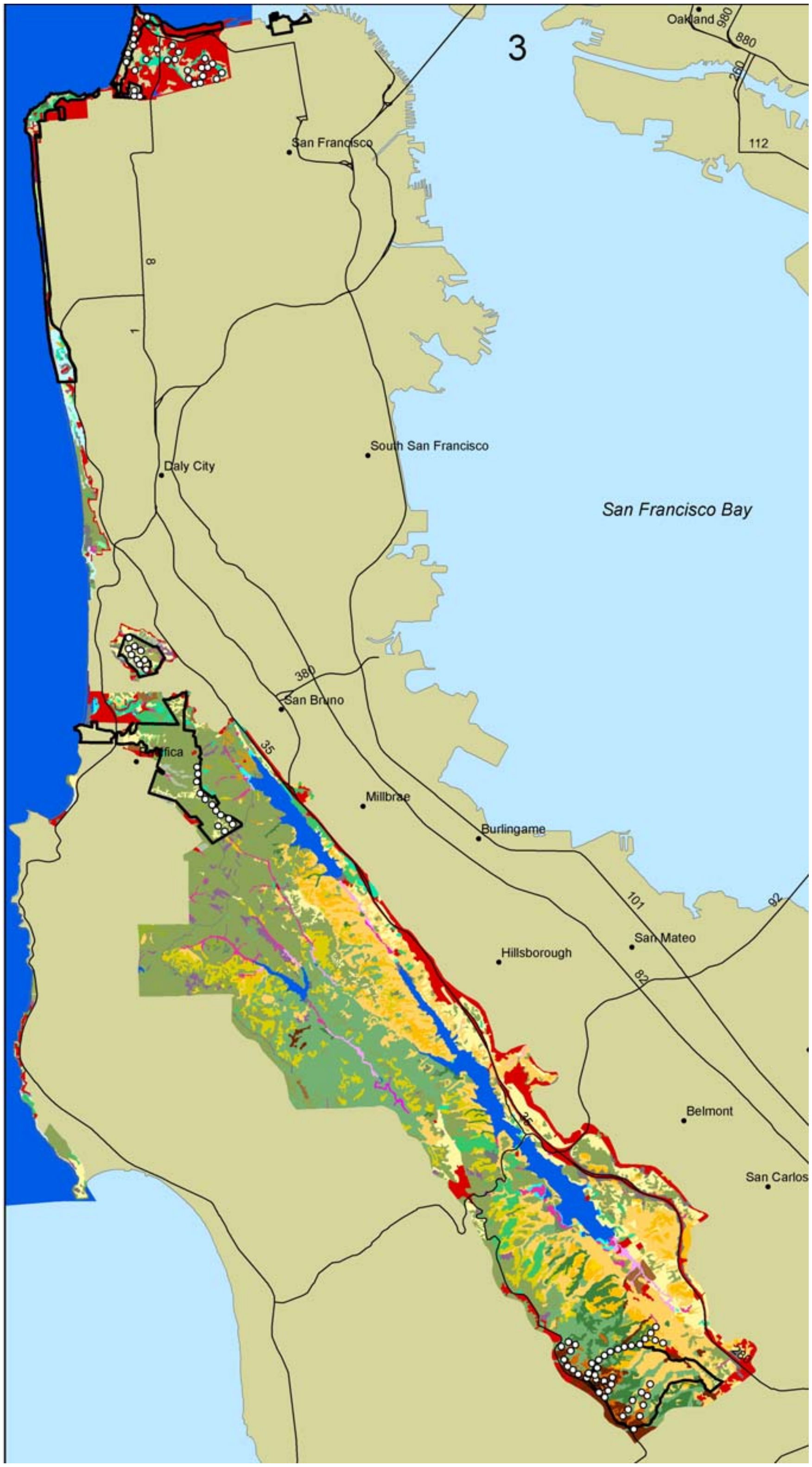


Figure 1c. NPS vegetation map (Schirokauer et al. 2003) representing the study area for development of habitat-based species distribution and diversity models. Study area covers NPS parks in Marin, San Francisco, and San Mateo counties. PRBO point count locations shown as white dots.

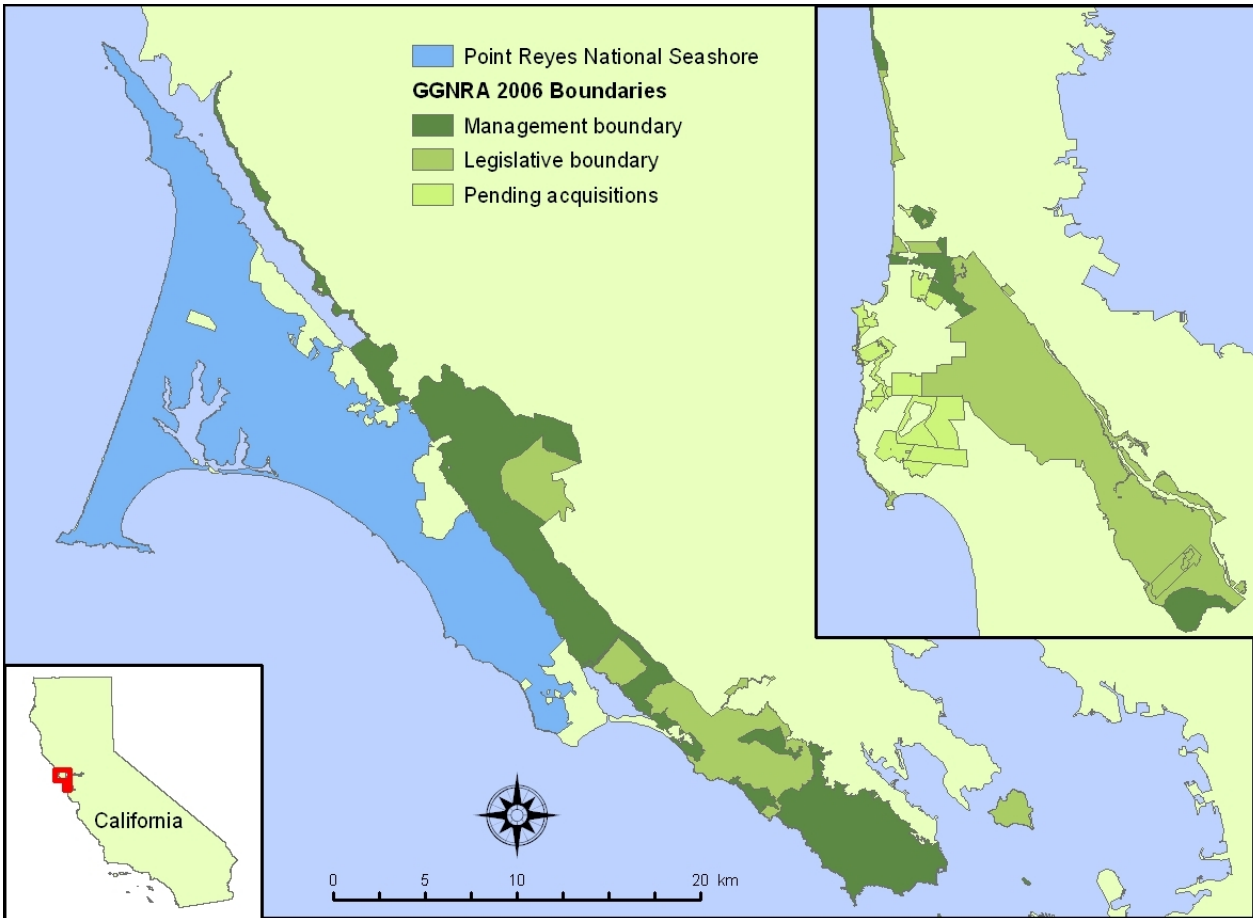


Figure 2. 2006 PORE and GOGA (GGNRA) boundaries. Some mapped areas (pending acquisitions) were not covered by the NPS vegetation map and thus were not included in model predictions.

Selection of model response metrics

To facilitate the planning of management activities, and to encompass a range of habitat requirements and life history strategies among avian species, we identified management-sensitive individual species that have also been selected as focal species (Lambeck 1997) by California Partners in Flight (CPIF) for its habitat-based conservation plans (http://www.prbo.org/calpif/plans.html, Chase and Geupel 2005). Individual species' distribution models were developed for each management-sensitive focal species, and then combined in an additive manner to generate several metrics representing cumulative responses across species. These combined management sensitivity metrics were complemented by several targeted avian species richness and diversity metrics calculated across (1) all native species, and (2) habitat-specific suites of CPIF focal species. Separate models were constructed for each richness/diversity metric.

Species richness and diversity

The most general metric that we examined was the overall richness of native avian species. For each point surveyed, this comprised the total number of native species that were detected across all surveys and years (i.e., cumulative species richness). Species that are not well sampled (e.g., non-territorial, colonial) by the point count method were excluded. This metric can be used to indicate areas and habitats that are occupied by many avian species, which may indicate high structural vegetation diversity or the presence of habitat ecotones. Hence, when the goal is to manage for many species, this metric may be useful.

Using the same native avian species that were included in the species richness metric, we also calculated species diversity, which measures the number of species detected (species richness) weighted by the number of individuals of each species. A high diversity score indicates a more equal representation of the species, and may represent high ecological diversity. Species diversity was calculated using the Shannon-Wiener index: $H' = -\sum_{i=1}^{S} p_i \ln p_i$, where p_i = the relative abundance of species i and S = the number of species (also called Shannon-Weaver index or Shannon index, Krebs 1989).

California Partners in Flight Focal Species Richness

Because the use of overall species richness and diversity metrics may obscure habitat relationships exhibited by groups of species that occupy similar habitats, we also calculated species richness of CPIF focal species by general habitat type (as defined by existing bird conservation plans): scrub/chaparral, grassland, oak woodland, riparian habitat, and coniferous forest (Table 2). Habitat-specific focal species are defined as those species that meet one or more of the following criteria: (1) use a given habitat type (e.g., riparian) as their primary breeding habitat, (2) have special management status, (3) have experienced a reduction from their historical breeding range, (4) commonly breed throughout a given habitat type, allowing adequate sample sizes for statistical comparisons and therefore the ability to rapidly assess responses to management changes, and (5) have breeding requirements that represent the full range of successional stages (Chase and Geupel 2005). For each habitat type, we summed the total number of CPIF focal species that were detected at each point across all surveys and years, excluding species that do not breed within the PORE/GOGA study area. These habitat-specific metrics may be used to identify areas of high value to avian species within a given habitat type of interest, and may be used to set habitat-specific management priorities. Because the habitats vary in the total possible number of focal species, species richness values should not be compared among habitat groupings.

Management-sensitive individual species

We used several criteria to identify management-sensitive CPIF focal species (Table 3):

1. ***Species on the California Department of Fish and Game's Bird Species of Special Concern (BSSC) list*** (Shuford and Gardali in press). We included only species that are known to occur within the study area and are adequately sampled by the point count method. State- and federally-listed threatened and endangered species were also excluded because their distributions within the parks are relatively well-known.
2. ***Species that appear to be declining.*** We used the Breeding Bird Survey (Sauer et al. 2005) and several other local studies (see references in Table 3) to identify species that are declining in California and/or locally.
3. ***Species that place their nests on or near the ground.*** We used Shuford (1993) and Poole and Gill (2003) to obtain nest heights. Species that nest on or near the ground were included because they are prone to disturbance from several common management practices as well as from park visitors.
4. ***Species that are sensitive to human disturbance and/or alterations.*** This included species reported to avoid high use areas (e.g., heavily used trails), those with reported direct human/research impacts, and those that will not typically nest in human-altered patches. We used local expert opinion (Gardali) and two primary published sources for making these distinctions (Shuford 1993, Poole and Gill 2003).

Distribution models, expressed as the probability of species occurrence at a given location, were developed for each of these species with adequate point count survey detections. For each survey point, a species was considered either present or absent based on all surveys conducted. One detection in one year was enough to constitute a species' presence at a location.

Table 2. California Partners in Flight native focal species (http://www.prbo.org/calpif/plans.html) that are known to occur within the Golden Gate National Recreation Area and the Point Reyes National Seashore.

Common Name	Scientific Name	Plan / Habitat
Warbling Vireo	*Vireo gilvus*	Riparian
Tree Swallow	*Tachycineta bicolor*	Riparian
Swainson’s Thrush	*Catharus ustulatus*	Riparian
Yellow Warbler	*Dendroica petechia*	Riparian
Common Yellowthroat	*Geothlypis trichas*	Riparian, Scrub
Wilson’s Warbler	*Wilsonia pusilla*	Riparian
Song Sparrow	*Melospiza melodia*	Riparian, Scrub
Black-headed Grosbeak	*Pheuclicus melanocephalus*	Riparian
Acorn Woodpecker	*Melanerpes formicivorus*	Oak
Western Scrub-Jay	*Aphelocoma californica*	Oak, Scrub
Oak Titmouse	*Baeolophus inornatus*	Oak
Western Bluebird	*Sialia Mexicana*	Oak
Red-shouldered Hawk	*Buteo lineatus*	Oak
California Quail	*Callipepla californica*	Oak, Scrub
Band-tailed Pigeon	*Columba fasciata*	Oak
Nuttall’s Woodpecker	*Picoides nuttallii*	Oak
Ash-throated Flycatcher	*Myiarchus cinerascens*	Oak
Hutton’s Vireo	*Vireo huttoni*	Oak
Bewick’s Wren	*Thryomanes bewickii*	Oak, Scrub
California Towhee	*Pipilo crissalis*	Oak
Wrentit	*Chamaea fasciata*	Scrub
Rufous-crowned Sparrow	*Aimophila ruficeps*	Scrub
Nuttall’s White-crowned Sparrow	*Zonotrichia leucophrys nuttalli*	Scrub
Allen’s Hummingbird	*Selasphorus sasin*	Scrub
Spotted Towhee	*Pipilo maculates*	Scrub
California Towhee	*Pipilo crissalis*	Scrub
Grasshopper Sparrow	*Ammodramus savannarum*	Grass
Northern Harrier	*Circus cyaneus*	Grass
Savannah Sparrow	*Passerculus sandwichensis*	Grass
Western Meadowlark	*Sturnella neglecta*	Grass
White-tailed Kite	*Elanus leucurus*	Grass
Brown Creeper	*Certhia Americana*	Conifer
Black-throated Gray Warbler	*Dendroica nigrescens*	Conifer
Dark-eyed Junco	*Junco hyemalis*	Conifer
Golden-crowned Kinglet	*Regulus satrapa*	Conifer
MacGillivray's Warbler	*Oporornis tolmiei*	Conifer
Olive-sided Flycatcher	*Contopus cooperi*	Conifer
Pileated Woodpecker	*Dryocopus pileatus*	Conifer
Red-breasted Nuthatch	*Sitta Canadensis*	Conifer
Purple Finch	*Carpodacus purpureus*	Conifer
Stellar’s Jay	*Cyanocitta stelleri*	Conifer

Table 3. California Partners in Flight focal species known to occur within the Golden Gate National Recreation Area and the Point Reyes National Seashore that were considered management sensitive according to one or more criteria (as listed in columns).

Common Name	BSSC[1]	Declining[2]	Ground/low nester[3]	Disturbance sensitive[4]
Common Yellowthroat	X	X	X	X
Northern Harrier	X	X	X	X
Olive-sided flycatcher	X	X		
Yellow Warbler	X	X		
Grasshopper Sparrow	X	X	X	X
Warbling Vireo		X		
Hutton's Vireo		X		X
Brown Creeper		X		X
Bewick's Wren		X	X	
Black-throated Gray Warbler		X		X
Wilson's Warbler		X	X	X
Nuttall's White-crowned Sparrow		X[5]	X	
Swainson's Thrush			X	X
Golden-crowned Kinglet		X		X
Rufous-crowned Sparrow			X	X
Western Meadowlark		X	X	X
MacGillivray's Warbler			X	X
Pileated Woodpecker				X
Oak Titmouse		X		
Dark-eyed Junco		X	X	
Savannah Sparrow		X	X	

[1]BSSC = California Department of Fish and Games Bird Species of Special Concern (Shuford and Gardali in press).
[2]Declining = Declines reported in the Breeding Bird Survey for California, 1966-2004 (Sauer et al. 2005), from studies within the study area (Gardali et al. 2000, Ballard et al. 2003, Michaud et al. 2004), and/or from individual species account in BSSC (Shuford and Gardali in press).
[3]Ground/low = nest typically placed below 2.5 meters (Shuford 1993, Poole 2003).
[4]Disturbance sensitive = will not typically nest in human-altered patches (Shuford 1993, Poole 2003, expert opinion).
[5]Both subspecies (*nuttalli* and *pugetensis*) combined.

Combined species metrics

Model predictions for individual management-sensitive species (expressed as probability of occurrence) were combined to generate four different cumulative indices of management sensitivity: one for each of the above-described criteria (BSSC and declining species combined), plus one overall management-sensitivity index. This approach should enable GOGA managers to use different indices for different management questions. For example, the combined index of disturbance sensitive species can be used to indicate areas where anthropogenic disturbance should be minimized. Similarly, the combined index of ground/low-nesting species can be used to indicate areas where ground-level disturbances should be avoided during the breeding season. The BSSC and declining species indices may be useful for long-term, proactive conservation planning to prevent future listings of threatened and endangered species, especially in light of NPS stewardship responsibilities for species at risk.

Model Development

Independent Variables

Because our goal was to develop models that could be used to develop spatial predictions across the study area, we were constrained to variables that were available as geographic information system (GIS) layers. Independent variables were derived primarily from the NPS vegetation layer (Schirokauer et al. 2003), but also from other GIS layers, including park trails, the national elevation dataset (NED, http://ned.usgs.gov/), and the national hydrography dataset (NHD, http://nhd.usgs.gov/).

Throughout California habitats, landscape composition and structure have been shown to be important predictors of breeding bird occurrence and density, both on their own and when combined with local habitat conditions (Bolger et al. 1997, Stralberg and Williams 2002, Spautz et al. 2006). Thus most of the independent variables were calculated using a 1-km radius moving window, to encompass a larger area of potential influence on the survey point locations. However, we also included in all models a categorical variable representing the vegetation class or general habitat type at the point location. Because the NPS vegetation layer did not have high classification accuracy at the alliance level (Schirokauer et al. 2003), and because it contains too many different vegetation alliances to have statistical power as a categorical variable, we grouped alliances into general habitat categories for this purpose (Appendix 2). These habitat categories closely resemble the land cover categories represented in the USGS National Land Cover Dataset (http://landcover.usgs.gov/classes.php). Landscape variables considered for each model consisted of vegetation composition and diversity (at the alliance level), habitat composition and patch structure (aggregated to general habitat categories) (Table 4). According to national vegetation classification guidelines (Jennings et al. 2006), a vegetation alliance is defined as:

> *a vegetation classification unit containing one or more associations, and defined by a characteristic range of species composition, habitat conditions, physiognomy, and diagnostic species, typically at least one of which is found in the uppermost or dominant stratum of the vegetation.*

Thus the vegetation alliance generally characterizes overstory conditions, and the percent of a particular vegetation alliance within a 1-km radius is not equivalent to the percent of its dominant species (e.g., coyote brush), within a 1-km radius. Many alliances are comprised of several co-dominant species, particularly in an area as floristically and structurally diverse as coastal California.

In addition to vegetation and habitat variables, we calculated a set of topographic and anthropogenic variables that included point characteristics (aspect and distance to nearest stream), as well as 1-km moving window metrics (slope and elevation, trail and stream density) (Table 4).

Additional variables calculated and evaluated, but not used for modeling purposes due to data quality issues, included fire frequency, trailhead density, road density and urban development proportion. The former was not found to have any explanatory power in exploratory analyses, the second was not consistently mapped, and the latter two had variable ranges that were not well-sampled by our point count locations. Landscape variables were calculated for each 30-m by 30-m grid cell within the study area using FragStats moving window landscape metrics (McGarigal and Marks 1995) (vegetation-based metrics) or standard ArcGIS 9 (ESRI 2005) Spatial Analyst operations.

For each avian metric, we chose a set of variables from the full set, that we *a priori* deemed useful in predicting distribution (Appendix 3). In most cases, we included non-native vegetation types (at least one) and trail density because of their relevance to management. Pearson correlation coefficients were used to identify and filter out highly correlated variables ($R > 0.50$), and to help select the most appropriate among candidate variables for each model. In addition to environmental predictor variables, we also included a covariate representing the survey effort (i.e., number of surveys conducted across years) at each point. Because we had such a large sample size for our avian survey data ($n = 675$), we were able to consider a large number of independent variables (maximum of 13) for each avian metric. This resulted in a relatively high minimum variable to sample size ratio (>50).

Table 4. Independent variables considered for development of avian species richness, diversity, and probability of occurrence models. Non-native vegetation types are marked with an asterisk. See Appendix 2 for correspondence between vegetation alliances and vegetation classes.

Variable name	Description
NUMVISITS	Number of surveys (across seasons and years) conducted at point
Vegetation composition and diversity	
VEGCLASS	Local vegetation class (general habitat type at point) 1 = grassland; 2 = riparian; 3 = conifer; 4 = scrub; 5 = wetland; 6 = hardwood
PNNATANNGR	Percent of non-native annual grassland vegetation within 1-km radius
PNATANNGRA	Percent of partly-native annual grassland vegetation within 1-km radius
PNNATPERGR	Percent of non-native perennial grassland vegetation within 1-km radius
PRUSH	Percent of rush (*Juncus* spp.) vegetation within 1-km radius
PREDALDER	Percent of red alder (*Alnus rubra*) vegetation within 1-km radius
PALLWILLOW	Percent of willow (*Salix* spp.) vegetation within 1-km radius
PREDWOOD	Percent of coast redwood (*Sequoia sempervirens*) vegetation within 1-km radius
PDOUGFIR	Percent of Douglas-fir (*Pseudotsuga menziesii*) vegetation within 1-km radius
PBISHOPPIN	Percent of bishop pine (*Pinus muricata*) vegetation within 1-km radius
PCOYOTEBRU	Percent of coyote brush (*Baccharis pilularis*) vegetation within 1-km radius
PCSAGEBRUS	Percent of California sagebrush (*Artemisia californica*) vegetation within 1-km radius
PCOFFEEBER	Percent of coffeeberry (*Rhamnus californica*) vegetation within 1-km radius
PSALMON	Percent of salmonberry (*Rubus spectabilis*) vegetation within 1-km radius
PPOISONOAK	Percent of poison oak (*Toxicodendron diversilobum*) vegetation within 1-km radius
PYBLUPINE	Percent of yellow bush lupine (*Lupinus arboreus*) vegetation within 1-km radius
PBULRUSH	Percent of bulrush (*Bolboschoenus* or *Scirpus* spp. / cattail (*Typha* spp.) / spikerush (*Eleocharis* spp.) vegetation within 1-km radius
PCALIFBAY	Percent of California bay laurel (*Umbellularia californica*) vegetation within 1-km radius
PTANOAK	Percent of tanoak (*Lithocarpus densiflorus*) vegetation within 1-km radius
PCLIVEOAK	Percent of coast live oak (*Quercus agrifolia*) vegetation within 1-km radius
PACTIVEPAS*	Percent of non-native active pasture within 1-km radius
PBROOM*	Percent of non-native broom (*Cytisus* and *Genista* spp.) vegetation within 1-km radius
PEUCALYPTU*	Percent of non-native eucalyptus (*Eucalyptus* spp.) vegetation within 1-km radius
PMYCYPRESS*	Percent of non-native Monterey cypress (*Cupressus macrocarpa*) vegetation within 1-km radius
SIDI	Vegetation alliance diversity (modified Simpson index) within 1-km radius

Table 4, continued.

Variable name	Description
Habitat composition and patch structure (for definitions see McGarigal and Marks 1995)	
PGRASS	Percent of grassland vegetation alliances (combined) within 1-km radius
PRIPARIAN	Percent of riparian vegetation alliances (combined) within 1-km radius
PCONIFER	Percent of conifer vegetation alliances (combined) within 1-km radius
PSCRUB	Percent of scrub vegetation alliances (combined) within 1-km radius
PWETLAND	Percent of wetland vegetation alliances (combined) with 1-km radius
PHARDWOOD	Percent of hardwood vegetation alliances (combined) within 1-km radius
GRASSCOHES	Patch cohesion of grassland vegetation alliances (combined) within 1-km radius
RIPARIANCOHES	Patch cohesion of riparian vegetation alliances (combined) within 1-km radius
CONIFERCOHES	Patch cohesion of conifer vegetation alliances (combined) within 1-km radius
SCRUBCOHES	Patch cohesion of scrub vegetation alliances (combined) within 1-km radius
WETLANDCOHES	Patch cohesion of wetland vegetation alliances (combined) within 1-km radius
GRASSSIZE	Mean patch size of grassland vegetation alliances (combined) within 1-km radius
RIPARIANSIZE	Mean patch size of riparian vegetation alliances (combined) within 1-km radius
CONIFERSIZE	Mean patch size of conifer vegetation alliances (combined) within 1-km radius
SCRUBSIZE	Mean patch size of scrub vegetation alliances (combined) within 1-km radius
WETLANDSIZE	Mean patch size of wetland vegetation alliances (combined) within 1-km radius
IJI	Interspersion / juxtaposition of vegetation classes within 1-km radius
Topography	
ELEV_MEAN	Mean elevation (m) within 1-km radius
SLOPE_MEAN	Mean slope (degrees) within 1-km radius
ELEV_CV	Elevation coefficient of variation within 1-km radius
SLOPE_CV	Slope coefficient of variation within 1-km radius
SOUTHASPEC	South aspect (difference from 180º) at point
WESTASPECT	West aspect (difference from 270º) at point
STREAMDENS	Stream density (km/km^2) within 1-km radius
STREAMDIST	Distance to nearest stream (m)
Anthropogenic factors	
TDENS1K	Trail density (km/km^2) within 1-km radius

Statistical model development

After some exploratory analyses using generalized linear models (GLM, McCullagh and Neder 1989) and maximum entropy models (MaxEnt, Phillips et al. 2006), we concluded that generalized additive models (GAM, Hastie and Tibshirani 1990) constituted the most suitable approach for our dataset, which consisted of both species' presence/absence (binary distribution) variables and species richness (approximately normal distribution). Our confidence that the absences in our dataset generally constituted true absences (based on multiple surveys and generally high detectability of avian species), led us to favor GAMs and GLMs over MaxEnt. MaxEnt is a machine learning approach that was developed primarily to accommodate presence-only occurrence data, which do not meet the assumptions of statistical approaches such as GLMs and GAMs. Our observation of non-linear relationships between landscape variables and species metrics, and our relative uncertainty about the nature of those non-linear relationships, led us to favor GAMs over GLMs. GAMs are semi-parametric extensions of GLMs that were developed to accommodate highly non-linear and non-monotonic relationships between explanatory and response variables (Guisan et al. 2002).

To implement GAMs, we used the generalized regression and spatial prediction (GRASP) module (Lehmann et al. 2002, Lehmann et al. 2003) for the R statistical package (http://www.r-project.org/), to develop, validate and predict models of species occurrence/distribution, richness, and diversity. GRASP is designed specifically to facilitate the production of spatial predictions from point data with the explicit goal to use these predictions for environmental management (Lehmann 2002). Using GRASP, we built multiple variable regression models to establish relationships between our response variables (avian metrics) and our spatial predictor variables (independent variables, Appendix 3).

For individual species' models we assumed a binomial distribution with a logistic link function (i.e., transformation of the predicted values, McCullagh and Neder 1989), and for richness and diversity models we assumed a Gaussian (normal) distribution with an identity link function. All models were fitted using a backwards stepwise variable selection procedure based on maximizing model parsimony using Akaike's Information Criterion (AIC). Three degrees of freedom (equivalent to a third order polynomial or cubic function) were used for the smoothing function. The R code used to develop these models is contained in Appendix 4.

Model assessment and validation

For each avian metric and each independent variable in the final model, we plotted the response curves and visually interpreted the relationships. We also evaluated the importance of each variable by comparing across a measure of model contribution calculated as the difference in prediction units (prior to back-transformation with the link function) resulting from the maximum and minimum values of that variable.

For the individual species models, we evaluated model performance using the receiver operating characteristic (ROC) or area under the curve statistic (Fielding and Bell 1997), which provides a threshold-independent measure of model accuracy (i.e., a measure of model accuracy that does not depend on a particular probability cut-off, e.g., 0.5, to distinguish between presence and absence). The larger the area under the curve (AUC), the higher the rate of correct classification for both presence and absence values, across a range of cut-off probabilities (because predictions are expressed as probabilities of occurrence, rather than strict presence or absence). The value of the AUC is always between 0.5 and 1.0. A value of 0.5 indicates a chance model performance while a value of 1.0 indicates perfect performance. A value of 0.8 means that 80% of the time a random selection from the presence group will have a higher probability of occurrence than a random selection from the absence group. For richness and diversity models, we used R^2 values to evaluate model performance.

In addition, we performed a 4-fold cross-validation of each model by separating the dataset into four equal portions, and repeating the model-building process four times, each time withholding one quarter of the data as a validation dataset. For individual species models, validation ROC AUC statistics were calculated by combining the outcomes of these four cross-validations. For richness and diversity models, we calculated correlation coefficients between the model predictions and validation dataset values.

Model prediction

For each avian metric, we used the GRASP tool for ArcView (Lehmann et al. 2003) to generate spatial predictions based on landscape inputs in ArcInfo grid format. Predictions were generated using a lookup table generated by the GRASP program. For number of survey visits, we used 13, half of the maximum 26 visits.

RESULTS

Richness and diversity models

Model assessment indicated strong predictive power for all of the species richness and diversity models, with R^2 values ranging from 0.64 for grassland species richness to 0.82 for riparian species richness (Table 5). Validation success scores for native avian species richness and diversity were equal and intermediate across the range. Cross-validation R^2 values were also high, ranging from 0.60 to 0.79 (Table 5).

Final model variables depended on *a priori* inputs, but the candidate variables common to all richness and diversity models—local vegetation class, number of survey visits, and trail density within a 1-km radius—were retained in all final models except coniferous forest focal species (no trail density), although model contribution was generally not high for these variables. Model-specific variables pertaining to non-native vegetation types (percent eucalyptus [*Eucalyptus* spp.], broom [*Cytisus* and *Genista* spp.], and active pasture) were also retained in most final models (except coniferous forest focal species), and in some cases had high model contributions. In general, however, the most important variables across all models were those representing the landscape-level composition or pattern of a vegetation class or habitat type (e.g., percent riparian or mean grassland patch size within a 1-km radius). Some landscape variables representing specific vegetation alliances (e.g., percent coast live oak [*Quercus agrifolia*] within a 1-km radius) were also retained, but their model contributions tended to be smaller.

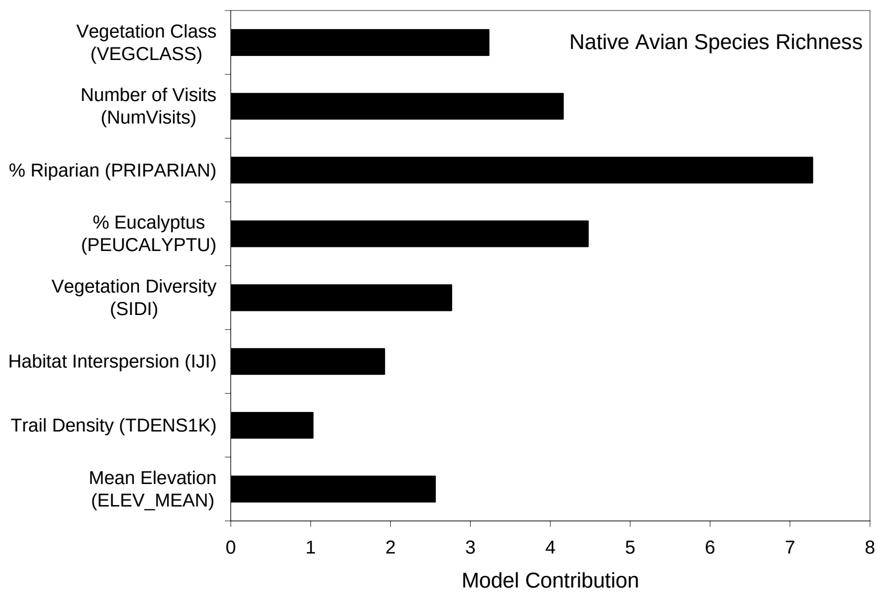
Table 5. Model diagnostics for species richness and diversity models. Model R^2 values were based on the entire model-building dataset. Cross-validation R^2 values were calculated using a 4-fold validation process, leaving out one quarter of the data at a time and using it to validate the model developed using the remaining three quarters of the data.

	Model R^2	Cross-validation R^2
Native avian species richness	0.73	0.71
Shannon-Wiener index of native avian species diversity	0.73	0.70
Oak woodland focal species richness	0.73	0.68
Grassland focal species richness	0.64	0.60
Coniferous forest focal species richness	0.73	0.68
Riparian focal species richness	0.82	0.79
Scrub focal species richness	0.68	0.65

Avian species richness

Eight variables were retained in the final model for native avian species richness, with the biggest contribution provided by percent riparian vegetation within a 1-km radius (Figure 3), which had a positive relationship with species richness (Figure 4). Other important variables included percent eucalyptus vegetation within a 1-km radius (Figure 3), which had a highly non-linear relationship with species richness, and the number of survey visits, which had a positive relationship with species richness, not leveling off even after 25 visits (Figure 4). Local vegetation class was also an important predictor, with hardwood vegetation providing the largest increase in species richness (Figure 4). The effect of trail density was relatively small and non-linear, with higher species richness predicted in the intermediate range of the variable (Figure 4). Predicted patterns of species richness are shown in Figure 5.

Figure 3. Model contributions of variables in the final model for native avian species richness. Each variable's contribution was defined as the difference in model-predicted species richness between the minimum and maximum values of that variable. Model contribution units are specific to each avian metric and are not comparable across different species and metrics.



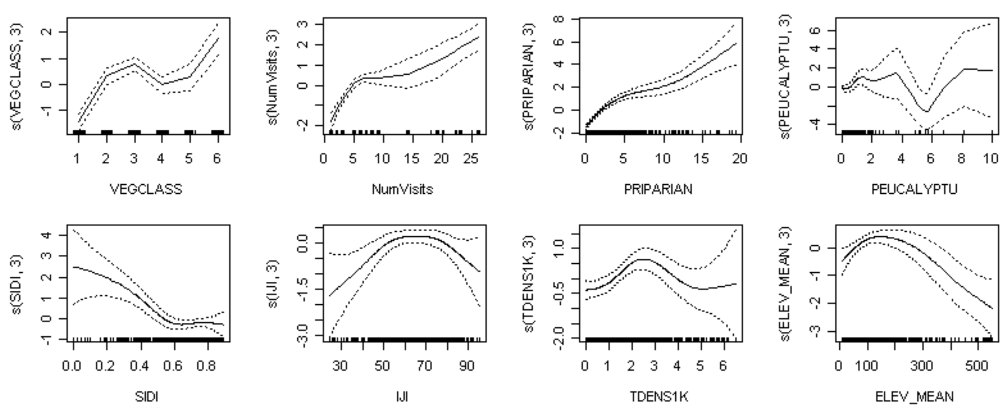


Figure 4. Partial response curves for variables in the final model for native avian species richness (holding all other variables at their mean values). See Table 4 for variable definitions. Y-axes represent deviations from mean species richness. Dashed lines represent upper and lower error bounds (2 SE). Tick marks along x-axes represent variable values for individual point count locations (more observations = higher model confidence).

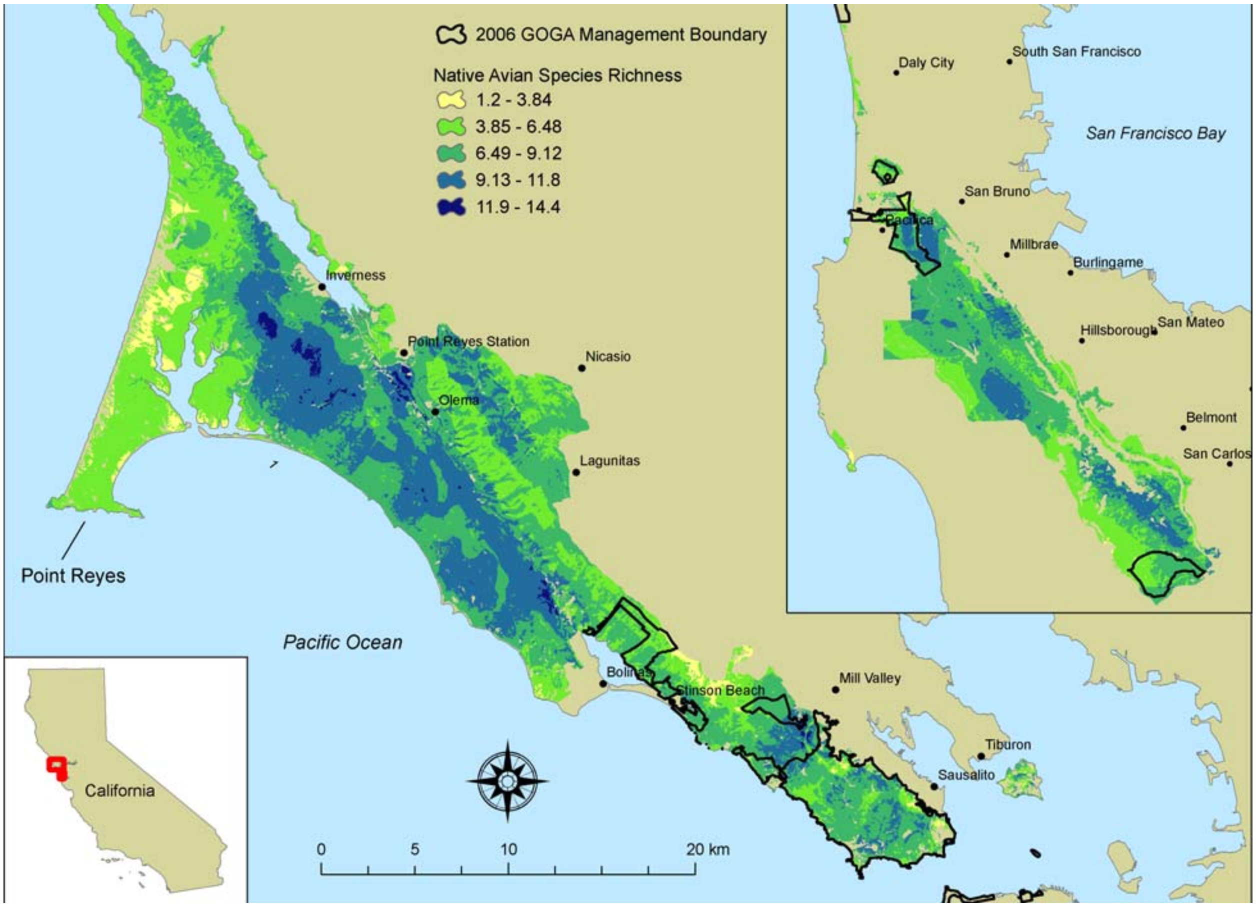
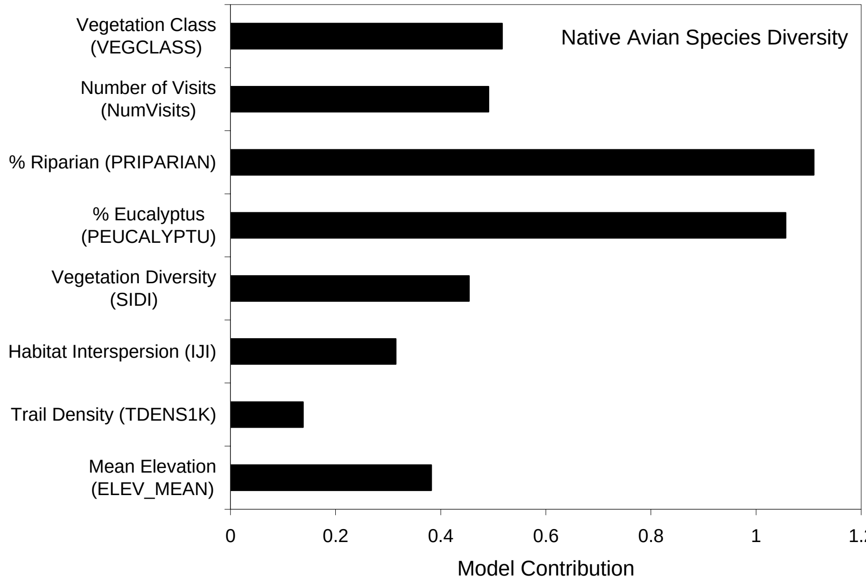


Figure 5. Predicted native avian species richness based on a generalized additive model with a Gaussian distribution and identity link function. Variables in the final model (Figures 3, 4) were selected from an *a priori* list (Appendix 3) using a stepwise backwards elimination AIC-minimizing procedure.

Avian species diversity

The same eight variables were retained in the final model for the Shannon-Wiener index of native species diversity as for species richness, and response curves were almost identical (Figures 6, 7). As with species richness, percent riparian vegetation within a 1-km radius made the largest contribution to the model, but percent eucalyptus vegetation with a 1-km radius was relatively more important (in a non-linear manner) than for species richness (Figures 6, 7). Predicted patterns of species diversity are shown in Figure 8.

Figure 6. Model contributions of variables in the final model for the Shannon-Wiener index of native avian species diversity. Each variable's contribution was defined as the difference in model-predicted species diversity between the minimum and maximum values of that variable. Model contribution units are specific to each avian metric and are not comparable across different species and metrics.



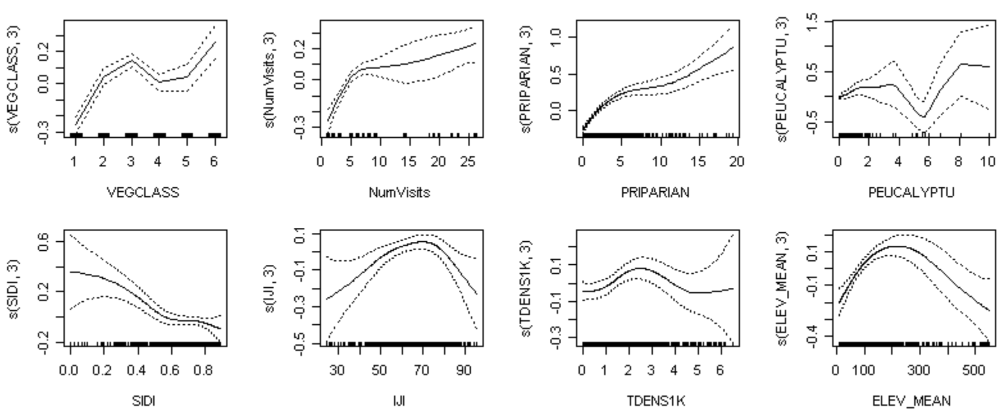


Figure 7. Partial response curves for variables in the final model for the Shannon-Wiener index of native avian species diversity (holding all other variables at their mean values). See Table 4 for variable definitions. Y-axes represent deviations from mean species diversity. Dashed lines represent upper and lower error bounds (2 SE). Tick marks along x-axes represent variable values for individual point count locations (more observations = higher model confidence).

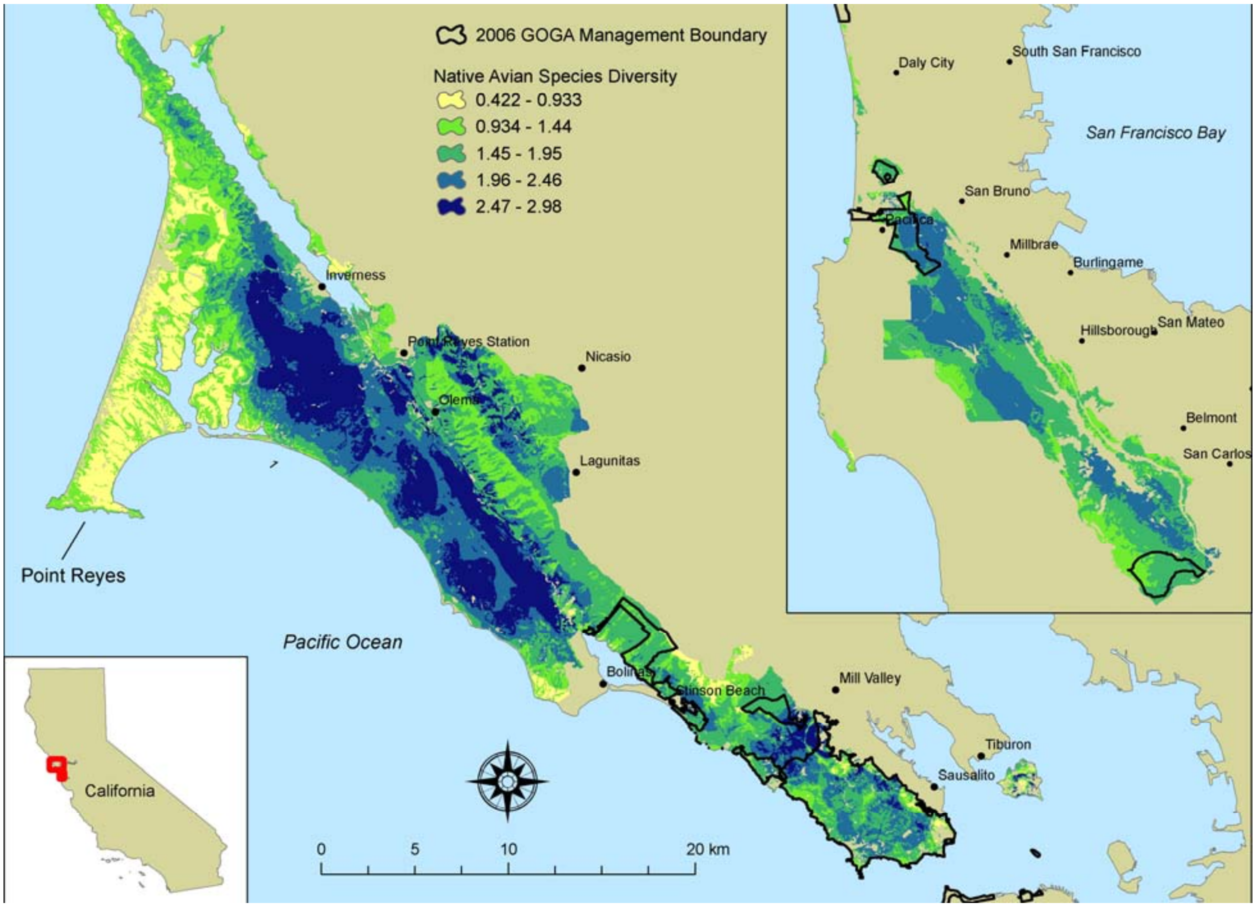
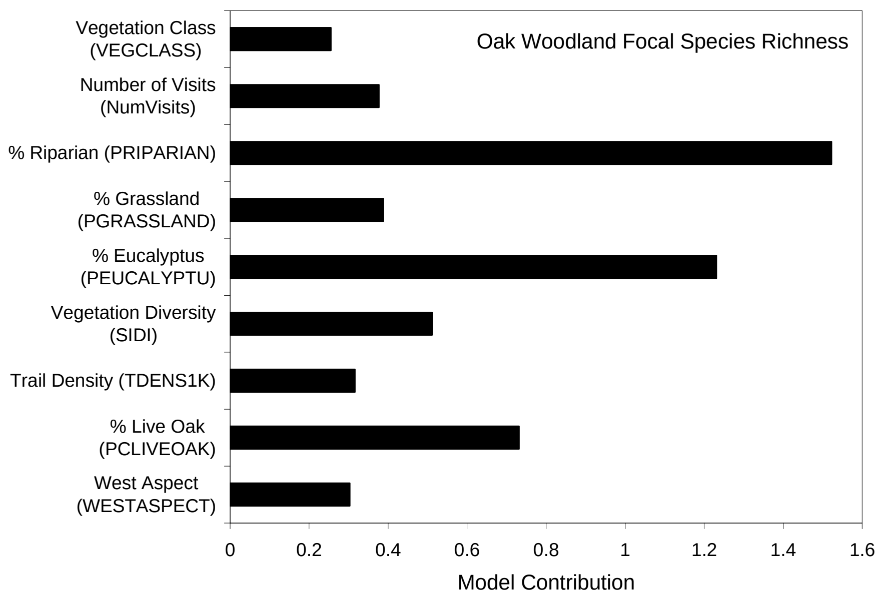


Figure 8. Predicted Shannon-Wiener index of native avian species diversity based on a generalized additive model with a Gaussian distribution and identity link function. Variables in the final model (Figures 6, 7) were selected from an *a priori* list (Appendix 3) using a stepwise backwards elimination AIC-minimizing procedure.

Oak woodland focal species richness

Nine variables were retained in the final model for oak woodland focal species richness (Figure 9). The largest model contribution was provided by percent riparian vegetation within a 1-km radius, followed by percent eucalyptus vegetation (Figure 9). The effect of riparian vegetation was positive, while the relationship with eucalyptus was non-linear, but primarily positive (Figure 10). Percent coast live oak vegetation had a relatively strong, but non-linear effect, and vegetation diversity also contributed to the model, with a primarily positive relationship (Figures 9, 10). Oak woodland focal species richness also increased with the number of survey visits, not leveling off after 25 visits (Figure 10). Local vegetation class had the smallest contribution to the model, but, of the six classes, hardwood provided the biggest increase in oak woodland species richness (Figure 10). Trail density made a relatively small contribution to the model, but the effect was primarily negative (Figure 10). Predicted patterns of oak woodland focal species richness are shown in Figure 11.

Figure 9. Model contributions of variables in the final model for oak woodland focal species richness. Each variable's contribution was defined as the difference in model-predicted species richness between the minimum and maximum values of that variable. Model contribution units are specific to each avian metric and are not comparable across different species and metrics.



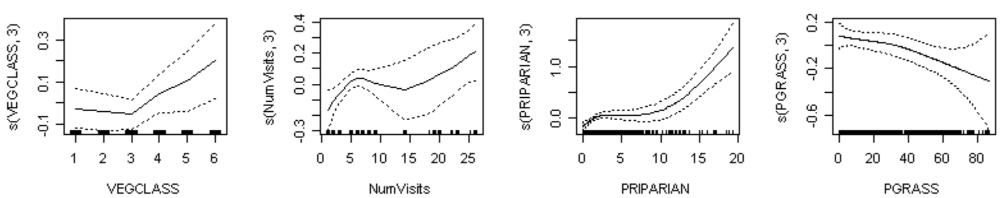


Figure 10. Partial response curves for variables in the final model for oak woodland focal species richness (holding all other variables at their mean values). See Table 4 for variable definitions. Y-axes represent deviations from mean species richness and are comparable across variables. Dashed lines represent upper and lower error bounds (2 SE). Tick marks along x-axes represent variable values for individual point count locations (more observations = higher model confidence).

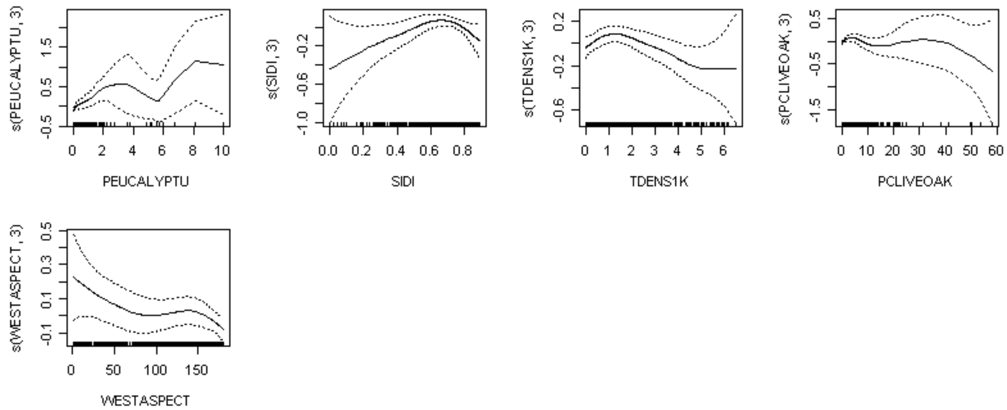


Figure 10. Continued.

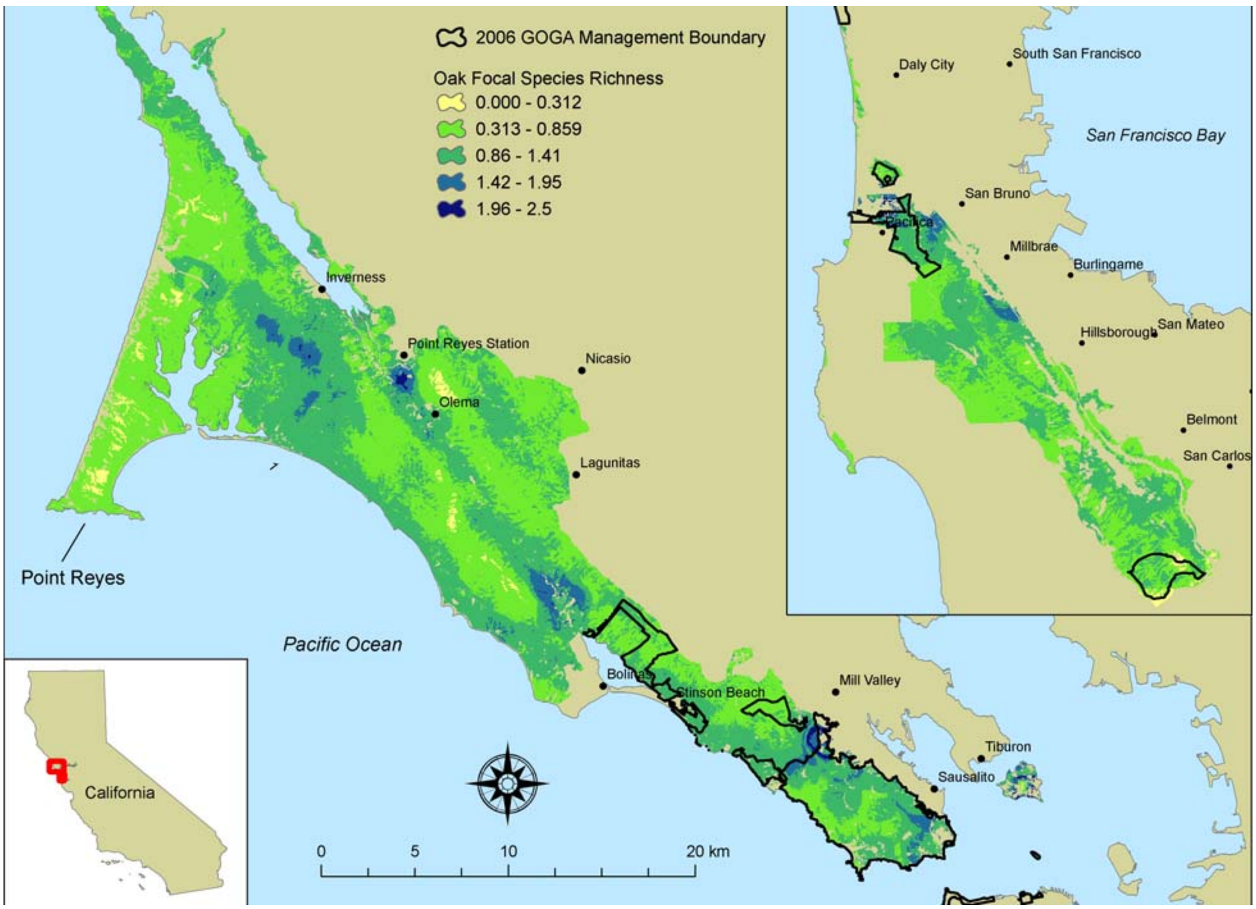
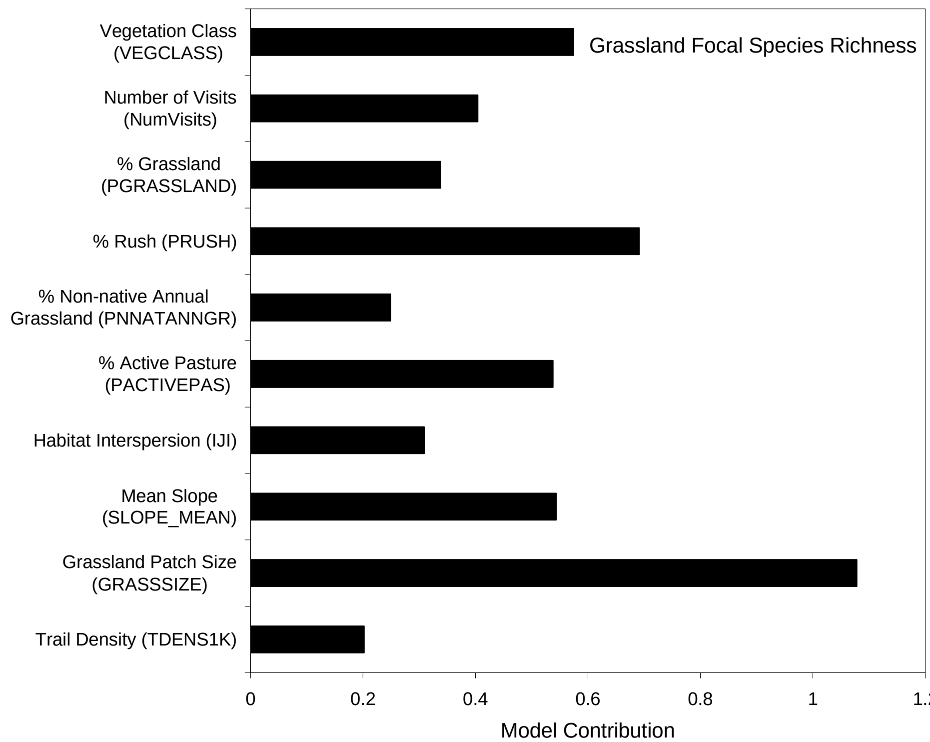


Figure 11. Predicted oak woodland focal species richness based on a generalized additive model with a Gaussian distribution and identity link function. Variables in the final model (Figures 9, 10) were selected from an *a priori* list (Appendix 3) using a stepwise backwards elimination AIC-minimizing procedure.

Grassland focal species richness

Ten variables were retained in the final model for grassland focal species richness, with the largest contribution provided by grassland patch size (Figure 12), which had a strong positive effect (Figure 13). Percent rush (*Juncus* spp.) vegetation within a 1-km radius had the next largest contribution (curvilinear, but positive at higher values), followed by local vegetation class (grassland vegetation providing the largest increase), mean slope within a 1-km radius (largely negative) and percent of active pasture within a 1-km radius (also largely negative) (Figures 12, 13). The number of survey visits was included in the final model, but actually exhibited a negative relationship with grassland species richness (Figures 12, 13). Trail density had the smallest model contribution, but the effect on grassland species richness was largely negative (Figures 12, 13). Predicted patterns of grassland focal species richness are shown in Figure 14.

Figure 12. Model contributions of variables in the final model for grassland focal species richness. Each variable's contribution was defined as the difference in model-predicted species richness between the minimum and maximum values of that variable. Model contribution units are specific to each avian metric and are not comparable across different species and metrics.



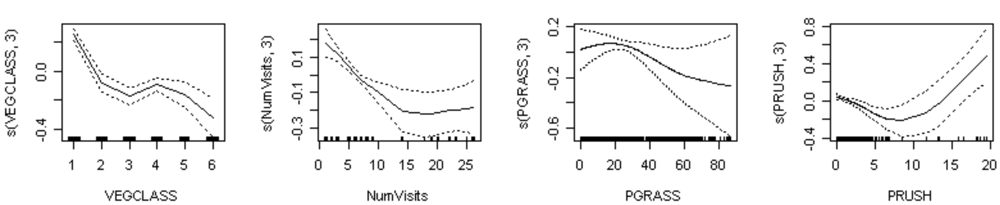


Figure 13. Partial response curves for variables in the final model for grassland focal species richness (holding all other variables at their mean values). See Table 4 for variable definitions. Y-axes represent deviations from mean species richness and are comparable across variables. Dashed lines represent upper and lower error bounds (2 SE). Tick marks along x-axes represent variable values for individual point count locations (more observations = higher model confidence).

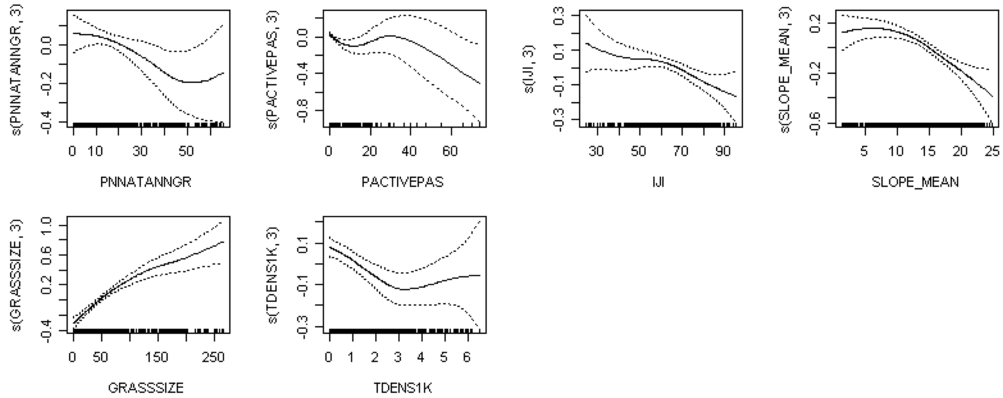


Figure 13. Continued.

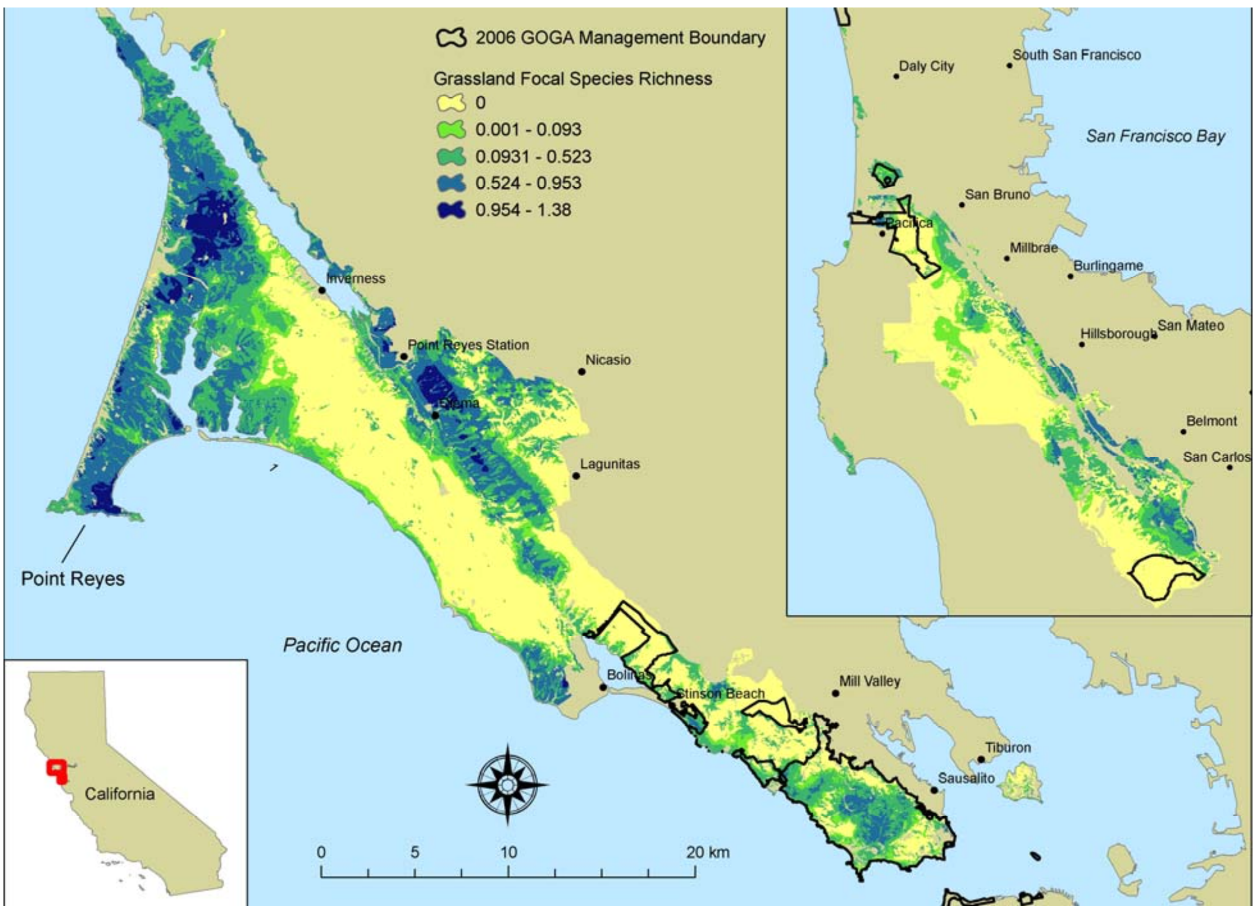
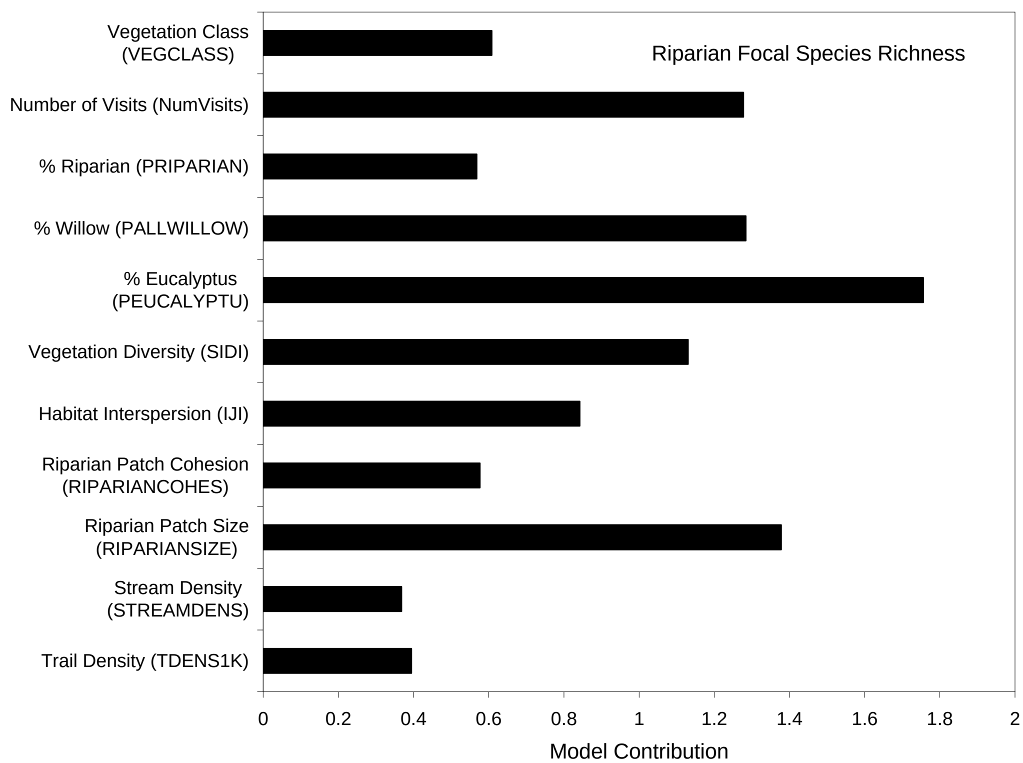


Figure 14. Predicted grassland focal species richness based on a generalized additive model with a Gaussian distribution and identity link function. Variables in the final model (Figures 12, 13) were selected from an *a priori* list (Appendix 3) using a stepwise backwards elimination AIC-minimizing procedure.

Riparian focal species richness

The final model for riparian focal species richness contained eleven variables, with the largest contribution provided by percent eucalyptus vegetation within a 1-km radius (Figure 15). The relationship with this variable was non-linear, but primarily negative in the intermediate range of values (Figure 16). Riparian patch size was the next most important variable (Figure 15), with a curvilinear relationship, increasing up to a point and then decreasing. Willow percent (mostly positive) and the number of survey visits (strongly positive) were also important variables in the final model. Local vegetation class had a smaller contribution to the model, with hardwood, followed by riparian, vegetation providing the biggest increase in riparian species richness (Figures 15, 16). Trail density was included in the final model, but the effect was not strong and highly non-linear (Figure 16). Predicted patterns of riparian focal species richness are shown in Figure 17.

Figure 15. Model contributions of variables in the final model for riparian focal species richness. Each variable's contribution was defined as the difference in model-predicted species richness between the minimum and maximum values of that variable. Model contribution units are specific to each avian metric and are not comparable across different species and metrics.



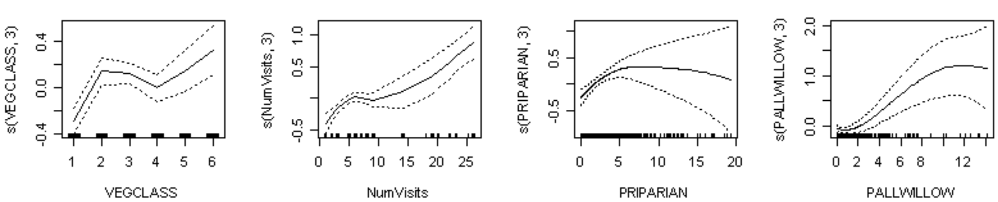


Figure 16. Partial response curves for variables in the final model for riparian focal species richness (holding all other variables at their mean values). See Table 4 for variable definitions. Y-axes represent deviations from mean species richness and are comparable across variables. Dashed lines represent upper and lower error bounds (2 SE). Tick marks along x-axes represent variable values for individual point count locations (more observations = higher model confidence).

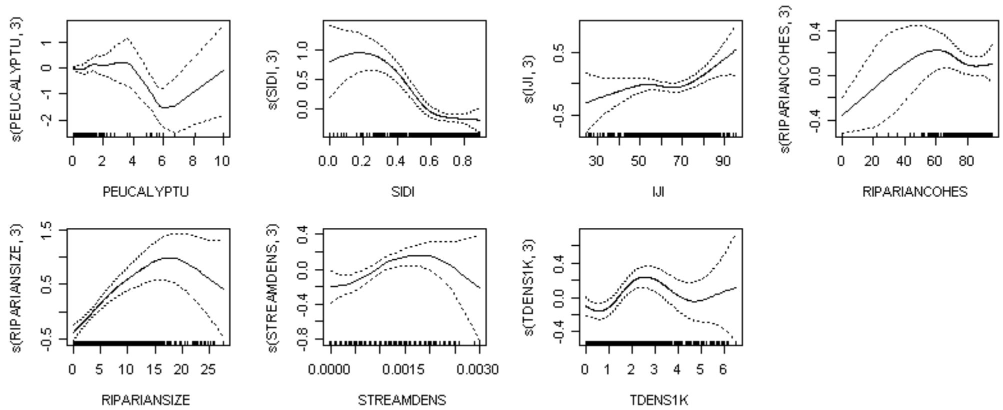


Figure 16. Continued.

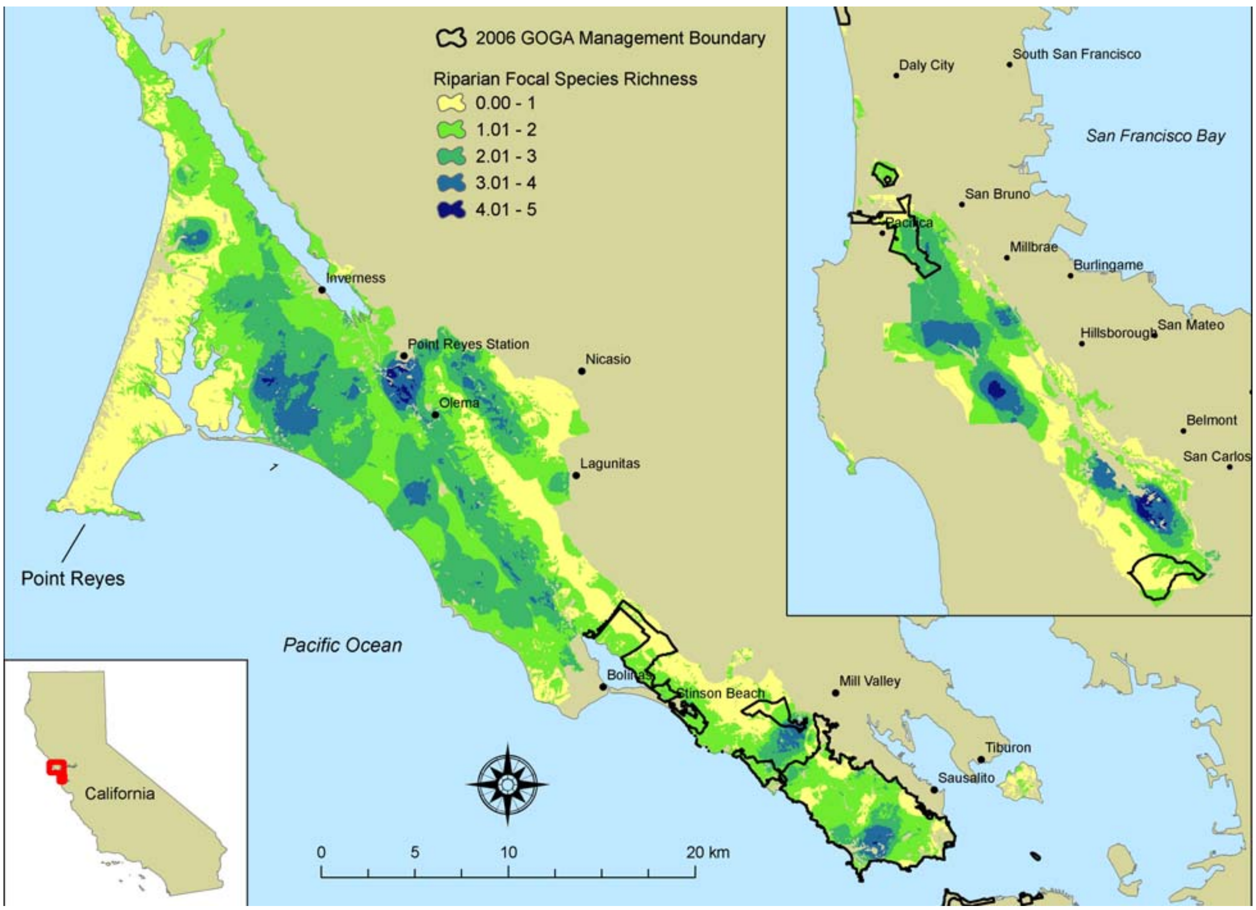


Figure 17. Predicted riparian focal species richness based on a generalized additive model with a Gaussian distribution and identity link function. Variables in the final model (Figures 15, 16) were selected from an *a priori* list (Appendix 3) using a stepwise backwards elimination AIC-minimizing procedure.

Scrub focal species richness

The final model for scrub focal species richness contained ten variables, with the largest contribution provided by percent California sagebrush (*Artemisia californica*) within a 1-km radius (Figure 18). The effect of this variable was strongly positive (Figure 19). Other variables with high model contributions included scrub patch size (positive) and percent coyote brush (*Baccharis pilularis*) (positive, then leveling off at intermediate values) (Figures 18, 19). The number of survey visits had a positive effect up until approximately 15 visits, then decreased slightly (Figure 19). Local vegetation class had the smallest model contribution, with wetland, followed by scrub, vegetation responsible for the largest increases in scrub focal species richness (Figure 19). The effect of trail density was relatively small, and non-linear, but negative in the upper ranges of the variable (Figure 19). Predicted patterns of scrub focal species richness are shown in Figure 20.

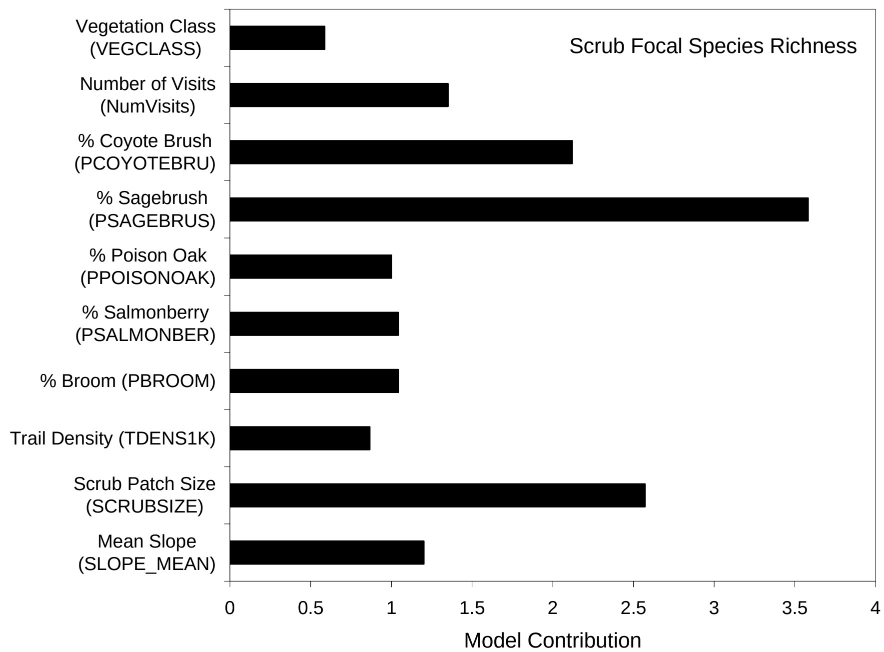


Figure 18. Model contributions of variables in the final model for scrub focal species richness. Each variable's contribution was defined as the difference in model-predicted species richness between the minimum and maximum values of that variable. Model contribution units are specific to each avian metric and are not comparable across different species and metrics.

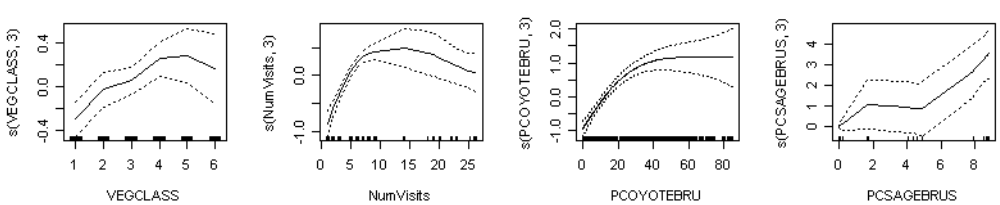


Figure 19. Partial response curves for variables in the final model for scrub focal species richness (holding all other variables at their mean values). See Table 4 for variable definitions. Y-axes represent deviations from mean species richness and are comparable across variables. Dashed lines represent upper and lower error bounds (2 SE). Tick marks along x-axes represent variable values for individual point count locations (more observations = higher model confidence).

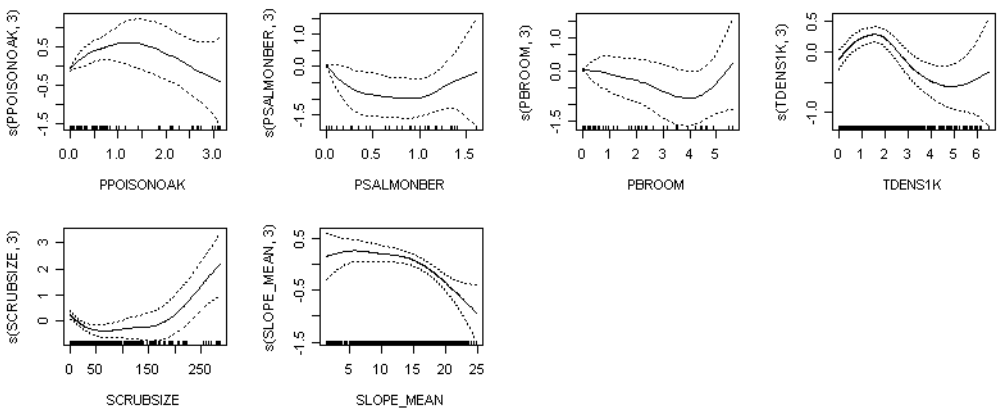


Figure 19. Continued.

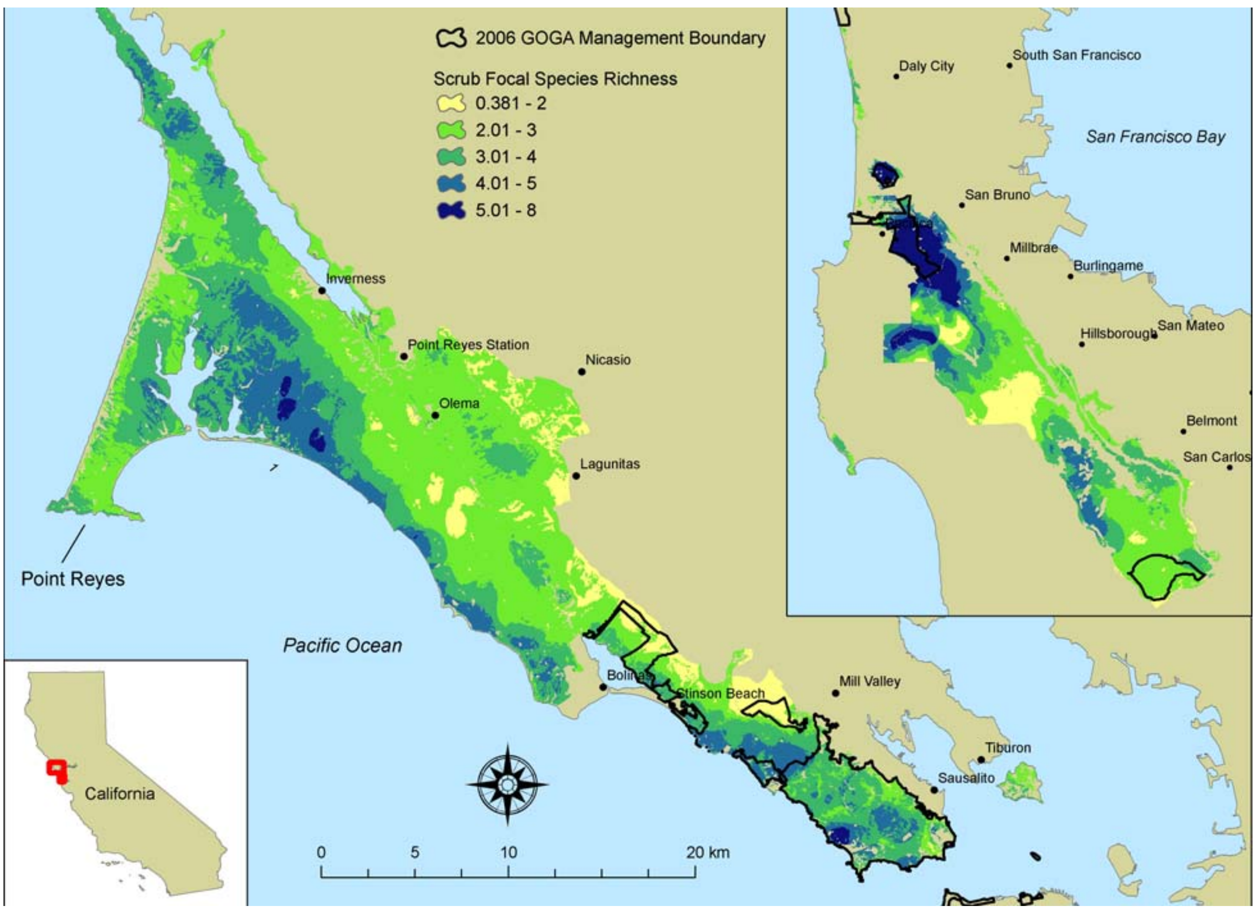
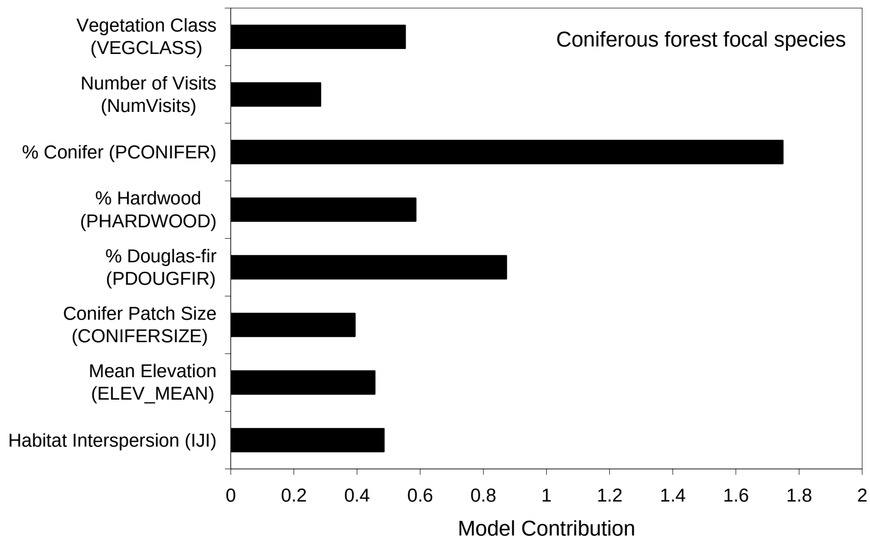


Figure 20. Predicted scrub focal species richness based on a generalized additive model with a Gaussian distribution and identity link function. Variables in the final model (Figures 18, 19) were selected from an *a priori* list (Appendix 3) using a stepwise backwards elimination AIC-minimizing procedure.

Coniferous forest focal species richness

Eight variables were retained in the final model for coniferous forest focal species richness (Figure 21). Percent conifer vegetation within a 1-km radius made the largest contribution to the model, followed by percent Douglas-fir (*Pseudotsuga menziesii*) and percent hardwood vegetation (Figure 21). The effects of conifer and Douglas-fir vegetation were largely positive, while the relationship with hardwood vegetation was highly non-linear (Figure 22). The number of survey visits had the smallest contribution, with a non-linear, but mostly positive effect (Figure 22). The model contribution of local vegetation class was intermediate, with hardwood, followed by conifer, vegetation classes responsible for the largest increases in coniferous forest focal species richness (Figures 21, 22). The trail density variable was not retained in the final model. Predicted patterns of coniferous forest focal species richness are shown in Figure 23.

Figure 21. Model contributions of variables in the final model for coniferous forest focal species richness. Each variable's contribution was defined as the difference in model-predicted species richness between the minimum and maximum values of that variable. Model contribution units are specific to each avian metric and are not comparable across different species and metrics.



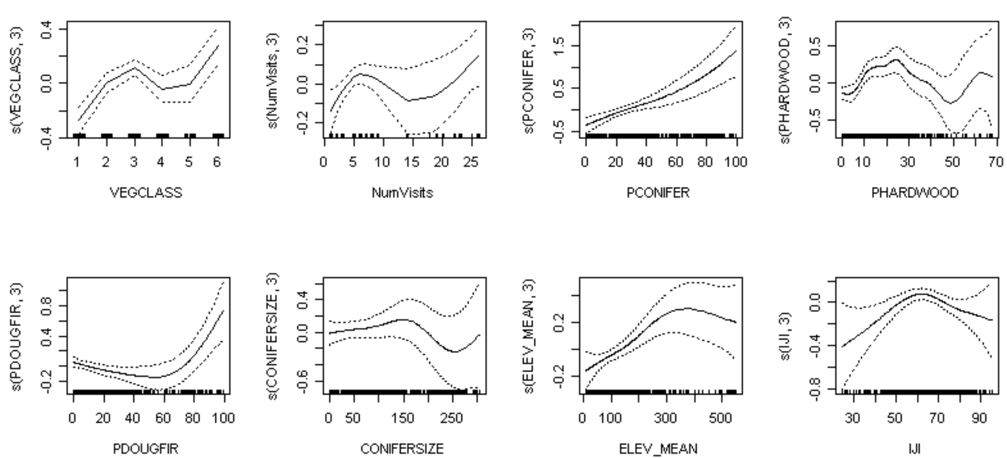


Figure 22. Partial response curves for variables in the final model for coniferous forest focal species richness (holding all other variables at their mean values). See Table 4 for variable definitions. Y-axes represent deviations from mean species richness and are comparable across variables. Dashed lines represent upper and lower error bounds (2 SE). Tick marks along x-axes represent variable values for individual point count locations (more observations = higher model confidence).

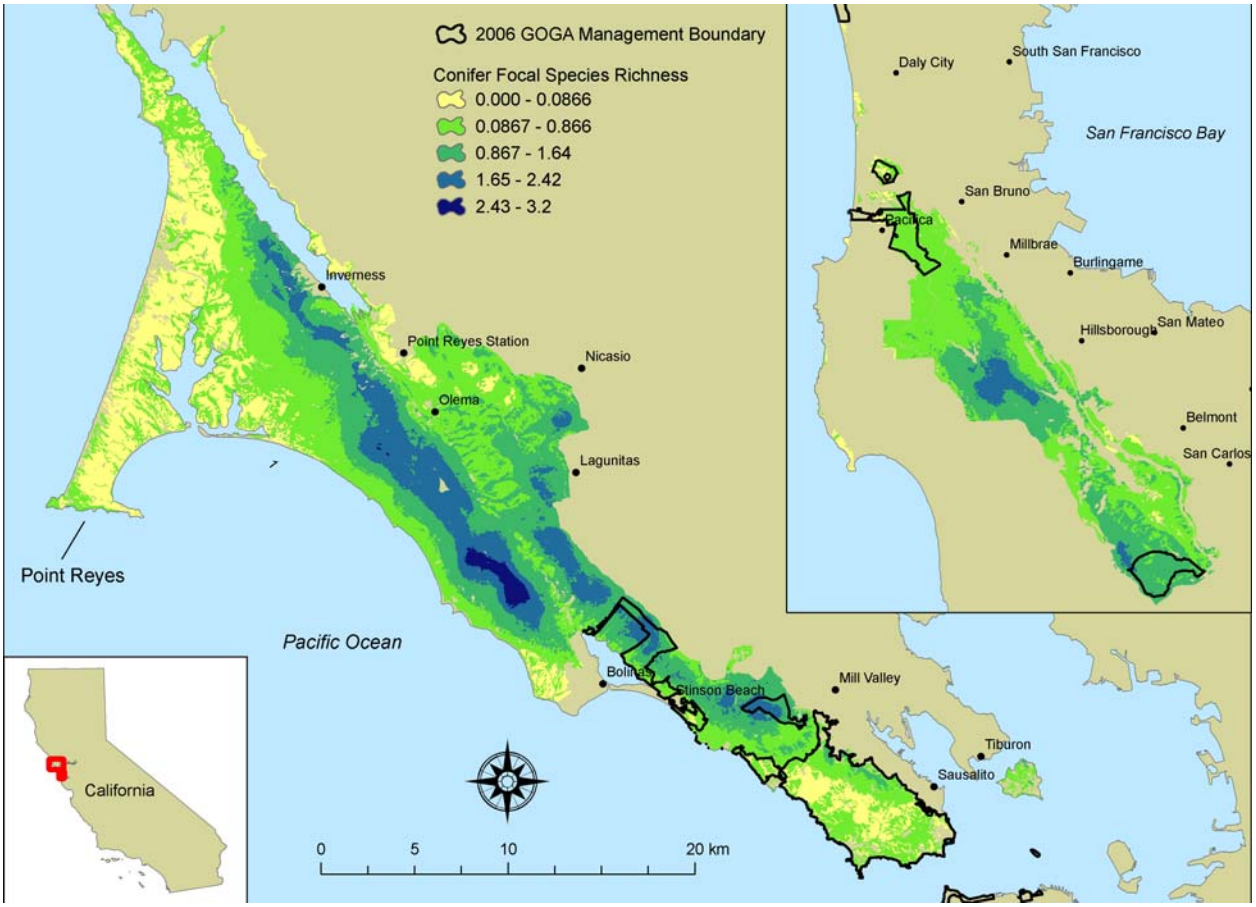


Figure 23. Predicted coniferous forest focal species richness based on a generalized additive model with a Gaussian distribution and identity link function. Variables in the final model (Figures 21, 22) were selected from an *a priori* list (Appendix 3) using a stepwise backwards elimination AIC-minimizing procedure.

Management-sensitive individual species models

Prevalence values for individual species varied widely, ranging from 0.14 (14% of surveyed points) for Golden-crowned Kinglet (*Regulus satrapa*) to 0.57 (57% of surveyed points) for Wilson's Warbler (*Wilsonia pusilla*) (Table 6). Model assessment indicated strong predictive power for all of the species-specific models, with model ROC area under the curve (AUC) values ranging from 0.86 for Dark-eyed Junco (*Junco hyemalis*) and Bewick's Wren (*Thryomanes bewickii*) to 0.97 for Golden-crowned Kinglet (Table 6). Cross-validation results indicated robust models for all species, with AUC values ranging from 0.82 for Bewick's Wren to 0.96 for Golden-crowned Kinglet (Table 6).

Final model variables depended on *a priori* inputs, but local vegetation class was present in all models, and number of survey visits was present in models for all species except Common Yellowthroat (*Geothlypis trichas*), Dark-eyed Junco, and Savannah Sparrow (*Passerculus sandwichensis*). Overall, trail density was less important for individual species than for richness and diversity metrics. Likewise, model-specific variables pertaining to non-native vegetation types were only retained in models for Common Yellowthroat (broom) and Swainson's Thrush (*Catharus ustulatus*) (eucalyptus), although model contribution was quite high for both variables. In general, as with species richness and diversity metrics, landscape-level vegetation class metrics had higher model contributions than did metrics based on specific vegetation alliances.

Table 6. Model diagnostics for individual species models.

Species	Prevalence (proportion of survey sites occupied)	Model ROC AUC	Cross-validation ROC AUC
Bewick's Wren	0.37	0.86	0.82
Brown Creeper	0.16	0.91	0.89
Common Yellowthroat	0.15	0.92	0.90
Dark-eyed Junco	0.20	0.86	0.84
Golden-crowned Kinglet	0.14	0.97	0.96
Nuttall's White-crowned Sparrow	0.29	0.93	0.92
Savannah Sparrow	0.18	0.91	0.90
Swainson's Thrush	0.44	0.95	0.93
Warbling Vireo	0.24	0.90	0.89
Wilson's Warbler	0.57	0.93	0.90

Zac Denning

Bewick's Wren

The final model for Bewick's Wren contained nine variables, of which percent scrub vegetation within a 1-km radius was the strongest positive predictor, followed by percent hardwood, percent California sagebrush, and elevation coefficient of variation (Figure 24). The number of survey visits also played an important role in this species' model, as did trail density and percent broom vegetation, while the local vegetation class was least important of the variables included. For the majority of variables, responses were curvilinear, but monotonically increasing (Figure 25). Predicted patterns of Bewick's Wren probability of occurrence are shown in Figure 26.

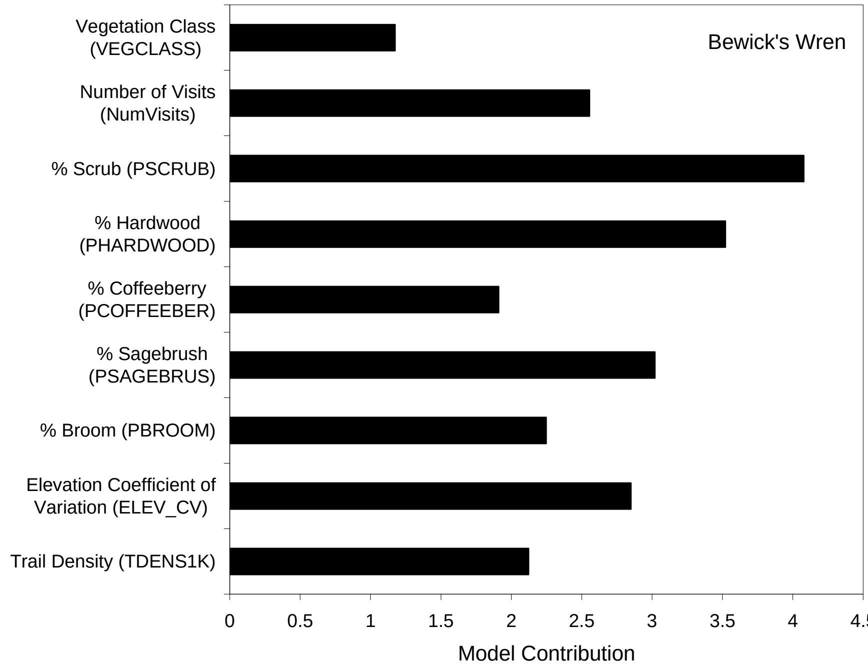


Figure 24. Model contributions of variables in the final model for Bewick's Wren probability of occurrence. Each variable's contribution was defined as the difference in model-predicted probability of occurrence (before back-transformation) between the minimum and maximum values of that variable. Model contribution units are specific to each avian metric and are not comparable across different species and metrics.

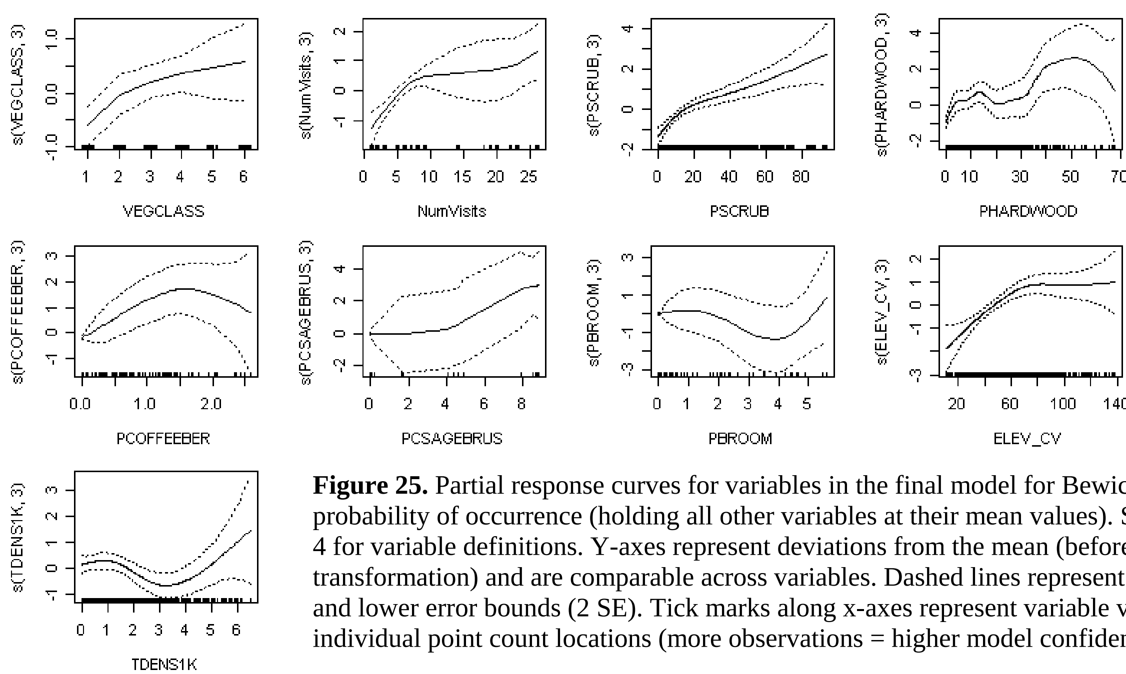


Figure 25. Partial response curves for variables in the final model for Bewick's Wren probability of occurrence (holding all other variables at their mean values). See Table 4 for variable definitions. Y-axes represent deviations from the mean (before back-transformation) and are comparable across variables. Dashed lines represent upper and lower error bounds (2 SE). Tick marks along x-axes represent variable values for individual point count locations (more observations = higher model confidence).

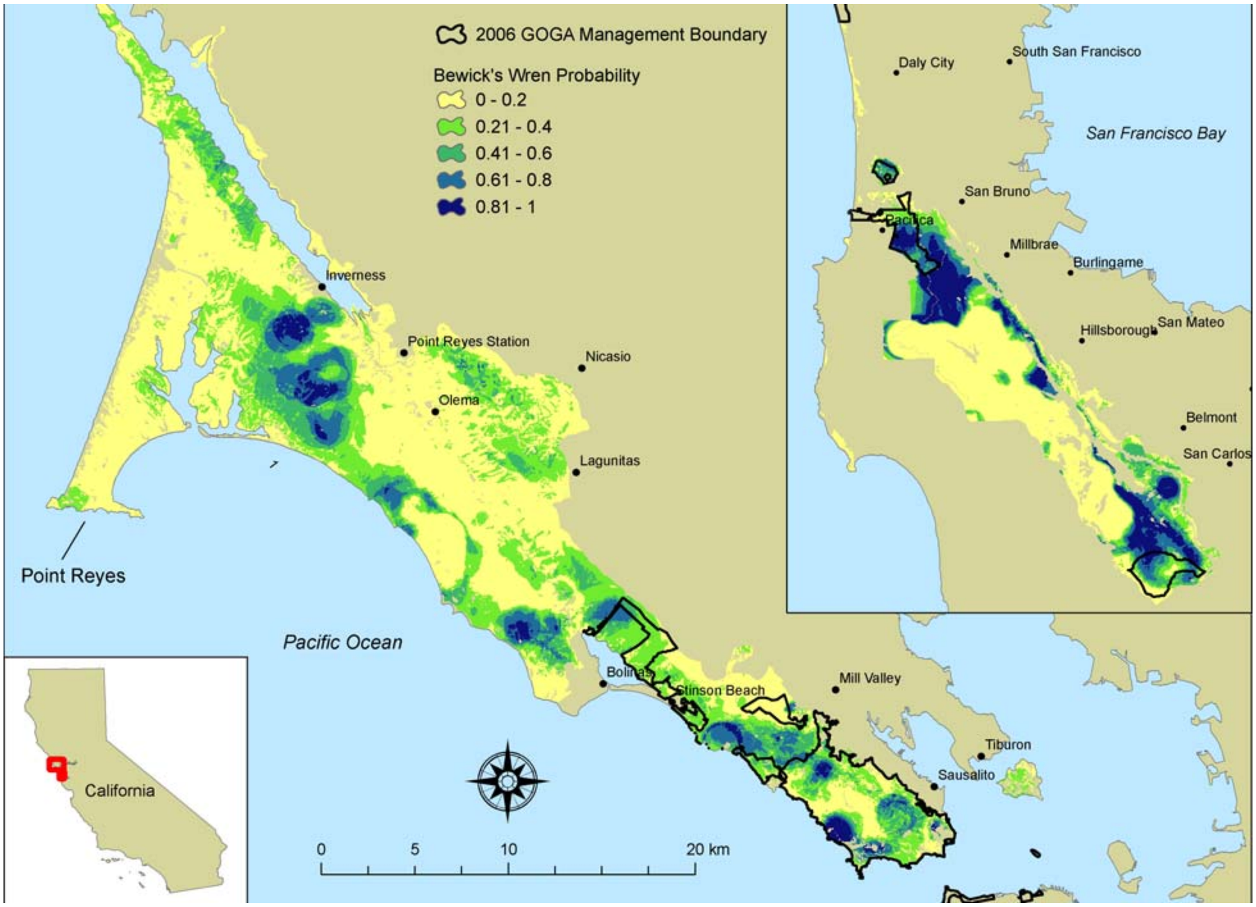


Figure 26. Predicted probability of Bewick's Wren occurrence based on a generalized additive model with a binomial distribution and logistic link function. Variables in the final model (Figures 24, 25) were selected from an *a priori* list (Appendix 3) using a stepwise backwards elimination AIC-minimizing procedure.

Brown Creeper

Just three variables were retained in the final model for Brown Creeper: conifer patch cohesion, number of survey visits, and local vegetation class, in order of model contribution (Figure 27). The relationships with conifer cohesion and number of survey visits were generally positive (Figure 28). Hardwood, followed by conifer vegetation classes provided the biggest increase in probability of occurrence (Figure 28). Trail density was not an important variable for this species. Predicted patterns of Brown Creeper probability of occurrence are shown in Figure 29.

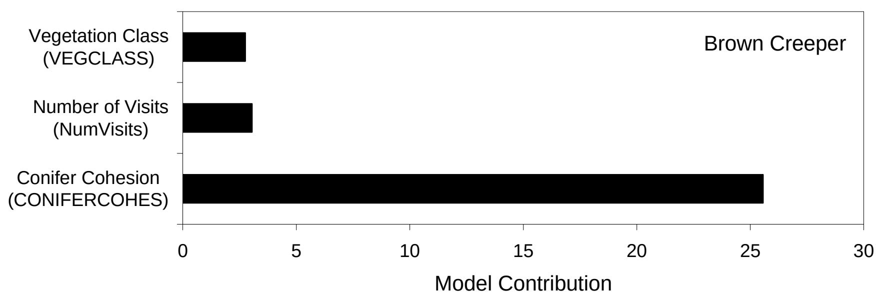


Figure 27. Model contributions of variables in the final model for Brown Creeper probability of occurrence. Each variable's contribution was defined as the difference in model-predicted probability of occurrence (before back-transformation) between the minimum and maximum values of that variable. Model contribution units are specific to each avian metric and are not comparable across different species and metrics.

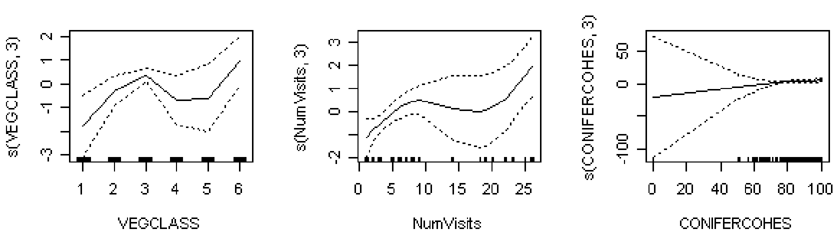


Figure 28. Partial response curves for variables in the final model for Brown Creeper probability of occurrence (holding all other variables at their mean values). See Table 4 for variable definitions. Y-axes represent deviations from the mean (before back-transformation) and are comparable across variables. Dashed lines represent upper and lower error bounds (2 SE). Tick marks along x-axes represent variable values for individual point count locations (more observations = higher model confidence).

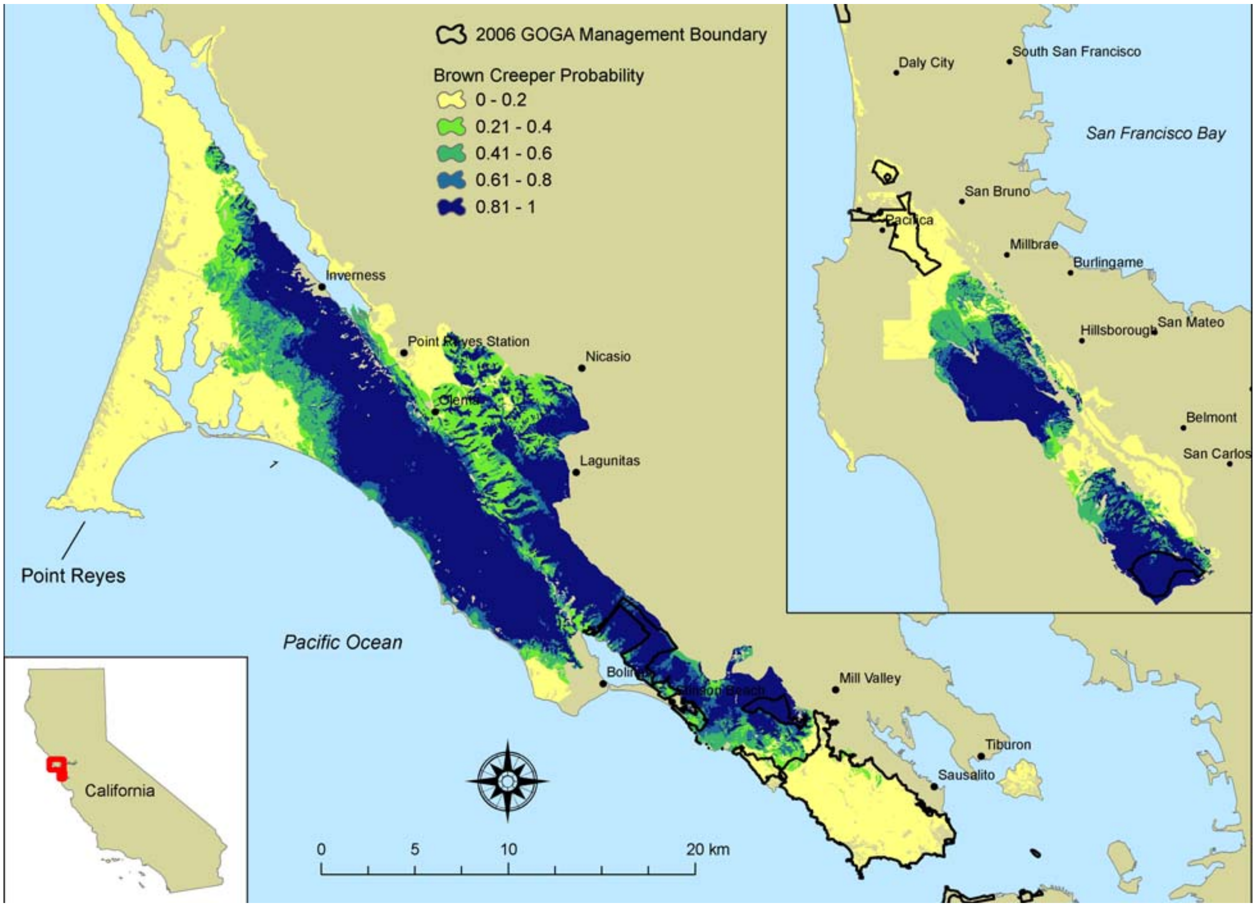


Figure 29. Predicted probability of Brown Creeper occurrence based on a generalized additive model with a binomial distribution and logistic link function. Variables in the final model (Figures 27, 28) were selected from an *a priori* list (Appendix 3) using a stepwise backwards elimination AIC-minimizing procedure.

Common Yellowthroat

Five variables were retained in the final model for Common Yellowthroat probability of occurrence. By far the largest contribution was from the percent broom variable, which had a negative effect (Figures 30, 31). Percent wetland within a 1-km radius (positive), stream distance (negative), and trail density (positive) were also important variables for this species (Figure 30, 31). Local vegetation class had the smallest model contribution, but of the six vegetation classes, wetland, followed by scrub and grassland, led to the biggest increase in probability of occurrence. Predicted patterns of Common Yellowthroat probability of occurrence are shown in Figure 32.

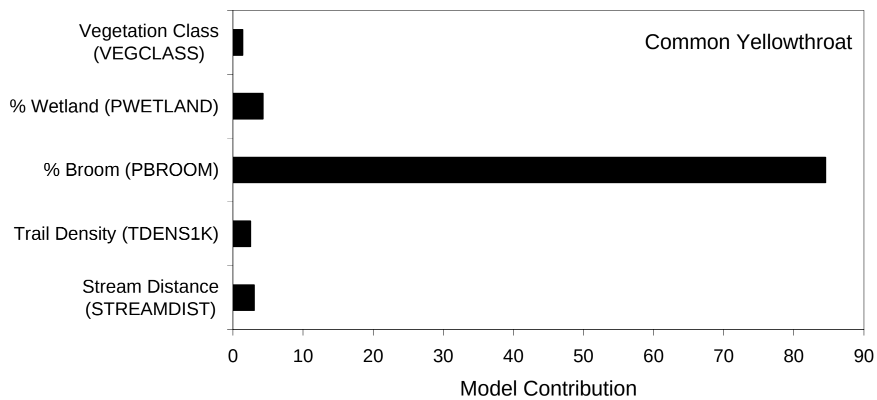


Figure 30. Model contributions of variables in the final model for Common Yellowthroat probability of occurrence. Each variable's contribution was defined as the difference in model-predicted probability of occurrence (before back-transformation) between the minimum and maximum values of that variable. Model contribution units are specific to each avian metric and are not comparable across different species and metrics.

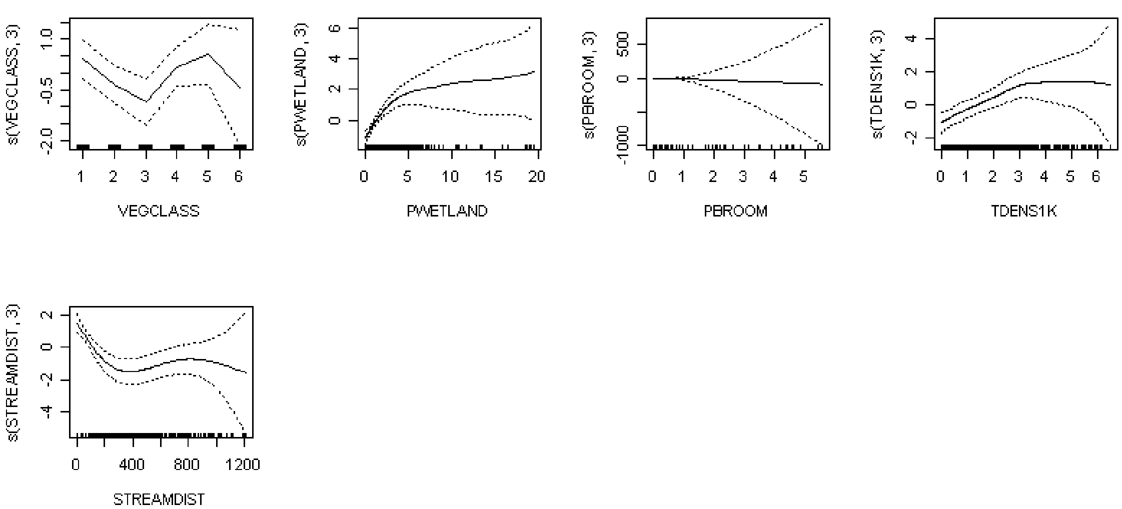


Figure 31. Partial response curves for variables in the final model for Common Yellowthroat probability of occurrence (holding all other variables at their mean values). See Table 4 for variable definitions. Y-axes represent deviations from the mean (before back-transformation) and are comparable across variables. Dashed lines represent upper and lower error bounds (2 SE). Tick marks along x-axes represent variable values for individual point count locations (more observations = higher model confidence).

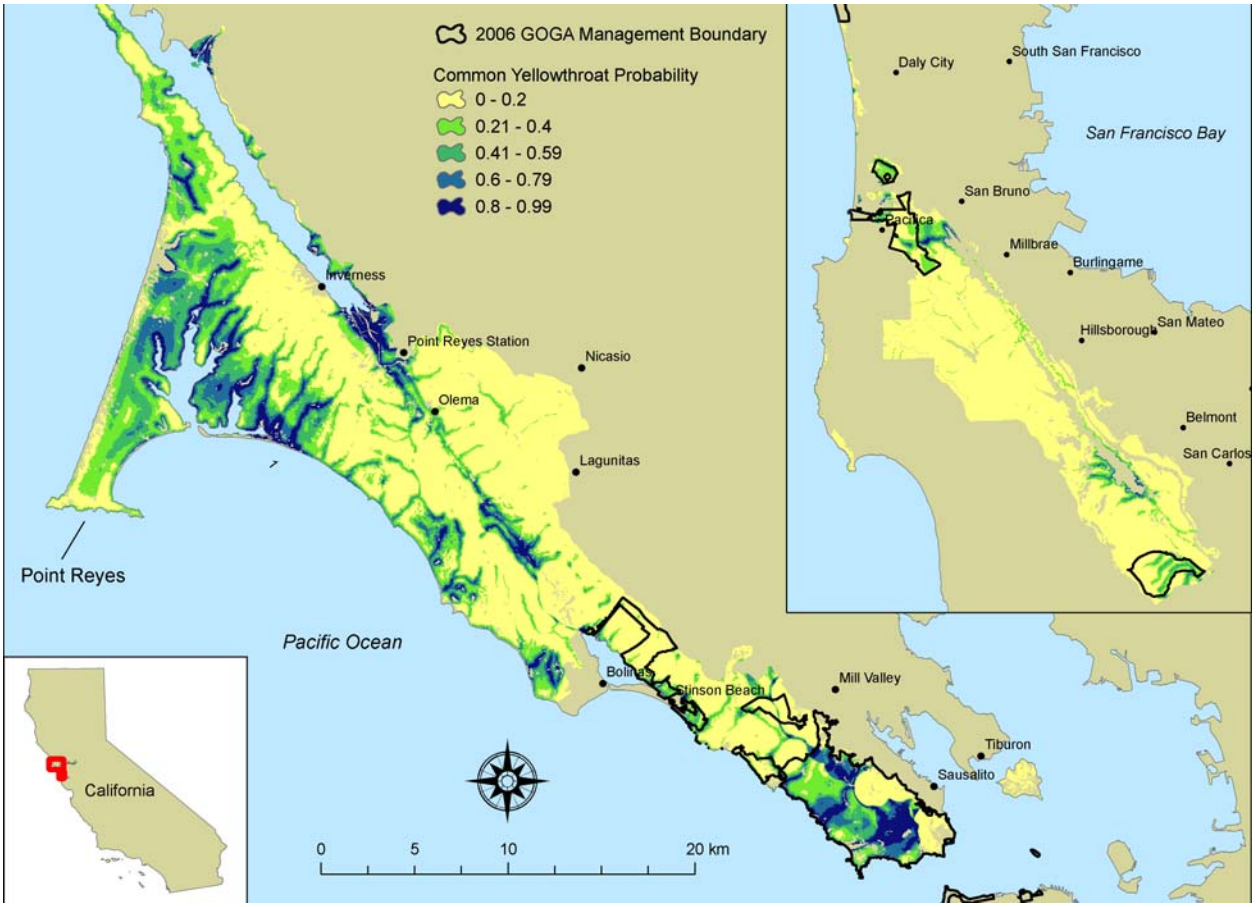


Figure 32. Predicted probability of Common Yellowthroat occurrence based on a generalized additive model with a binomial distribution and logistic link function. Variables in the final model (Figures 30, 31) were selected from an *a priori* list (Appendix 3) using a stepwise backwards elimination AIC-minimizing procedure.

Golden-crowned Kinglet

Four variables were retained in the final model for Golden-crowned Kinglet probability of occurrence, with the largest model contribution provided by mean elevation within a 1-km radius (positive), followed by local vegetation class, number of survey visits (positive), and percent Douglas-fir vegetation (positive) (Figures 33, 34). Highest probability of occurrence was associated with the conifer vegetation class, followed by hardwood vegetation (Figure 34). Predicted patterns of Golden-crowned Kinglet probability of occurrence are shown in Figure 35.

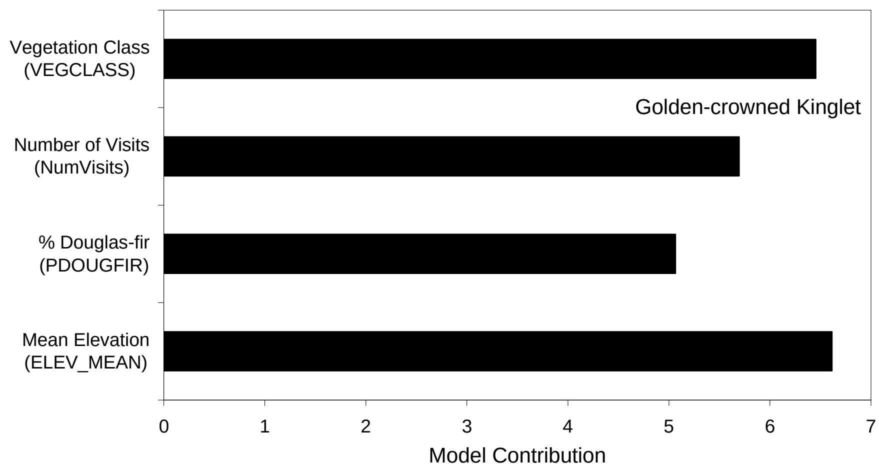


Figure 33. Model contributions of variables in the final model for Golden-crowned Kinglet probability of occurrence. Each variable's contribution was defined as the difference in model-predicted probability of occurrence (before back-transformation) between the minimum and maximum values of that variable. Model contribution units are specific to each avian metric and are not comparable across different species and metrics.

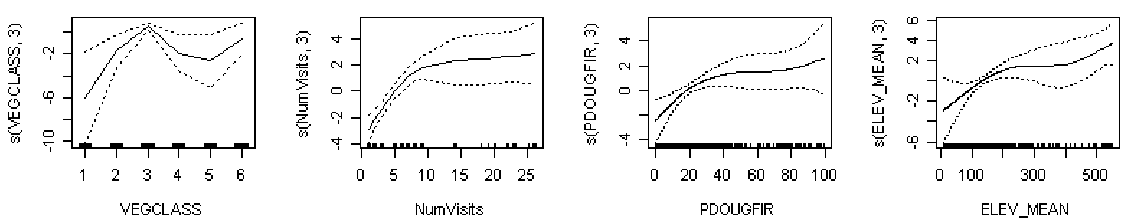


Figure 34. Partial response curves for variables in the final model for Golden-crowned Kinglet probability of occurrence (holding all other variables at their mean values). See Table 4 for variable definitions. Y-axes represent deviations from the mean (before back-transformation) and are comparable across variables. Dashed lines represent upper and lower error bounds (2 SE). Tick marks along x-axes represent variable values for individual point count locations (more observations = higher model confidence).

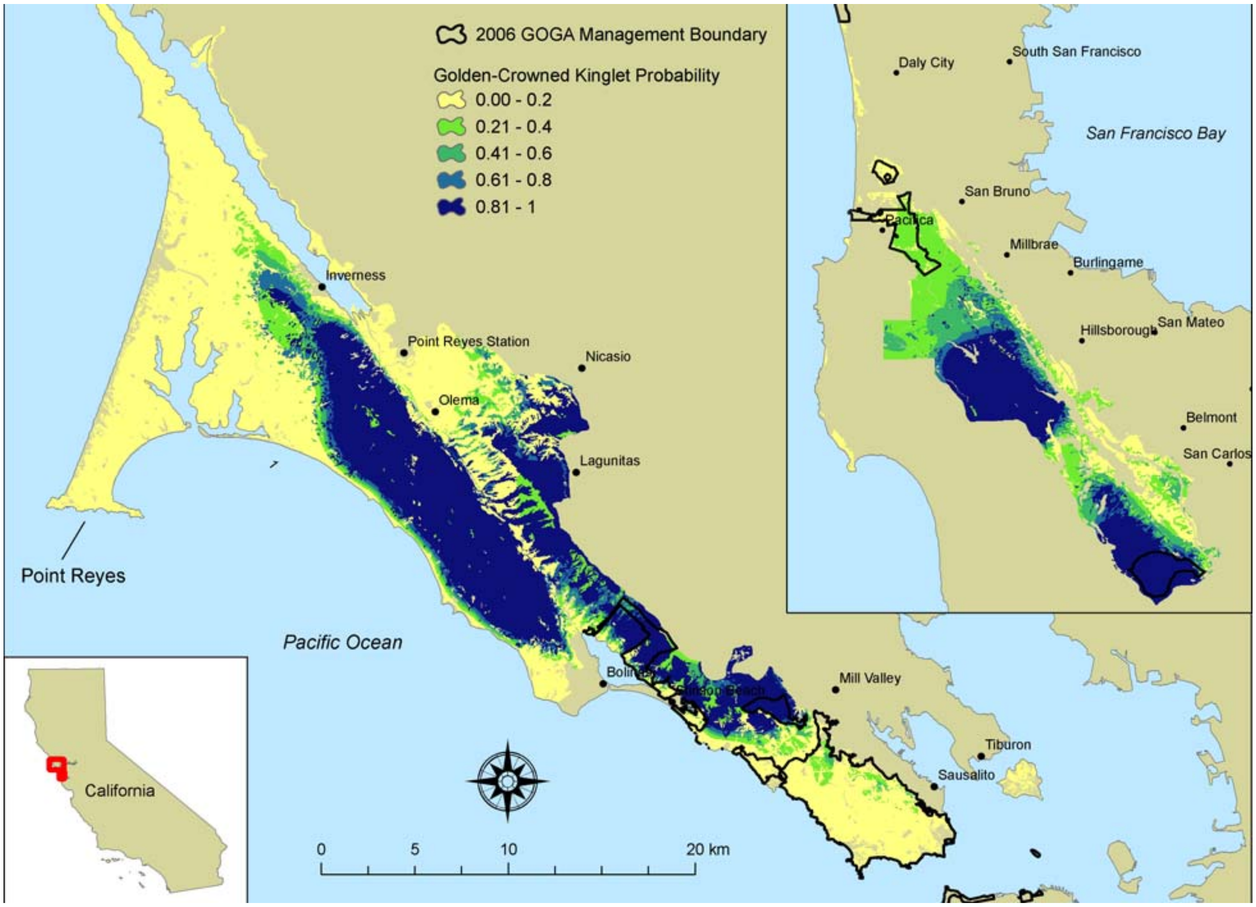
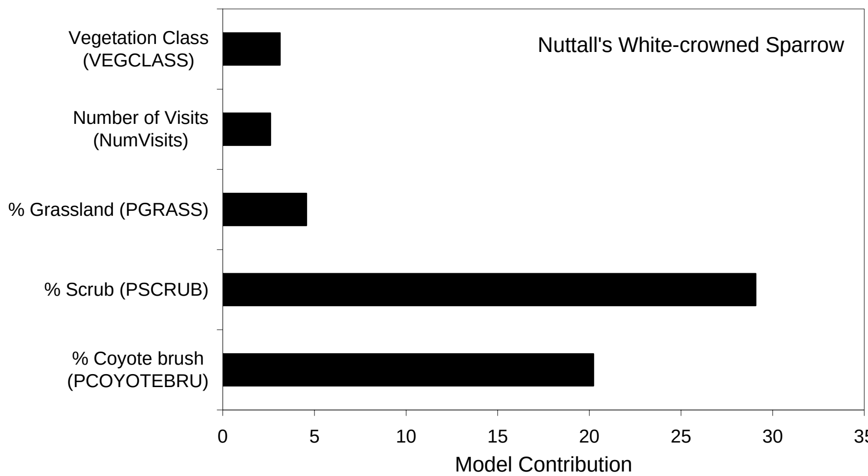


Figure 35. Predicted probability of Golden-crowned Kinglet occurrence based on a generalized additive model with a binomial distribution and logistic link function. Variables in the final model (Figures 33, 34) were selected from an *a priori* list (Appendix 3) using a stepwise backwards elimination AIC-minimizing procedure.

Nuttall's White-crowned Sparrow

The final model for Nuttall's White-crowned Sparrow probability of occurrence contained five variables, with the highest contribution provided by percent scrub vegetation (positive effect), followed by percent coyote brush (negative effect) (Figures 36, 37). Percent grassland (positive), number of survey visits (increasing until approximately 20 visits, then declining), and vegetation class were also included in the final model, with smaller relative contributions (Figures 36, 37). Scrub vegetation, followed by grassland, led to the highest increase in probability of occurrence. Predicted patterns of Nuttall's White-crowned Sparrow probability of occurrence are shown in Figure 38.

Figure 36. Model contributions of variables in the final model for Nuttall's White-crowned Sparrow probability of occurrence. Each variable's contribution was defined as the difference in model-predicted probability of occurrence (before back-transformation) between the minimum and maximum values of that variable. Model contribution units are specific to each avian metric and are not comparable across different species and metrics.



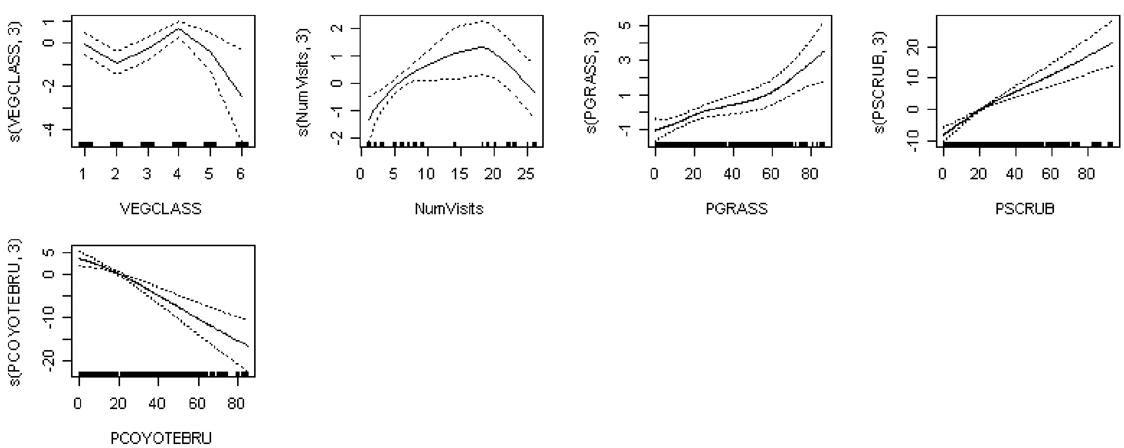


Figure 37. Partial response curves for variables in the final model for Nuttall's White-crowned Sparrow probability of occurrence (holding all other variables at their mean values). See Table 4 for variable definitions. Y-axes represent deviations from the mean (before back-transformation) and are comparable across variables. Dashed lines represent upper and lower error bounds (2 SE). Tick marks along x-axes represent variable values for individual point count locations (more observations = higher model confidence).

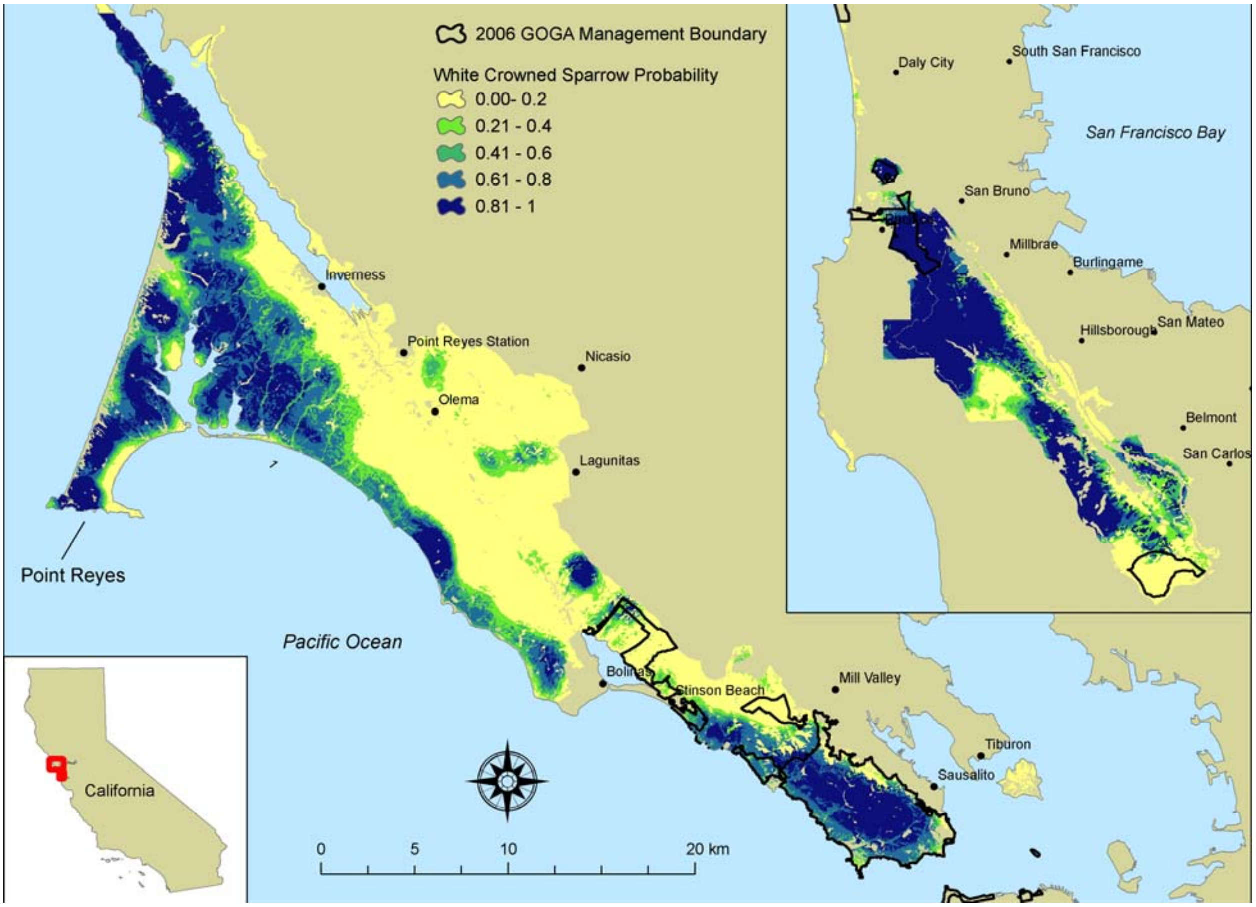


Figure 38. Predicted probability of Nuttall's White-crowned Sparrow occurrence based on a generalized additive model with a binomial distribution and logistic link function. Variables in the final model (Figures 36, 37) were selected from an *a priori* list (Appendix 3) using a stepwise backwards elimination AIC-minimizing procedure.

Dark-eyed Junco

Just three variables were retained in the final model for Dark-eyed Junco probability of occurrence: conifer patch cohesion within a 1-km radius (positive), mean slope within a 1-km radius (positive), and vegetation class (Figures 39, 40). The most important vegetation class was hardwood. The number of survey visits was not included in the final model; neither was trail density. Predicted patterns of Dark-eyed Junco probability of occurrence are shown in Figure 41.

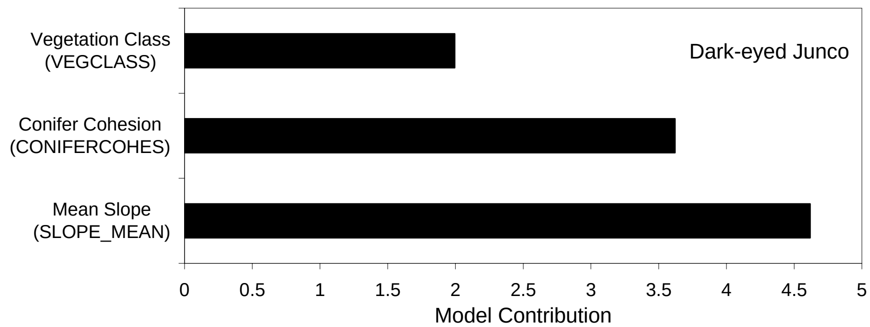


Figure 39. Model contributions of variables in the final model for Dark-eyed Junco probability of occurrence. Each variable's contribution was defined as the difference in model-predicted probability of occurrence (before back-transformation) between the minimum and maximum values of that variable. Model contribution units are specific to each avian metric and are not comparable across different species and metrics.

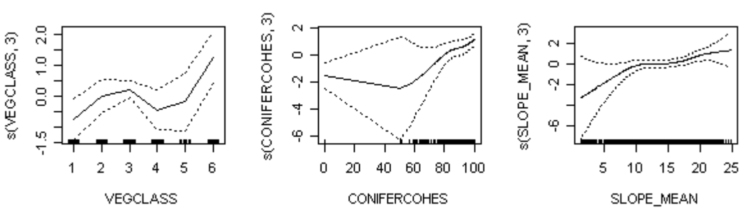


Figure 40. Partial response curves for variables in the final model for Dark-eyed Junco probability of occurrence (holding all other variables at their mean values). See Table 4 for variable definitions. Y-axes represent deviations from the mean (before back-transformation) and are comparable across variables. Dashed lines represent upper and lower error bounds (2 SE). Tick marks along x-axes represent variable values for individual point count locations (more observations = higher model confidence).

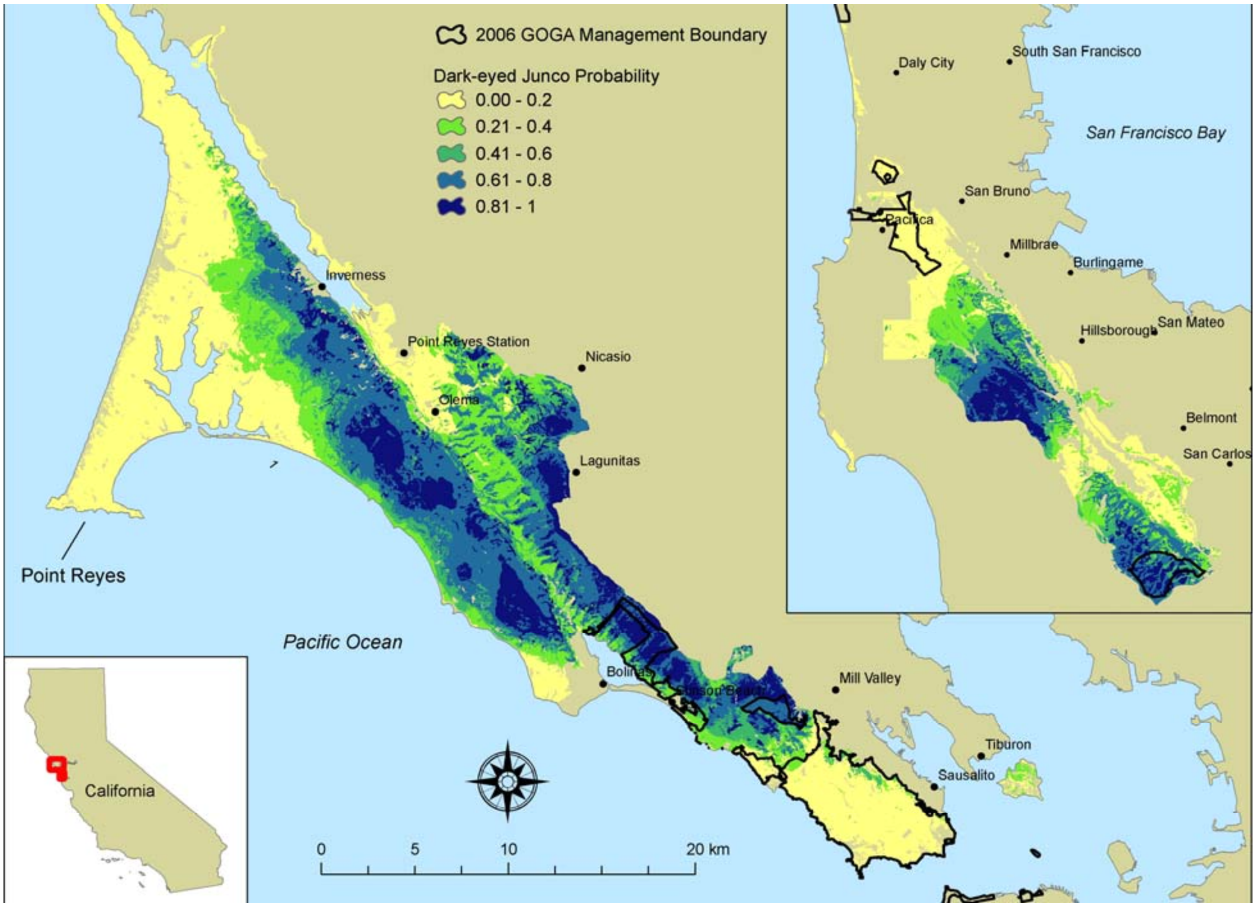
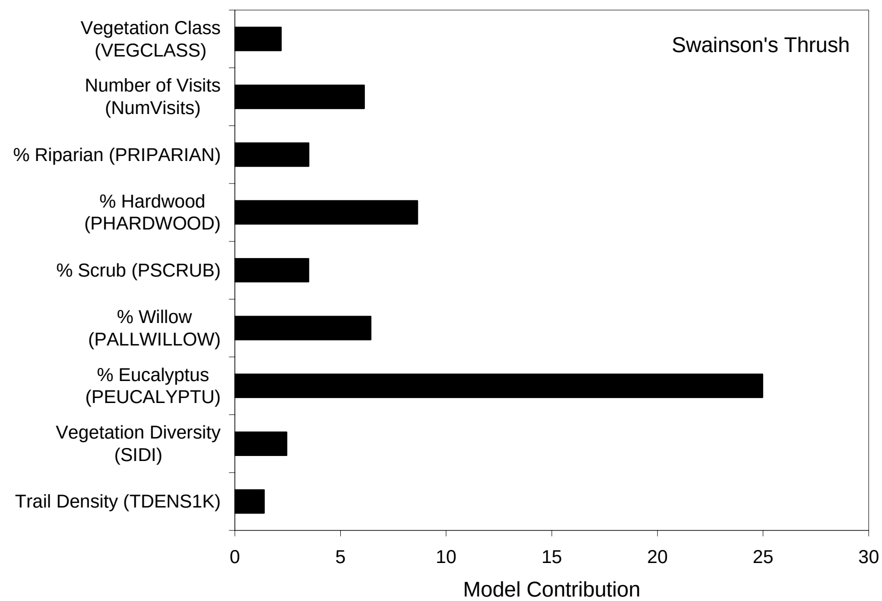


Figure 41. Predicted probability of Dark-eyed Junco occurrence based on a generalized additive model with a binomial distribution and logistic link function. Variables in the final model (Figures 39, 40) were selected from an *a priori* list (Appendix 3) using a stepwise backwards elimination AIC-minimizing procedure.

Swainson's Thrush

Nine variables were included in the final model for Swainson's Thrush probability of occurrence (Figures 42, 43). Percent eucalyptus within a 1-km radius had, by far, the largest model contribution, with a negative effect (Figures 42, 43). Percent hardwood (negative), percent willow (positive), and the number of survey visits (positive) also had high model contributions (Figures 42, 43). The effect of the number of visits was steeply positive, not leveling off, even after 25 visits. The effect of trail density was positive in the lower ranges of the variable, but negative in its upper ranges (Figure 43). In terms of vegetation class, hardwood was the most important, followed by riparian and conifer (Figure 43). Predicted patterns of Swainson's Thrush probability of occurrence are shown in Figure 44.

Figure 42. Model contributions of variables in the final model for Swainson's Thrush probability of occurrence. Each variable's contribution was defined as the difference in model-predicted probability of occurrence (before back-transformation) between the minimum and maximum values of that variable. Model contribution units are specific to each avian metric and are not comparable across different species and metrics.



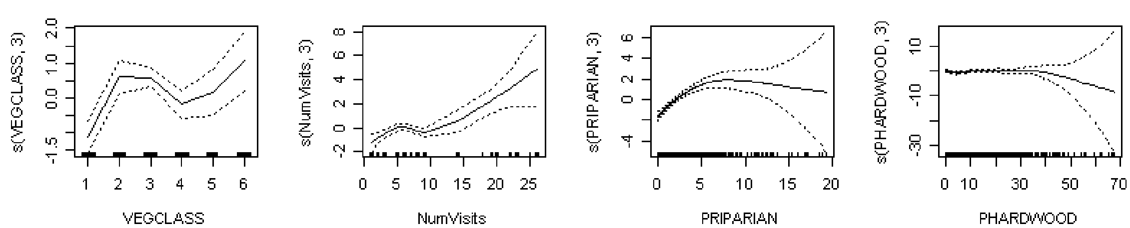


Figure 43. Partial response curves for variables in the final model for Swainson's Thrush probability of occurrence (holding all other variables at their mean values). See Table 4 for variable definitions. Y-axes represent deviations from the mean (before back-transformation) and are comparable across variables. Dashed lines represent upper and lower error bounds (2 SE). Tick marks along x-axes represent variable values for individual point count locations (more observations = higher model confidence).

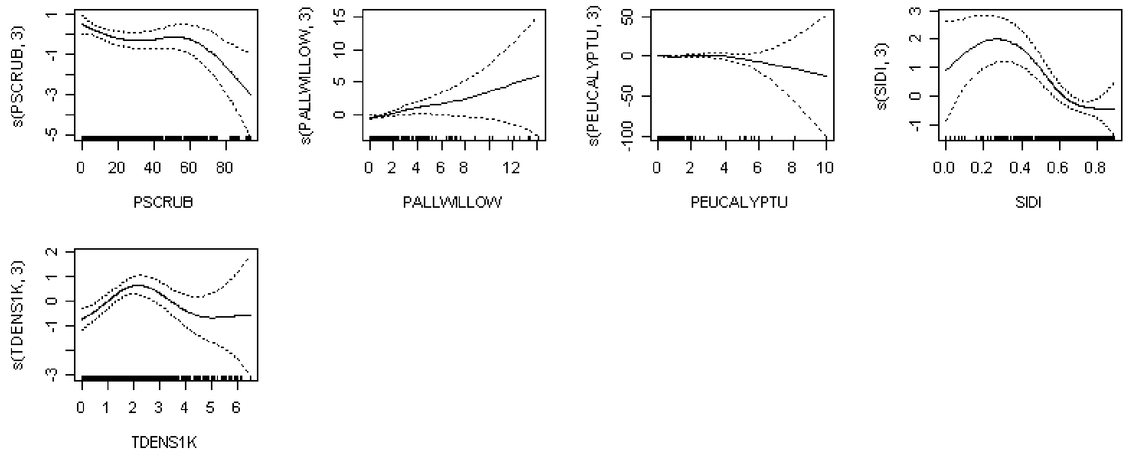


Figure 43. Continued.

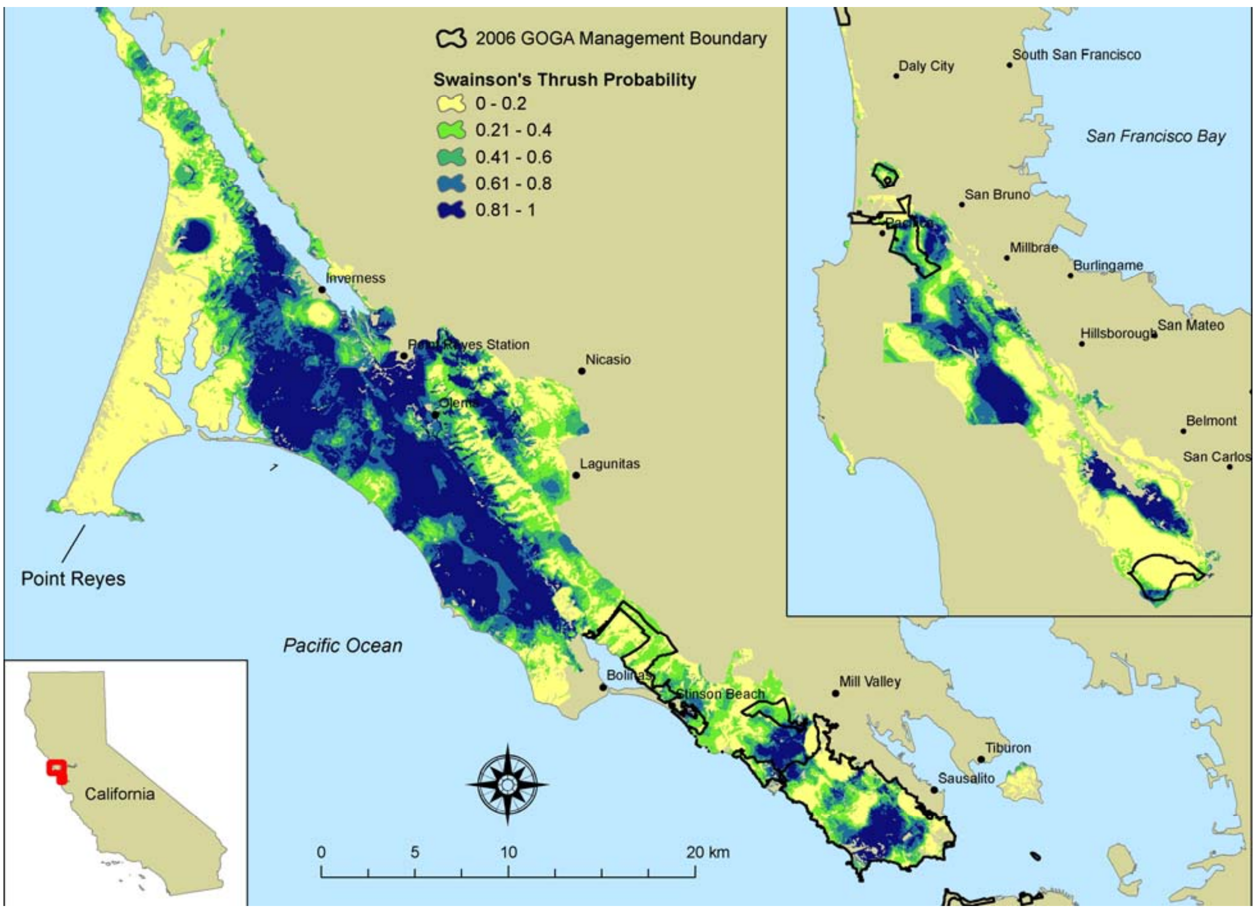


Figure 44. Predicted probability of Swainson's Thrush occurrence based on a generalized additive model with a binomial distribution and logistic link function. Variables in the final model (Figures 42, 43) were selected from an *a priori* list (Appendix 3) using a stepwise backwards elimination AIC-minimizing procedure.

Warbling Vireo

There were four variables retained in the final model for Warbling Vireo probability of occurrence (Figure 45). The variable with the highest model contribution was stream distance (sharply negative), followed by number of visits (sharply positive), percent California bay laurel (*Umbellularia californica*) within a 1-km radius (positive), and vegetation class (Figures 45, 46). Hardwood, followed by conifer, vegetation classes were the most important for this species (Figure 46). Predicted patterns of Warbling Vireo probability of occurrence are shown in Figure 47.

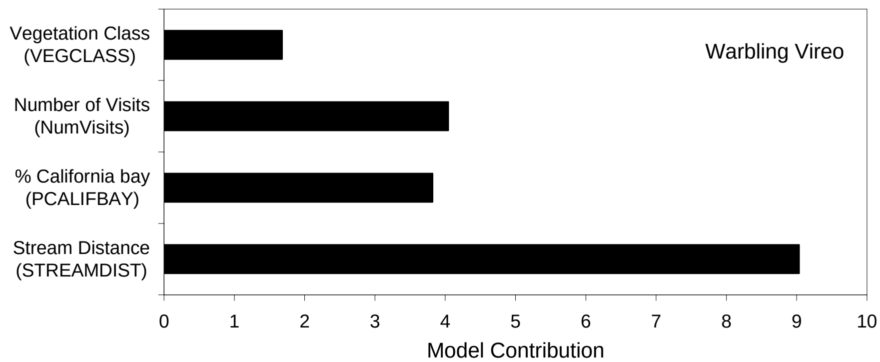


Figure 45. Model contributions of variables in the final model for Warbling Vireo probability of occurrence. Each variable's contribution was defined as the difference in model-predicted probability of occurrence (before back-transformation) between the minimum and maximum values of that variable. Model contribution units are specific to each avian metric and are not comparable across different species and metrics.

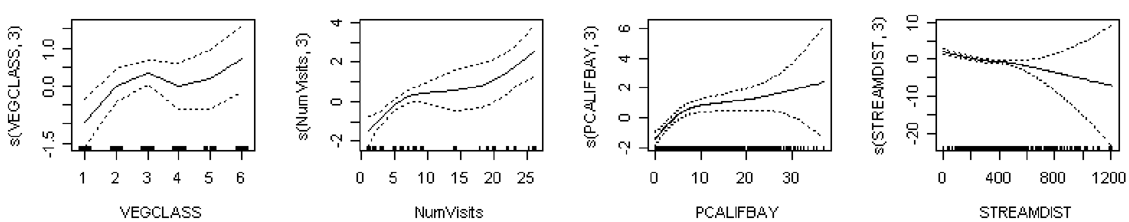


Figure 46. Partial response curves for variables in the final model for Warbling Vireo probability of occurrence (holding all other variables at their mean values). See Table 4 for variable definitions. Y-axes represent deviations from the mean (before back-transformation) and are comparable across variables. Dashed lines represent upper and lower error bounds (2 SE). Tick marks along x-axes represent variable values for individual point count locations (more observations = higher model confidence).

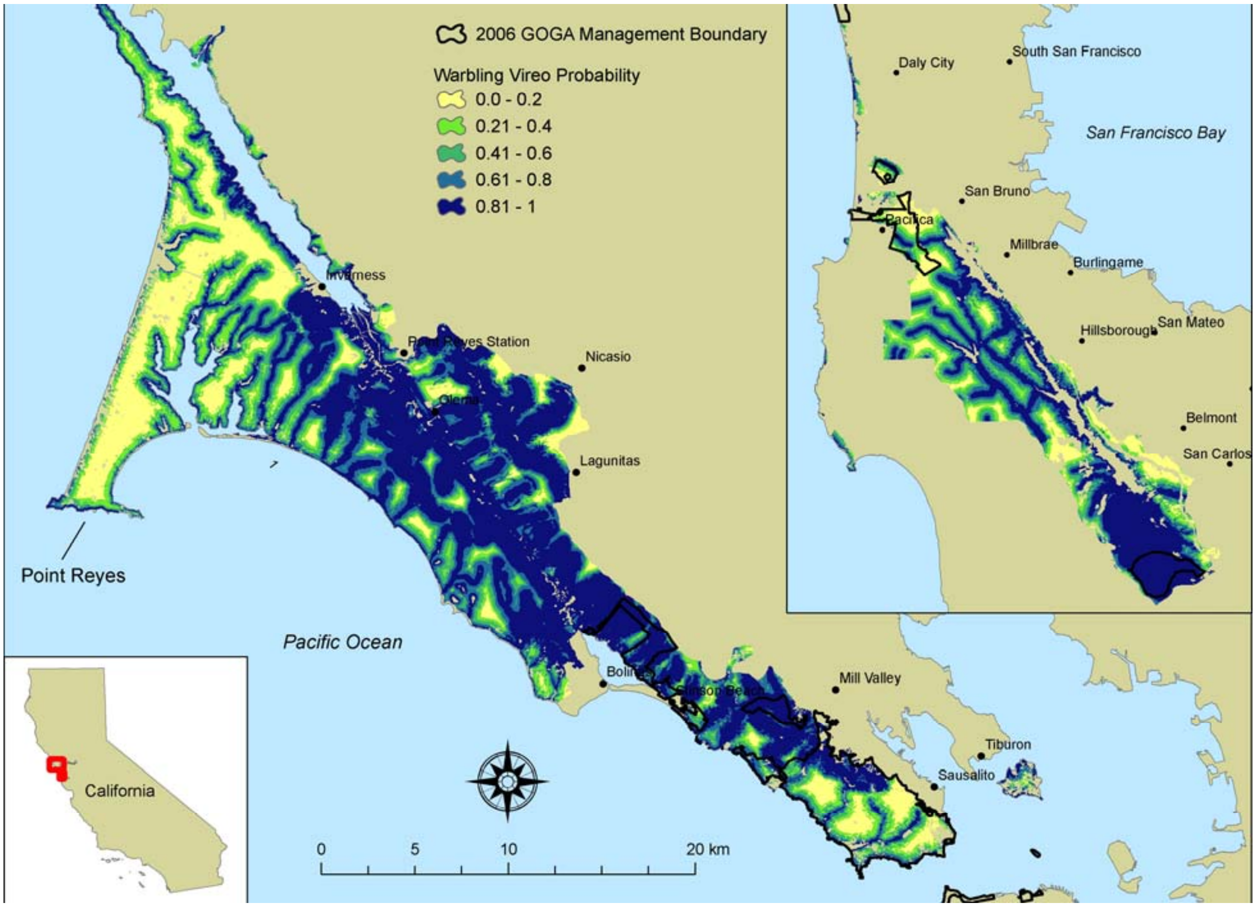
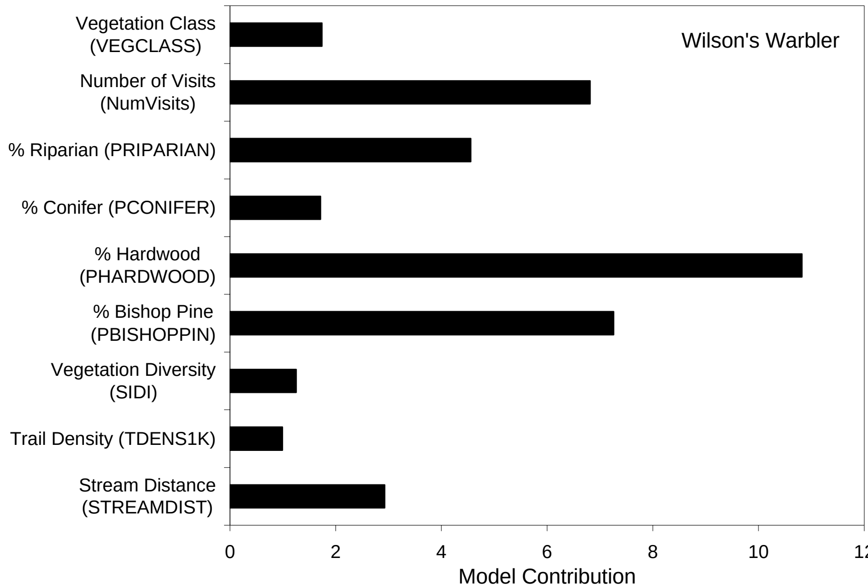


Figure 47. Predicted probability of Warbling Vireo occurrence based on a generalized additive model with a binomial distribution and logistic link function. Variables in the final model (Figures 45, 46) were selected from an *a priori* list (Appendix 3) using a stepwise backwards elimination AIC-minimizing procedure.

Wilson's Warbler

The final model for Wilson's Warbler probability of occurrence contained nine variables (Figure 48), with the largest model contribution provided by percent hardwood vegetation within a 1-km radius (negative), followed by percent bishop pine (*Pinus muricata*) within 1-km (positive), and the number of survey visits (sharply positive) (Figures 48, 49). There was also a strong positive effect of percent riparian vegetation within a 1-km radius, while the effect of trail density was small and non-linear (Figures 48, 49). In terms of vegetation class, hardwood, followed by conifer and riparian classes, led to the largest increase in probability of occurrence. Predicted patterns of Wilson's Warbler probability of occurrence are shown in Figure 50.

Figure 48. Model contributions of variables in the final model for Wilson's Warbler probability of occurrence. Each variable's contribution was defined as the difference in model-predicted probability of occurrence (before back-transformation) between the minimum and maximum values of that variable. Model contribution units are specific to each avian metric and are not comparable across different species and metrics.



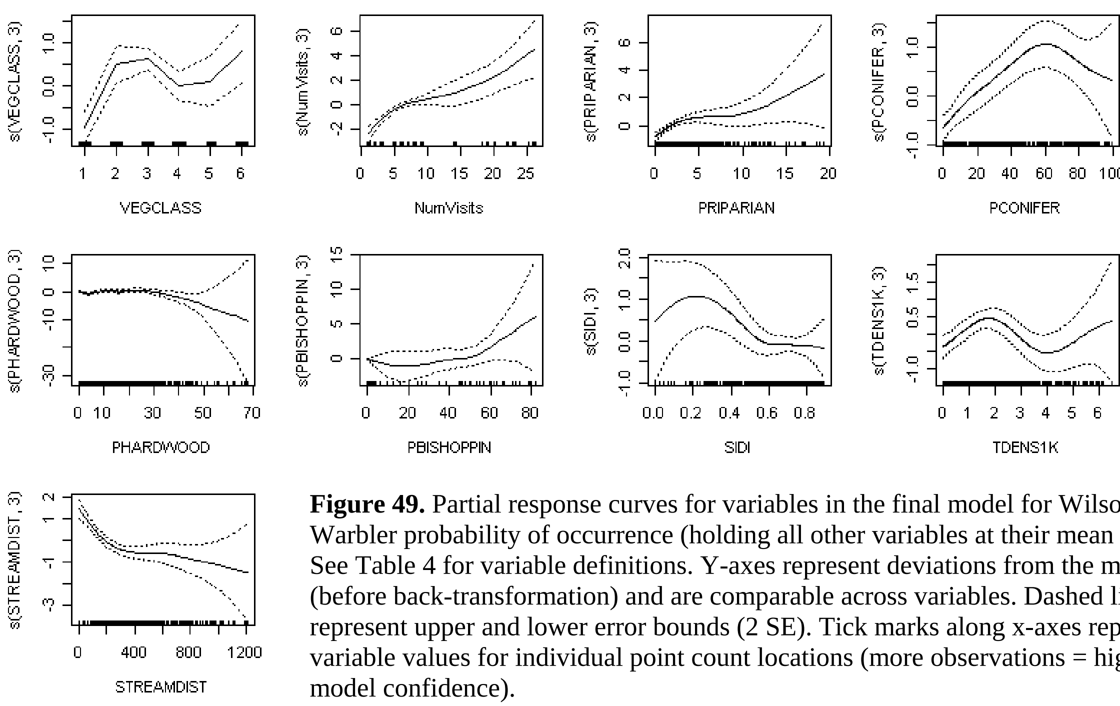


Figure 49. Partial response curves for variables in the final model for Wilson's Warbler probability of occurrence (holding all other variables at their mean values). See Table 4 for variable definitions. Y-axes represent deviations from the mean (before back-transformation) and are comparable across variables. Dashed lines represent upper and lower error bounds (2 SE). Tick marks along x-axes represent variable values for individual point count locations (more observations = higher model confidence).

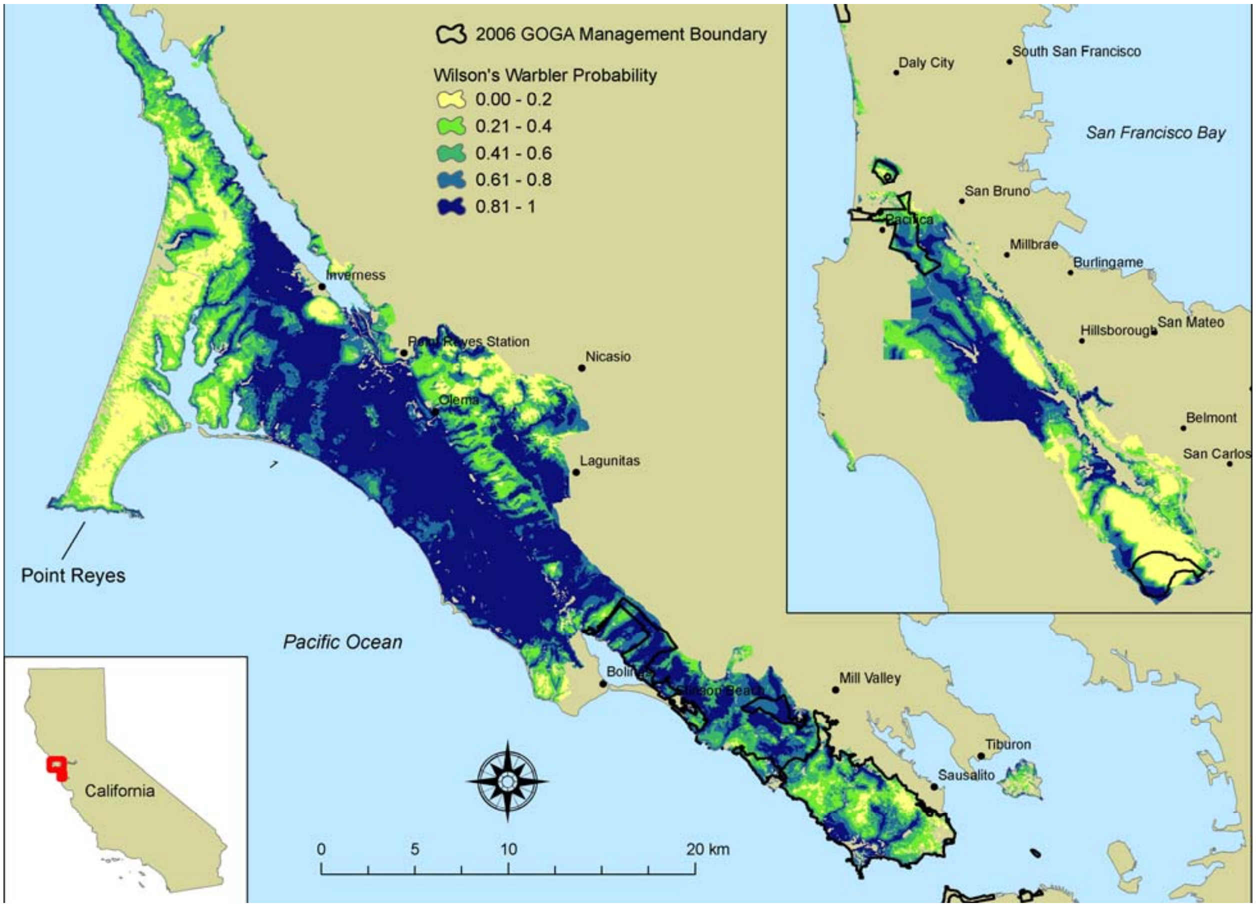


Figure 50. Predicted probability of Wilson's Warbler occurrence based on a generalized additive model with a binomial distribution and logistic link function. Variables in the final model (Figures 48, 49) were selected from an *a priori* list (Appendix 3) using a stepwise backwards elimination AIC-minimizing procedure.

Savannah Sparrow

The final model for Savannah Sparrow probability of occurrence contained just two variables: grassland cohesion within a 1-km radius (positive) and vegetation class (Figures 51, 52). The most important vegetation class was grassland, followed by scrub (Figure 52). Number of survey visits and trail density were not present in the final model. Predicted patterns of Savannah Sparrow probability of occurrence are shown in Figure 53.

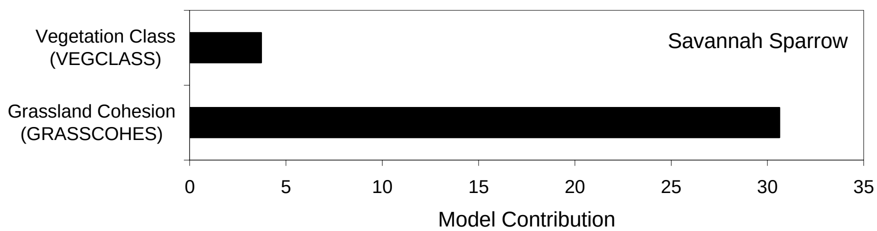


Figure 51. Model contributions of variables in the final model Savannah Sparrow probability of occurrence. Each variable's contribution was defined as the difference in model-predicted probability of occurrence (before back-transformation) between the minimum and maximum values of that variable. Model contribution units are specific to each avian metric and are not comparable across different species and metrics.

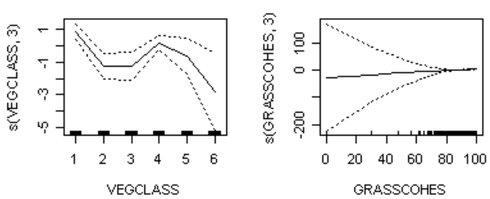


Figure 52. Partial response curves for variables in the final model for Savannah Sparrow probability of occurrence (holding all other variables at their mean values). See Table 4 for variable definitions. Y-axes represent deviations from the mean (before back-transformation) and are comparable across variables. Dashed lines represent upper and lower error bounds (2 SE). Tick marks along x-axes represent variable values for individual point count locations (more observations = higher model confidence).

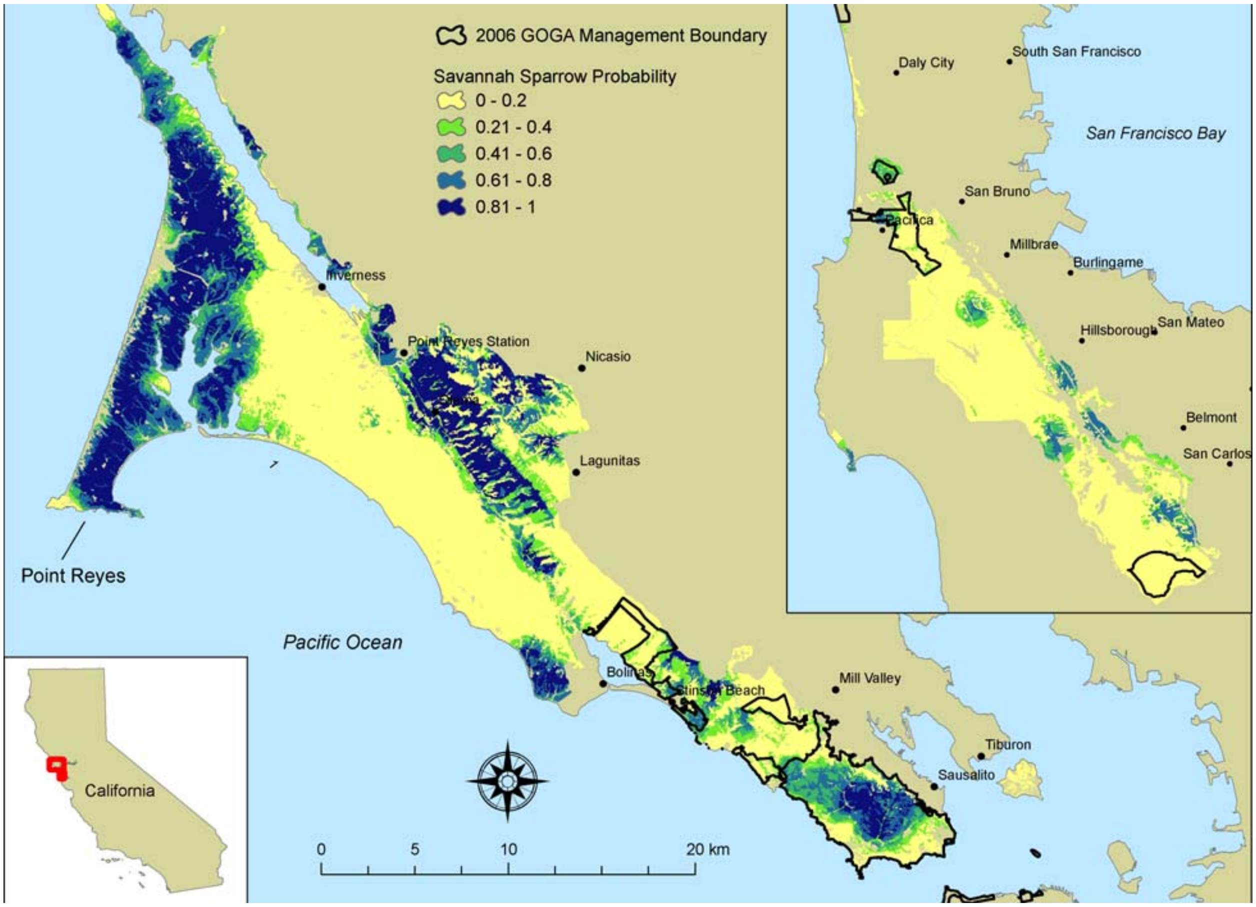


Figure 53. Predicted probability of Savannah Sparrow occurrence based on a generalized additive model with a binomial distribution and logistic link function. Variables in the final model (Figures 51, 52) were selected from an *a priori* list (Appendix 3) using a stepwise backwards elimination AIC-minimizing procedure.

Combined species indices

Summing up various combinations of management-sensitive species' probabilities of occurrence resulted in four different spatial representations of priority areas, each associated with different management goals. We found that topographically diverse areas, primarily along major drainages, on both slopes of the Inverness and Bolinas ridges of PORE and GOGA lands in Marin County, as well as parts of the San Francisco peninsula watershed in San Mateo County, contained the highest predicted proportion of declining species (Figure 54). The areas with the highest predicted proportion of low-nesting species overlapped somewhat, but was more concentrated at lower coastal elevations, along major drainages such as Muddy Hollow and Glenbrook creeks within PORE, Gerbode and Tennessee valleys within GOGA's Marin Headlands, and parts of the Mori and Sweeney ridge parks on the San Francisco peninsula (Figure 55). Disturbance-sensitive species were concentrated primarily within core park areas, generally away from roads, except for along highway 1 in the Olema Valley (Figure 56). Combining models for all management-sensitive focal species, additional "hotspots" emerged, including the Arroyo Honda drainage near the Palomarin field station within PORE, Steep Ravine near Muir Woods within GOGA, and southern parts of the San Francisco peninsula watershed (Figure 57).

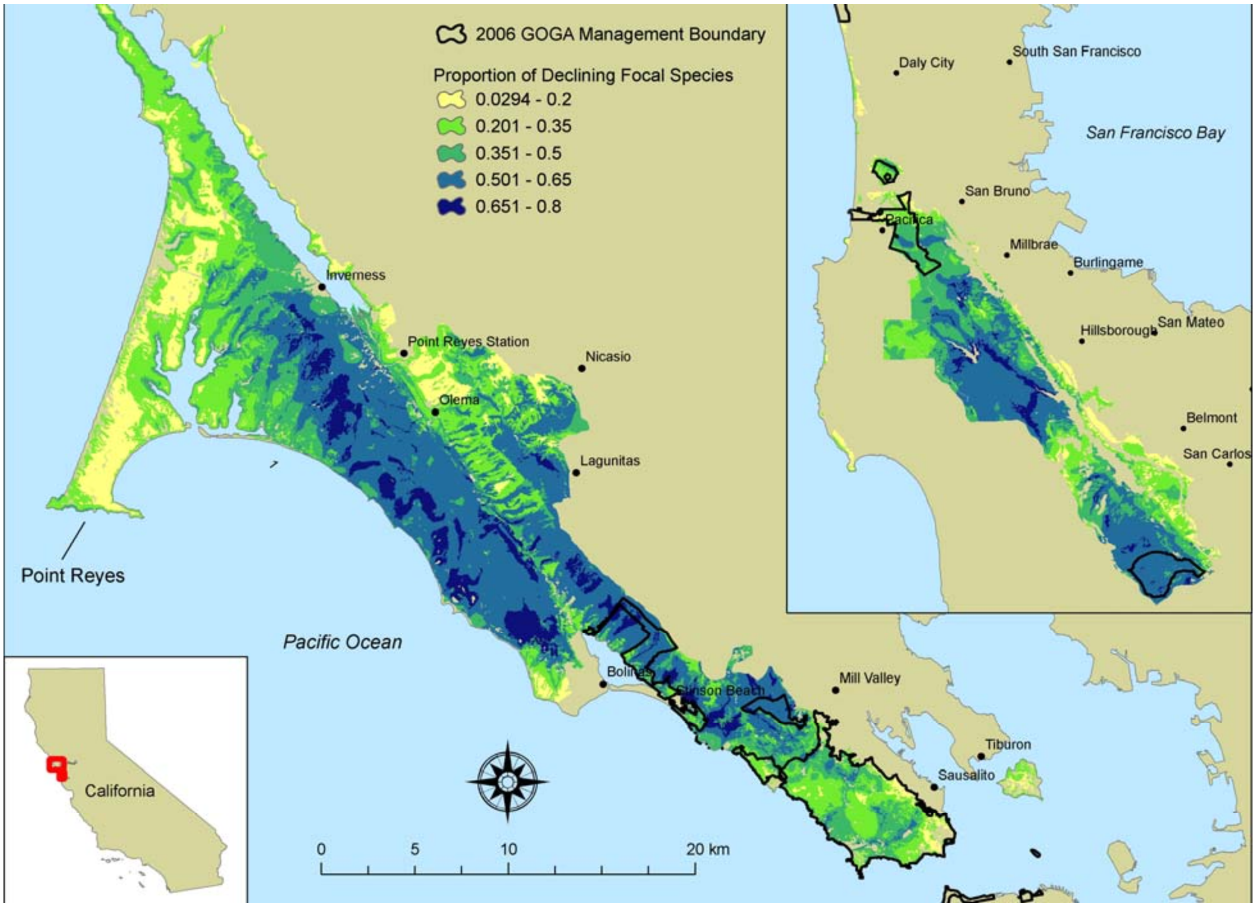


Figure 54a. Predicted proportion of declining focal species, based on the sum of model outputs for Common Yellowthroat, Warbling Vireo, Brown Creeper, Bewick's Wren, Wilson's Warbler, Nuttall's White-crowned Sparrow, Golden-crowned Kinglet, Dark-eyed Junco, and Savannah Sparrow.

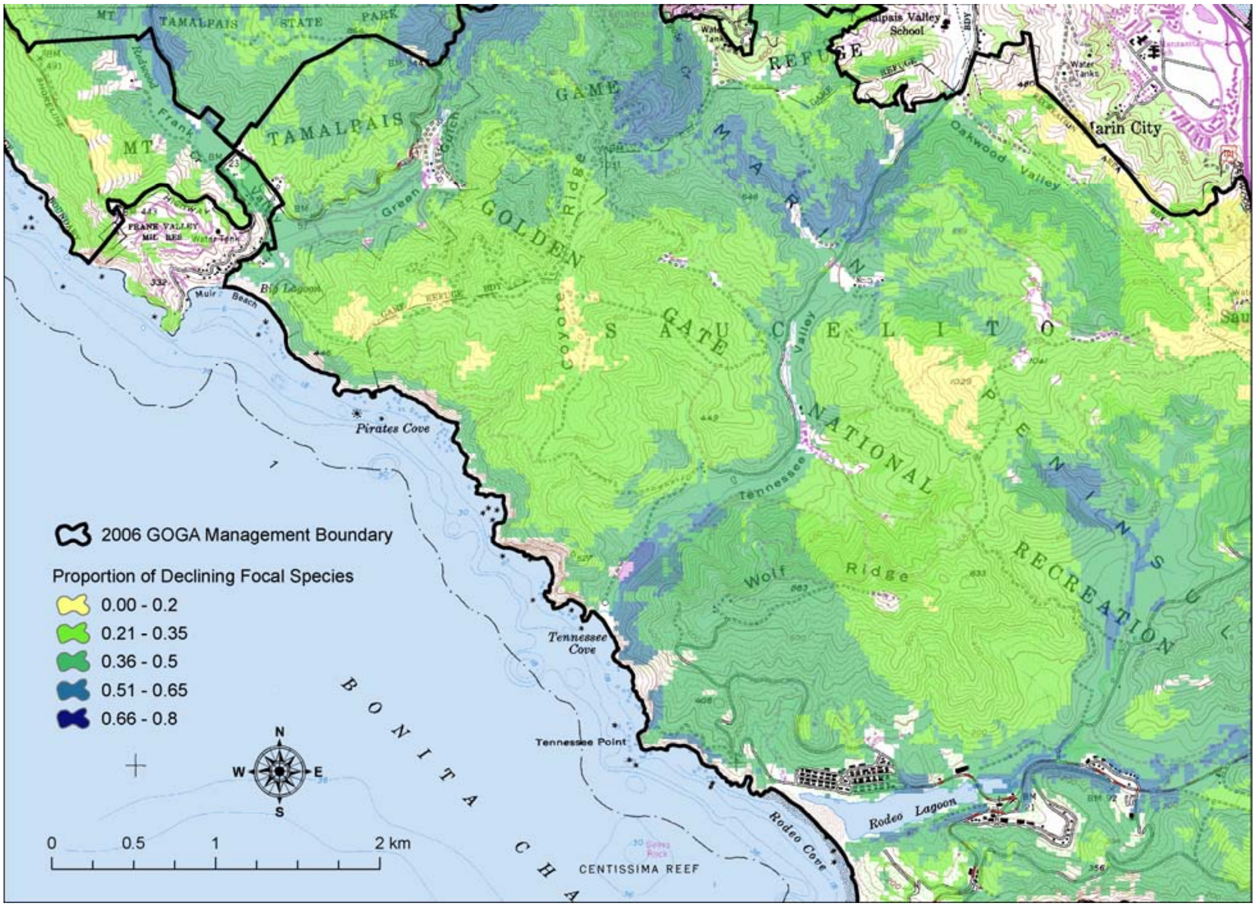


Figure 54b. Sample detail of predicted proportion of declining focal species, based on the sum of model outputs for Common Yellowthroat, Warbling Vireo, Brown Creeper, Bewick's Wren, Wilson's Warbler, Nuttall's White-crowned Sparrow, Golden-crowned Kinglet, Dark-eyed Junco, and Savannah Sparrow.

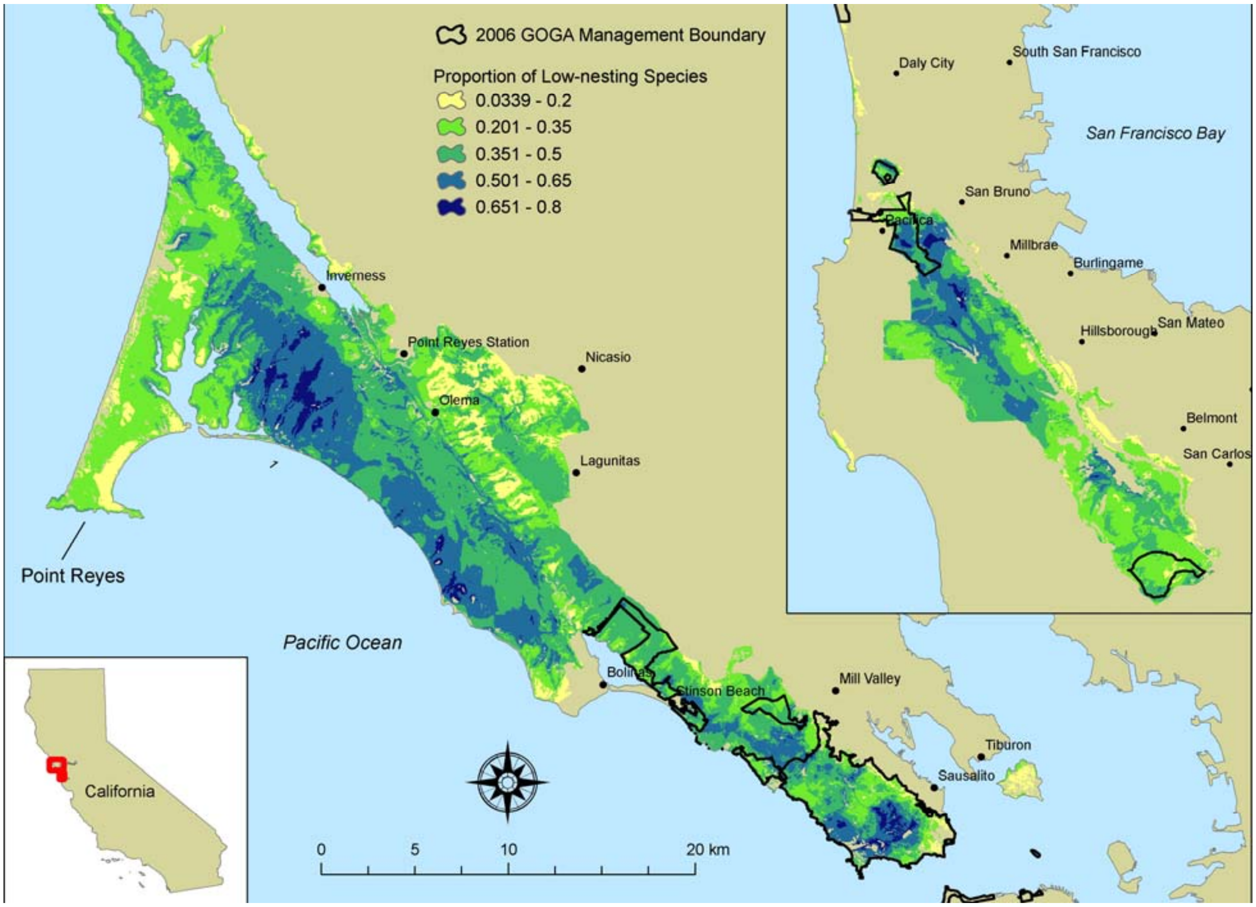


Figure 55a. Predicted proportion of low-nesting focal species, based on the sum of model outputs for Common Yellowthroat, Bewick's Wren, Wilson's Warbler, Nuttall's White-crowned Sparrow, Swainson's Thrush, Dark-eyed Junco, and Savannah Sparrow.

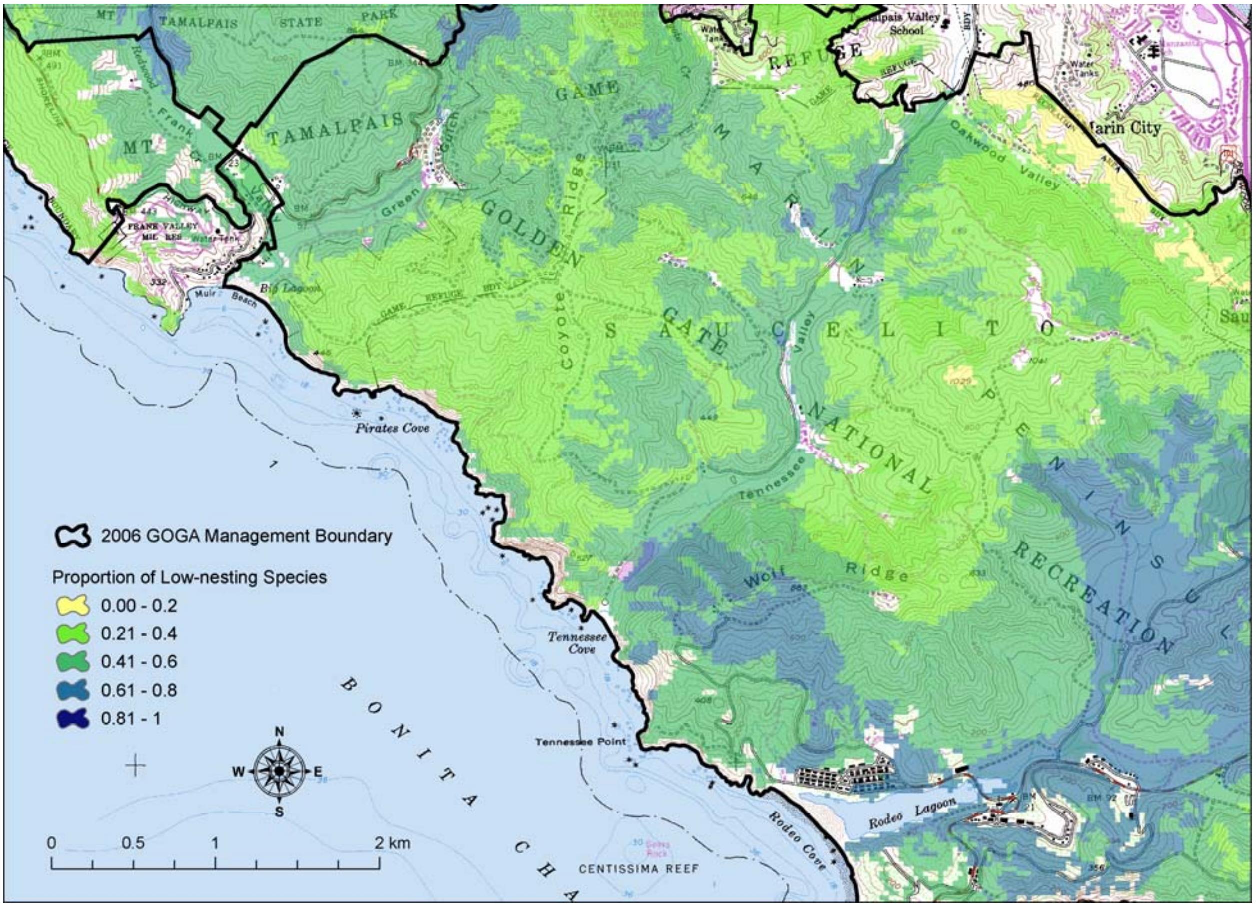


Figure 55b. Sample detail of predicted proportion of low-nesting focal species, based on the sum of model outputs for Common Yellowthroat, Bewick's Wren, Wilson's Warbler, Nuttall's White-crowned Sparrow, Swainson's Thrush, Dark-eyed Junco, and Savannah Sparrow.

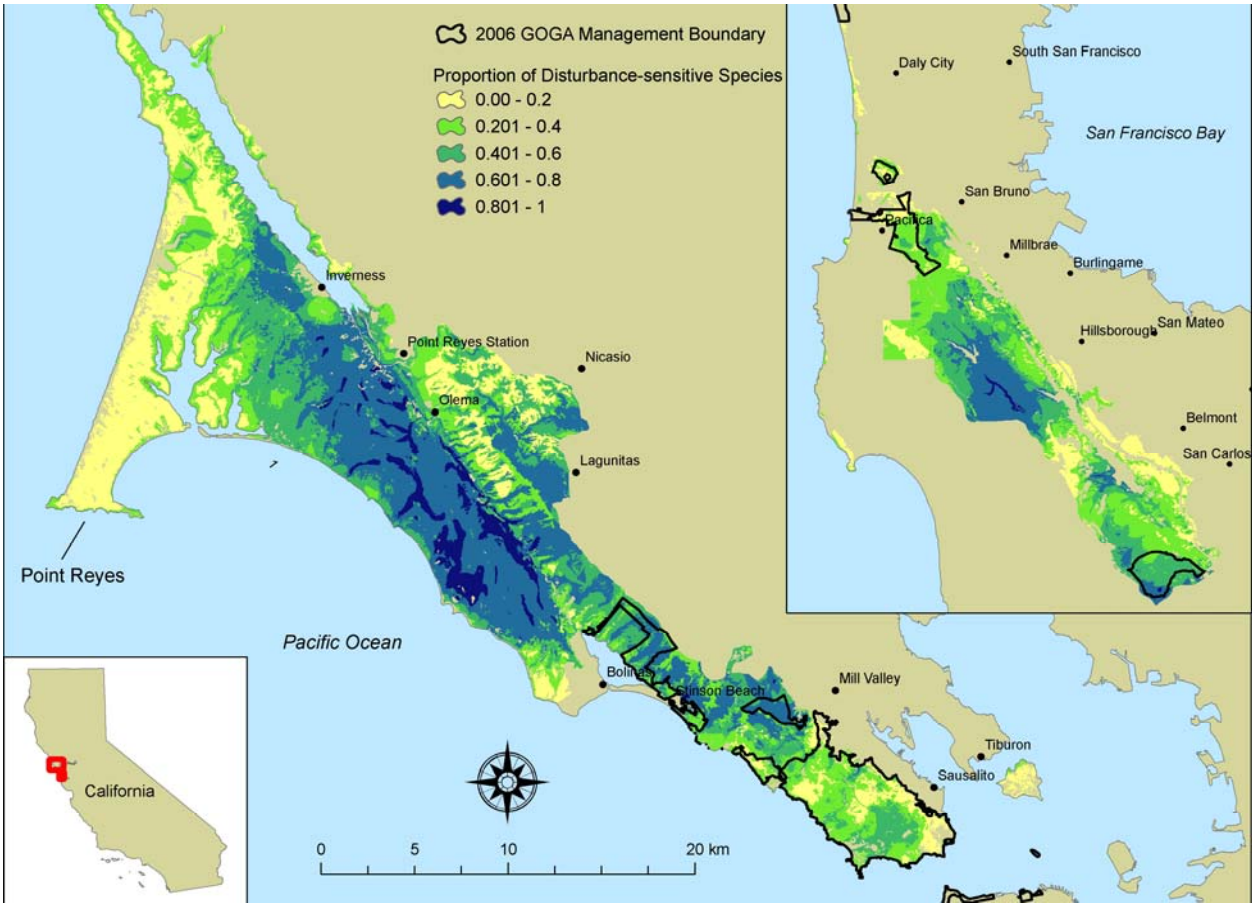


Figure 56a. Predicted proportion of disturbance-sensitive focal species, based on the sum of model outputs for Common Yellowthroat, Brown Creeper, Swainson's Thrush, and Golden-crowned Kinglet.

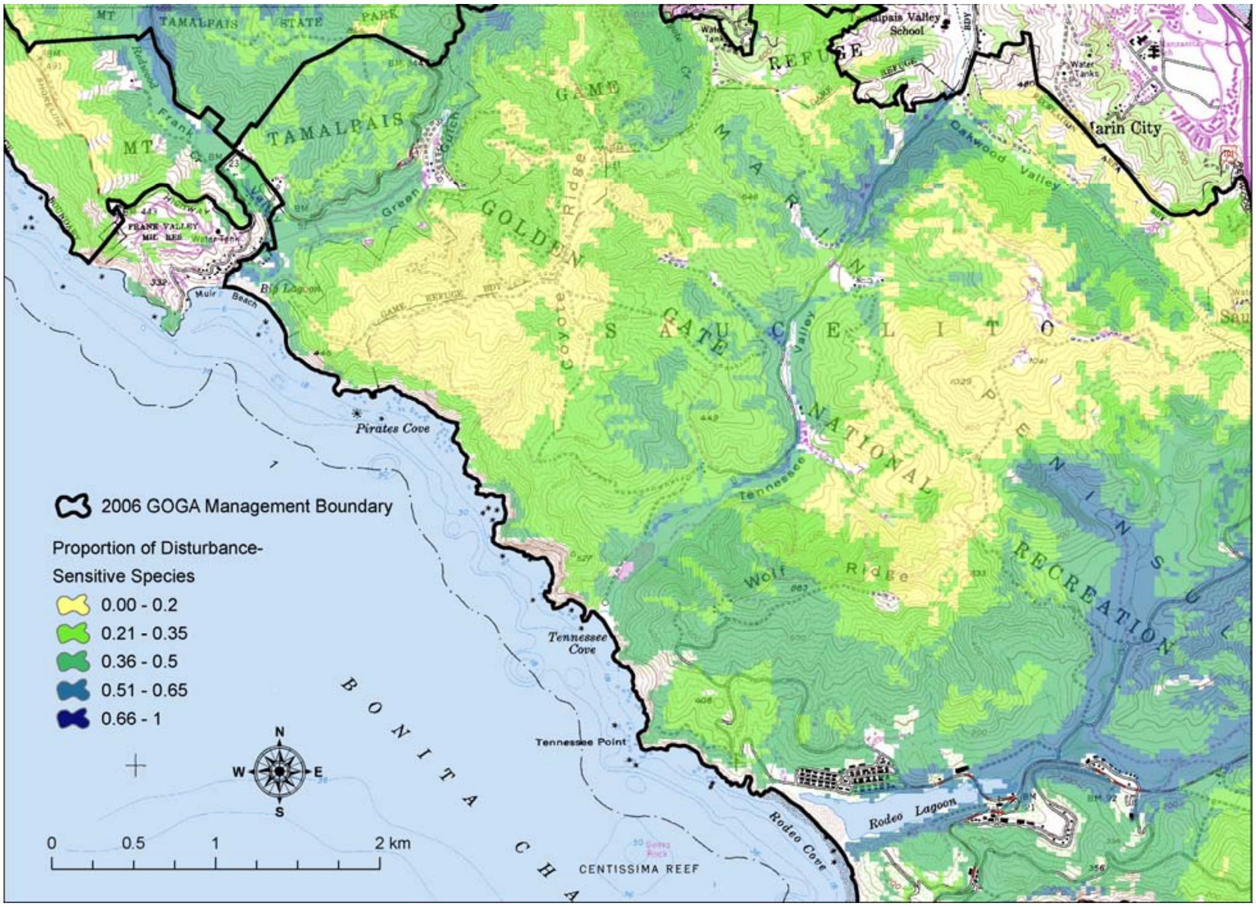


Figure 56b. Sample detail of predicted proportion of disturbance-sensitive focal species, based on the sum of model outputs for Common Yellowthroat, Brown Creeper, Swainson's Thrush, and Golden-crowned Kinglet.

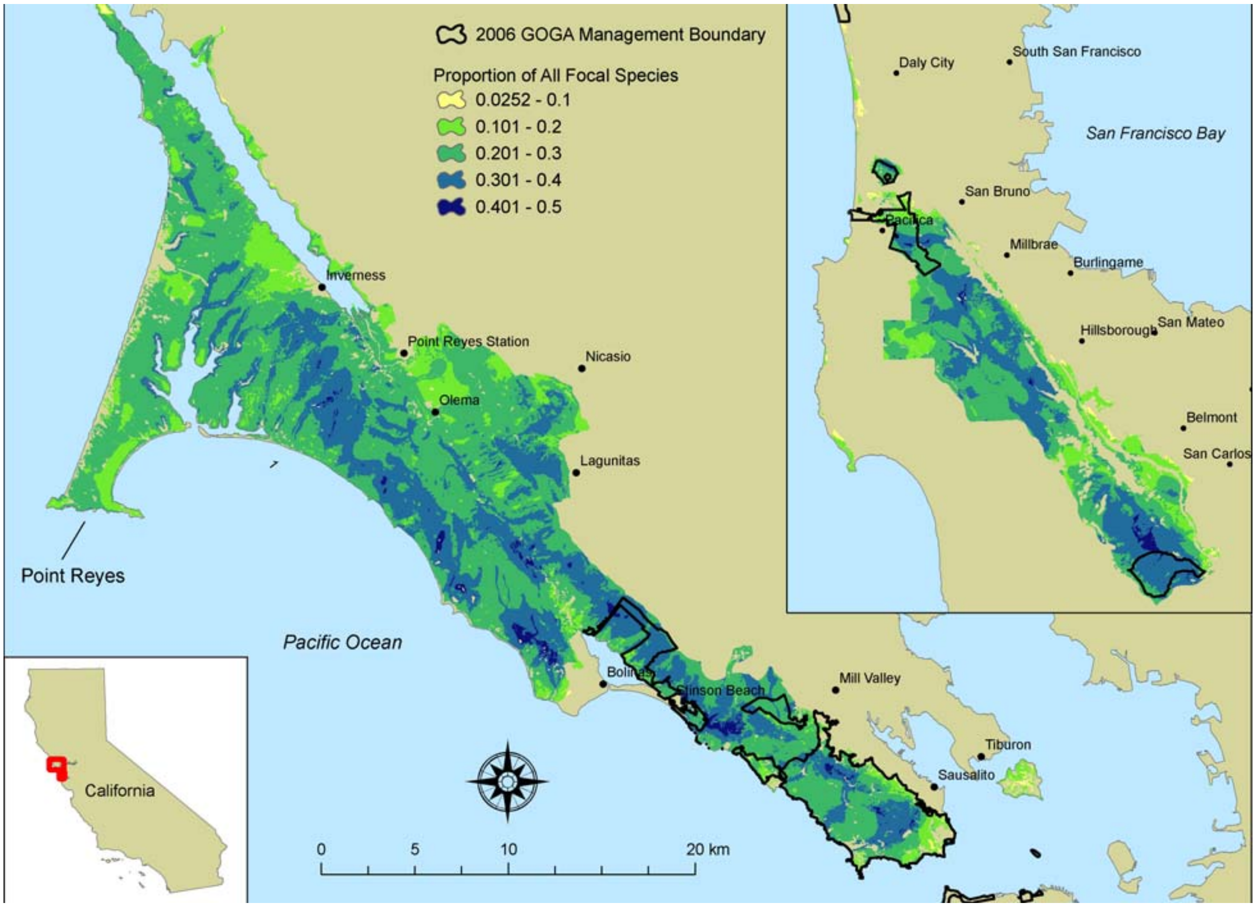


Figure 57a. Predicted proportion of all management-sensitive focal species, based on the sum of model outputs for Common Yellowthroat, Warbling Vireo, Brown Creeper, Bewick's Wren, Wilson's Warbler, Nuttall's White-crowned Sparrow, Swainson's Thrush, Golden-crowned Kinglet, Dark-eyed Junco, and Savannah Sparrow.

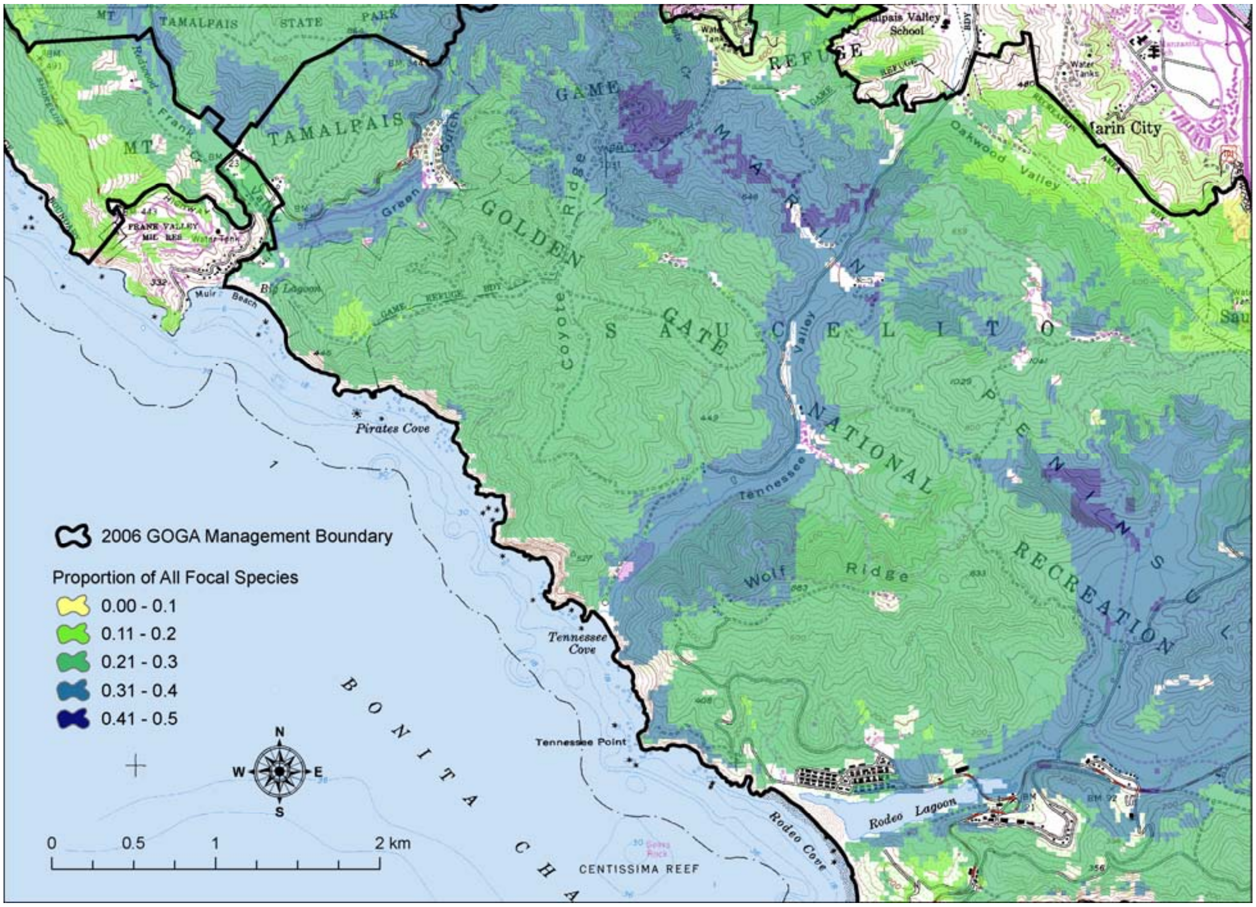


Figure 57b. Sample detail of predicted proportion of all management-sensitive focal species, based on the sum of model outputs for Common Yellowthroat, Warbling Vireo, Brown Creeper, Bewick's Wren, Wilson's Warbler, Nuttall's White-crowned Sparrow, Swainson's Thrush, Golden-crowned Kinglet, Dark-eyed Junco, and Savannah Sparrow.

DISCUSSION

Avian detectability

With respect to the avian survey data, there may have been detectability issues at some points, particularly those that were surveyed just one or two years such that not all recorded absences were true absences (Gu and Swihart 2004, MacKenzie 2005). The importance of the number of survey visits in several of our models, and the fact that the relationship did not level off in many cases, suggests that we may have had quite a few false absences. Alternatively, because many of the more intensively surveyed sites were riparian (the most species rich habitat type) and perhaps higher quality than less surveyed sites, this may be partly responsible for the positive relationships, which were strongest for overall species richness and diversity, riparian species richness, and riparian focal species' presence. However, given the large sample size and frequent surveys at most points, the effects of detection omissions on our model predictions are likely to have been minor.

Priority habitats

Across the species and metrics examined, we found that landscape-level vegetation characteristics (within a 1-km radius area, approximately 314 ha) were generally more important predictors than local vegetation type (at the 30-m pixel level), although the latter was an essential component of each model. Furthermore, at the landscape level, general vegetation classes or habitat types (i.e., conifer, hardwood, riparian, wetland, or scrub) appeared to be better predictors of both individual species distributions and various species richness and diversity metrics than did specific vegetation alliances or topographic characteristics. This may be due to several factors, including limitations of the NPS vegetation layer, which had a classification accuracy of only 64% at the alliance level (Schirokauer et al. 2003), as well as the smoothing effect of a 1-km radius. We did not evaluate the importance of local (pixel-level) vegetation alliance, due to the lack of statistical power to include a categorical variable with more than 50 cases in our models. Nor did we evaluate vegetation "superalliances," which are intermediate classifications between alliances and general vegetation classes, and had somewhat higher classification accuracy (71%, Schirokauer et al. 2003). In general, however, our findings seem to coincide with others that have demonstrated the importance of general vegetation structure, rather than plant species composition, at the landscape scale (Rotenberry and Wiens 1980). Furthermore, the importance of landscape metrics such as patch size and patch cohesion in most of the habitat-specific focal species richness models, as well as several individual species models, suggest that habitat configuration and pattern may matter as much if not more than general composition.

At the local level, the hardwood vegetation class, which included California bay laurel, coast live oak, and tanoak (*Lithocarpus densiflorus*) alliances, appeared to be most important across a range of species and metrics, including coniferous forest, oak woodland, and riparian focal species. This is supported by other studies that have demonstrated the importance of oaks and other hardwood tree species in providing nesting and foraging habitat for avian species (Verner 1980, Rosenstock 1998). Hardwoods within the study area often represent ecotones between or within other habitat types. Ecotones are known to be species-rich (Smith et al. 1997) and this result highlights the importance of habitat mosaics within the parks.

At the landscape level, variables of importance differed by species and associated habitat type, making generalizations difficult. Percent cover, patch size and cohesion of grassland, coniferous forest, scrub, and riparian vegetation were all important for at least one species or richness metric. In terms of overall species richness and diversity, however, percent riparian habitat within a 1-km radius stood out as an important factor, likely due to the proportionately high number of riparian-associated species within the study area. Indeed riparian habitats are known to contain some of the most diverse bird communities in the western United States (Knopf et al. 1988, Dobkin 1994). The diversity of vegetation alliances (Simpson's index) was actually negatively associated with overall avian species richness and diversity, while habitat interspersion, as measured by the interspersion-juxtaposition index (IJI, McGarigal and Marks 1995) had a generally positive relationship with overall richness and diversity, as well as riparian and coniferous forest focal species richness. The opposite pattern was seen for oak woodland focal species richness, however, suggesting that overall species richness is largely driven by riparian species, and is only one part of the picture.

Coastal scrub and grassland habitats were generally not identified as high priority with respect to overall species diversity or combined management-sensitive species indices. However, these habitats are of equally high importance to grassland- and scrub-dependent species, and results from habitat-specific focal species models can help differentiate among seemingly similar habitat areas. With respect to grasslands, flatter areas with larger grassland patches, less non-native annual grassland and active pasture, and lower trail density, had the highest predicted grassland focal species richness. Within scrub habitats, flatter areas with larger connected scrub patches, more California sagebrush and coyote brush, less broom, and lower trail densities had the highest predicted scrub focal species richness.

With respect to anthropogenic factors, the percent cover of non-native, introduced vegetation types, such as eucalyptus and broom, as well as active pasture, had strong, mostly negative (except for oak woodland focal species), effects on several species occurrence and richness metrics, suggesting a need to reduce and/or manage these vegetation types. However, the range of variation in these variables across survey locations was not great, and error bars were large at their upper limits, suggesting that these results must be interpreted with caution, and could be enhanced with further studies. Trail density, while present in all species richness and diversity models, as well as most individual species occurrence models, did not exhibit clear negative effects, except for grassland and scrub focal species. For other species and metrics, the effects were positive or non-linear, suggesting the presence of confounding factors, such as a bias in trail placement toward areas with higher avian diversity (e.g., near riparian zones). It also suggests that the presence of trails, *per se*, does not necessarily lead to reduced species diversity or deter many, if any species. However, we were not able to incorporate any quantitative measure of trail use or width into our models, which may have led to different results (Holmes and Geupel 2005).

Combined metrics for management-sensitive species were based on several species that often had differing, and even conflicting, habitat relationships. Thus it is more fruitful to evaluate the resulting spatial predictions and areas of high importance, rather than the component variables that resulted in those predictions.

Priority areas for habitat conservation and enhancement

Due to the high species diversity of riparian habitats, both overall species richness and diversity metrics, as well most of the combined management-sensitive species indices, indicated riparian zones as high priority areas for avian conservation. Some of the Marin County drainages highlighted by multiple models included Muddy Hollow Creek, Olema Creek, Pine Gulch Creek, Redwood Creek, and Gerbode Valley. In addition, areas of higher elevation and topographic diversity, primarily along the Inverness Ridge and around Mount Tamalpais, had high overall richness and diversity, as well as a large proportion of declining management-sensitive species. Finally, core areas of the Point Reyes National Seashore and San Francisco peninsula watershed, which are farther away from urban development and roads and also have higher habitat connectivity, were identified as having a large proportion of disturbance-sensitive species, as well as high overall species richness.

With respect to habitat-specific focal species groups, many additional areas were identified as important. For oak woodland focal species, Bear Valley, as well as southern Olema Valley, areas around Mount Vision, and eucalyptus groves near Mill Valley had high predicted species richness. We do not know why the eucalyptus groves near Mill Valley had high predicted oak woodland species richness but suspect is has to do with vegetation structure there and/or that oak-associated species concentrate in the patches of trees that exist in urban areas. Because the only oak woodland focal species to be modeled individually (Bewick's Wren) is also associated with scrub habitat, these two sets of predictions did not coincide very well. Areas of high importance for grassland focal species were mostly on the Tomales and Point Reyes peninsulas, as well as on the east side of the Olema Valley, north of Olema. These areas did not necessarily coincide with areas of high Savannah Sparrow or Nuttall's White-crowned Sparrow probability of occurrence, suggesting that less common grassland focal species such as Grasshopper Sparrow and Western Meadowlark may help to drive the combined focal species pattern. For riparian focal species, Olema Creek, Muddy Hollow Creek, Glenbrook Creek, Redwood Creek, Gerbode Valley, and parts of the San Francisco peninsula watershed had high predicted species richness. Important areas for scrub focal species were concentrated in the northern San Francisco peninsula, especially within the Milagra and Sweeney ridge areas, and to a lesser extent, in the Marin headlands and on the west side of the Inverness Ridge. Finally, for coniferous forest focal species, the Inverness Ridge, particularly the southern portion, had highest predicted species richness. Individual coniferous forest focal species (e.g., Brown Creeper and Golden-crowned Kinglet) had similar but broader predicted distributions, again highlighting the importance of a combination of focal species in driving the pattern.

Applying models to management activities

The models and associated distribution maps in this report can be used as important inputs to land management and planning decisions. They should, however, be used carefully with an understanding of their limitations. Models are simplifications of complex ecological systems and, as a result, no prediction is perfect. They are best estimates based on the best available data. Distribution models do not tell us about the processes that drive population change, and hence simply prioritizing specific areas may not lead to the project's desired outcome. Some models used for decision support systems suffer from a mismatch between management goals and modeling strategy and technique (Van Horne 2001). By providing distribution models for several avian metrics deemed *a priori* useful to management within GOGA and PORE, we have attempted to match general management objectives with model capabilities.

Due to the landbird focus, not all vegetation types and habitats were included in the modeling effort. Specifically, beaches, tidal flats, open water, and other unvegetated areas were excluded from our predictions, as were areas mapped as urban development. Thus our models can not be used to evaluate management activities associated with these habitats. Furthermore, special status species, as well as some rare species with insufficient data, were not included in this effort and should not be assumed to be covered with these metrics.

Because of the sheer number of models presented here (21) and the diverse array of metrics modeled, determining exactly how to use the models can be confusing. Of concern is that the models will be misused or not used at all because doing so seems daunting. As a first step in model use, it is necessary to (1) identify specific project goals, (2) consider the scale necessary to meet the goals, and (3) identify the appropriate metric or metrics to best inform management and planning.

Project goals

It is common that projects have multiple, sometimes competing goals, and the goals of a particular project may lead model use in different ways. For example, a primary project goal might be to realign a trail for reasons of visitor safety. Hence, the issue of visitor safety, with the primary goal of trail realignment, could create the associated secondary goal of minimizing impact to native wildlife. Other times the goal of a particular project might be to augment grasslands, to remove non-native invasive plant species, or to improve or maintain overall biodiversity.

As a first step to model use we recommend defining the primary project goals and then determining if there are any resulting secondary goals. We suggest trying to be as specific as possible when setting goals; doing so will help determine which avian metrics are most relevant. Even so, many project goals can not be addressed by these models, and we assume that landbird criteria will comprise just one component of a multi-faceted decision-making process.

Project scale

The model predictions presented herein are intended to be scaleable, and may be used to address management questions at a variety of different spatial scales. However, because the models do not include site-specific habitat quality characteristics such as vegetation height and structure, they should be used primarily as a coarse filter to identify potential target areas that may be investigated more thoroughly with site visits and surveys. They should not be used to identify specific small-scale features such as individual trees or groves for conservation/management action. A more appropriate application is the prioritization of larger habitat areas (e.g., 10-100 ha) with respect to various landbird criteria. Models may be used to evaluate potential landbird impacts of small-scale projects such as trail realignment or parking lot construction, when placed in the context of the surrounding landscape, but should not be interpreted at the individual pixel level.

For a specific management goal, we suggest asking the questions: What is the scale of the project and will the effects extend beyond project boundaries? Answers to these questions may vary from very small scales to all of GOGA and/or PORE (e.g., the General Management Plan). The GIS layers provided with this report allow the user to view the model predictions at any spatial scale down to the 30-m pixel level. We recommend looking at each project at both the scale of the project and at a larger spatial scale, to provide context for decision-making. It is also important to use appropriate map legends when viewing the GIS data, so that differences among pixels are not exaggerated or underemphasized.

Species metrics

The selection of relevant avian metrics is a function of project goals and associated spatial scale. We recommend using more than one metric per project in order to maximize available information for decision-making. However, we caution against using too many metrics as this may complicate the decision-making process unnecessarily. In some cases the choice of which metric to use will be easy. For example, if a project proposes to mow a particular area during the landbird breeding season, overlaying the “low-nesting species” metric would be a useful first step in determining impact. If the probability of occurrence for this group is very low, the choice to proceed with mowing might be made. On the other hand, if the probability is high, the decision to wait until autumn would be the most appropriate. However, if the probably lies somewhere in between high and low, a field visit might be warranted before deciding whether or not to mow. In the case of trail realignment, it would make sense to determine what general habitat type will be affected (metric: habitat-specific focal species) and also assess potential impacts to sensitive species groups (metrics: disturbance-sensitive species, declining species).

Landbirds and beyond

The models presented here are only for landbirds. Clearly, planning and management decisions would benefit from using other sources of information. We suggest using distribution data for other taxa as well, and matching these with the primary and secondary goals of the project, assigning weights as appropriate. The benefit of landbirds and of these models, however, is that planning can be based on multiple species that represent a diverse array of habitats, life history strategies, and ecosystem processes. Further, many of the metrics presented here are based on common species; thus their use in management decisions constitutes a proactive approach to preserving biodiversity and keeping common birds common.

It is inevitable that many management decisions will not have win-win outcomes. The use of these models can serve to reduce uncertainty, minimize impacts, and maximize benefits thereby empowering the user to make difficult management and planning decisions. Still, it will be necessary to be bold when defining specific goals, sticking to these goals, and using these models in the face of uncertainty and conflict.

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Appendix 1. List of NPS sites (transects) supplying data for development of habitat-based species distribution and diversity models, number of points per site, and number of years surveyed.

Site Code	Site Name	# Points	# Years	Site Code	Site Name	# Points	# Years
ABKE	Abbots / Kehoe	16	2	LOOL	Lower Olema Creek	15	6
ANIS	Angel Island	12	1	MCDU	McClure's Ranch Dunes	12	1
ARHO	Arroyo Hondo	6	8	MCTR	McCurdy Trail	6	1
ATT	AT+T	7	1	MEEU	Mesa Road Eucalyptus	2	1
ATTG	AT+T Grassland	7	1	MIRI	Milagra Ridge	9	1
ATTS	AT+T Scrub	4	1	MOGU	Morse's Gulch	15	2
BEAR	Bear Valley	17	1	MRAN	M Ranch	8	2
BEVA	Bear Valley	16	2	MTWI	Mt. Wittenberg	10	2
BIP1	Bishop Pine 1	8	1	MUHO	Muddy Hollow	17	9
BIP2	Bishop Pine 2	8	1	MWOT	Muir Woods Off Trail	15	3
BIP3	Bishop Pine 3	4	1	OLGR	Olema Grassland	10	1
BJTR	Ben Johnson Trail	15	3	OPDS	Outer Point Dune Scrub	12	1
BORN	Bolinas Ridge North	14	1	OPTR	Old Pine Trail	10	1
BOTR	Bootjack Trail	15	3	PAG5	Palomarin Grid 5	7	7
BVMT	Bear Valley Meadow Trail	11	2	PALO	Palomarin Grids	13	7
CGEU	Coast Guard Eucalyptus	8	1	PHES	Phleger Estates	9	1
COCA	Coast Camp	8	3	PIGU	Pine Gulch	5	9
CRTR	Coyote Ridge Trail	15	3	PRHN	Point Reyes Headlands North	15	2
CTLA	Coast Trail Lagunitas	13	3	PRHS	Point Reyes Headlands South	15	2
CTPA	Coastal Trail Palomarin	14	3	RATR	Randall Trail	8	1
DEGU	Deadman's Gulch	6	1	RECR	Redwood Creek	24	9
DUSC	Dune Scrub	7	1	RITR	Ridge Trail	8	1
ERSO	Elk Range South	12	1	RODE	Rodeo / Bobcat Trail	15	3
ESTE	Estero	9	3	SPBP	Samuel P. Taylor Bike Path	10	1
EUMV	Eucalyptus Mill Valley	10	1	STGU	Stinson Gulch	14	2
GERB	Gerbode Valley	18	3	STRA	Stewart Ranch	15	2
HORA	Home Ranch	10	1	SWRI	Sweeney Ridge	12	1
INRI	Inverness Ridge	4	1	TEVA	Tennesee Valley	13	2
JACR	Jack's Creek	6	1	TOMN	Tomales Point North	15	2
JEPS	Jepson Trail	6	1	TOMS	Tomales Point South	15	3
KIMO	Kings Mountain	32	1	UPOL	Upper Olema Creek	13	3
LACR	Lagunitas Creek	18	9	UPRT	Upper Ridge Trail	10	1
LIMG	Limantour Grassland	4	1				

Appendix 2. Vegetation classes and corresponding alliances from NPS vegetation layer (Schirokauer et al. 2003).

Code	Veg Class	Alliance
1	Grassland	Active Pasture or Agriculture
1	Grassland	California Annual Grassland Weedy Alliance
1	Grassland	California Annual Grasslands with Native Component
1	Grassland	Introduced Perennial Grassland
1	Grassland	Pacific Reedgrass Alliance
1	Grassland	Purple Needlegrass Alliance
1	Grassland	Rush Alliance
1	Grassland	Tufted Hairgrass Alliance
2	Riparian	Arroyo Willow Alliance
2	Riparian	Red Alder Alliance
2	Riparian	Salmonberry Alliance
2	Riparian	Willow Mapping Unit
3	Conifer	Bishop Pine Alliance
3	Conifer	Douglas/fir Alliance
3	Conifer	Monterey Cypress Grove
3	Conifer	*Sequoia sempervirens* Alliance
4	Scrub	Blue/blossom Alliance
4	Scrub	California Sagebrush Alliance
4	Scrub	California Wax Myrtle Alliance
4	Scrub	Chamise Alliance
4	Scrub	Coffeeberry Alliance
4	Scrub	Coyote Brush Alliance
4	Scrub	Dune Sagebrush Alliance or Dune Lupine/Goldenbush Alliance
4	Scrub	Eastwood Manzanita
4	Scrub	Hazel (Ethyl) Alliance
4	Scrub	Holly/leaf Cherry Alliance
4	Scrub	Mixed Manzanita mapping unit
4	Scrub	Poison Oak Alliance
4	Scrub	Sensitive Manzanita
4	Scrub	Yellow bush lupine Alliance
5	Wetland	Bullrush - Cattail - Spikerush Marsh mapping unit
5	Wetland	Cordgrass (*Spartina foliosa*) Alliance
5	Wetland	Pickleweed Alliance
5	Wetland	Saltgrass Alliance
6	Hardwood	California Bay Alliance
6	Hardwood	California Buckeye Alliance
6	Hardwood	Giant Chinquapin Alliance
6	Hardwood	Tanoak Alliance
6	Hardwood	Coast Live Oak Alliance

Appendix 3. Independent variables selected *a priori* based on expert opinion (Gardali) to be used in each distribution model.

Overall species richness / diversity

Variable name	Description
PRIPARIAN	1. Proportion of riparian vegetation alliances (combined) within 1-km radius
PWETLAND	2. Proportion of wetland vegetation alliances (combined) within 1-km radius
PEUCALYPTU	3. Proportion of *Eucalyptus* vegetation within 1-km radius
SIDI	4. Vegetation alliance diversity (modified Simpson index) within 1-km radius
IJI	5. Interspersion / juxtaposition of general habitat types within 1-km radius
TDENS1K	6. Trail density within 1-km radius
ELEV_MEAN	7. Mean elevation within 1-km radius
SLOPE_MEAN	8. Mean slope within 1-km radius
VEGCLASS	9. Local vegetation class (general habitat type at point)

Oak woodland focal species richness

Variable name	Description
PGRASS	1. Proportion of grassland vegetation alliances (combined) within 1-km radius
PRIPARIAN	2. Proportion of riparian vegetation alliances (combined) within 1-km radius
PCLIVEOAK	3. Proportion of coast live oak vegetation within 1-km radius
PTANOAK	4. Proportion of tanoak vegetation within 1-km radius
PCALIFBAY	5. Proportion of California bay laurel vegetation within 1-km radius
PEUCALYPTU	6. Proportion of eucalyptus vegetation within 1-km radius
SIDI	8. Vegetation alliance diversity (modified Simpson index) within 1-km radius
IJI	9. Interspersion / juxtaposition of general habitat types within 1-km radius
TDENS1K	10. Trail density within 1-km radius
ELEV_CV	11. Elevation coefficient of variation (topographic diversity) within 1-km radius
SOUTHASPEC	12. South aspect (difference from 180º) at point
WETASPECT	13. West aspect (difference from 270º) at point
VEGCLASS	14. Local vegetation class (general habitat type at point)

Grassland focal species richness

Variable name	Description
PGRASS	1. Proportion of grassland vegetation alliances (combined) within 1-km radius
PNNATANNGR	2. Proportion of non-native annual grassland vegetation within 1-km radius
PRUSH	3. Proportion of rush vegetation within 1-km radius
PACTIVEPAS	4. Proportion of active pasture or agriculture within 1-km radius
IJI	5. Interspersion / juxtaposition of general habitat types within 1-km radius
GRASSCOHES	6. Patch cohesion of grassland vegetation alliances (combined) within 1-km radius
GRASSSIZE	7. Mean patch size of grassland vegetation alliances (combined) within 1-km radius
TDENS1K	8. Trail density within 1-km radius
SLOPE_MEAN	9. Mean slope within 1-km radius
VEGCLASS	10. Local vegetation class (general habitat type at point)

Riparian focal species richness

Variable name	Description
PRIPARIAN	1. Proportion of riparian vegetation alliances (combined) within 1-km radius
PREDALDER	2. Proportion of red alder vegetation within 1-km radius
PALLWILLOW	3. Proportion of willow vegetation within 1-km radius
PEUCALYPTU	4. Proportion of eucalyptus vegetation within 1-km radius
SIDI	5. Vegetation alliance diversity (modified Simpson index) within 1-km radius
IJI	6. Interspersion / juxtaposition of general habitat types within 1-km radius
RIPARIANCOHES	7. Patch cohesion of riparian vegetation alliances (combined) within 1-km radius
RIPARIANSIZE	8. Mean patch size of riparian vegetation alliances (combined) within 1-km radius
TDENS1K	9. Trail density within 1-km radius
STREAMDENS	10. Stream density within 1-km radius
VEGCLASS	11. Local vegetation class (general habitat type at point)

Scrub focal species richness

Variable name	Description
PSCRUB	1. Proportion of scrub vegetation alliances (combined) within 1-km radius
PCOYOTEBRU	2. Proportion of coyote brush vegetation within 1-km radius
PCSAGEBRUS	3. Proportion of California sagebrush vegetation within 1-km radius
PSALMON	4. Proportion of salmonberry vegetation within 1-km radius
PPOISONOAK	5. Proportion of poison oak vegetation within 1-km radius
PBROOM	6. Proportion of broom vegetation within 1-km radius
SIDI	7. Vegetation alliance diversity (modified Simpson index) within 1-km radius
IJI	8. Interspersion / juxtaposition of general habitat types within 1-km radius
SCRUBSIZE	9. Mean patch size of scrub vegetation alliances (combined) within 1-km radius
TDENS1K	10. Trail density within 1-km radius
SLOPE_MEAN	11. Mean slope within 1-km radius
SOUTHASPEC	12. South aspect (difference from 180°) at point
VEGCLASS	13. Local vegetation class (general habitat type at point)

Coniferous forest focal species richness

Variable name	Description
PCONIFER	1. Proportion of conifer vegetation alliances (combined) within 1-km radius
PREDWOOD	3. Proportion of coast redwood vegetation within 1-km radius
PDOUGFIR	4. Proportion of Douglas-fir vegetation within 1-km radius
PHARDWOOD	5. Proportion of hardwood vegetation alliances (combined) within 1-km radius
PEUCALYPTU	6. Proportion of eucalyptus vegetation within 1-km radius
SIDI	7. Vegetation alliance diversity (modified Simpson index) within 1-km radius
IJI	8. Interspersion / juxtaposition of general habitat types within 1-km radius
CONIFERSIZE	9. Mean patch size of conifer vegetation alliances (combined) within 1-km radius
TDENS1K	10. Trail density within 1-km radius
SLOPE_MEAN	11. Mean slope within 1-km radius
ELEV_MEAN	12. Mean elevation within 1-km radius
VEGCLASS	13. Local vegetation class (general habitat type at point)

Bewick's Wren

Variable name	Description
PHARDWOOD	1. Proportion of hardwood vegetation alliances (combined) within 1-km radius
PSCRUB	2. Proportion of scrub vegetation alliances (combined) within 1-km radius
PCOYOTEBRU	3. Proportion of coyote brush vegetation within 1-km radius
PSAGEBRUS	4. Proportion of California sagebrush vegetation within 1-km radius
PCOFFEEBER	5. Proportion of coffeeberry vegetation within 1-km radius
PPOISONOAK	6. Proportion of poison oak vegetation within 1-km radius
PBROOM	7. Proportion of broom vegetation within 1-km radius
SIDI	8. Vegetation alliance diversity (modified Simpson index) within 1-km radius
IJI	9. Interspersion / juxtaposition of general habitat types within 1-km radius
TDENS1K	10. Trail density within 1-km radius
ELEV_CV	11. Elevation coefficient of variation (topographic diversity)
VEGCLASS	12. Local vegetation class (general habitat type at point)

Brown Creeper

Variable name	Description
PCONIFER	1. Proportion of conifer vegetation alliances (combined) within 1-km radius
PBISHOPPIN	2. Proportion of bishop pine vegetation within 1-km radius
PREDWOOD	3. Proportion of coast redwood vegetation within 1-km radius
PDOUGFIR	4. Proportion of douglas-fir vegetation within 1-km radius
PEUCALYPTU	5. Proportion of eucalyptus vegetation within 1-km radius
PMYCYPRESS	6. Proportion of Monterey Cypress vegetation within 1-km radius
IJI	7. Interspersion / juxtaposition of general habitat types within 1-km radius
CONIFERSIZE	8. Mean patch size of conifer vegetation alliances (combined) within 1-km radius
CONIFERCOHES	9. Mean patch cohesion of conifer vegetation alliances (combined) within 1-km radius
TDENS1K	10. Trail density within 1-km radius
VEGCLASS	11. Local vegetation class (general habitat type at point)

Common Yellowthroat

Variable name	Description
PRIPARIAN	1. Proportion of riparian vegetation alliances (combined) within 1-km radius
PGRASS	2. Proportion grassland vegetation alliances (combined) within 1-km radius
PWETLAND	3. Proportion of wetland vegetation alliances (combined) within 1-km radius
PBULRUSH	4. Proportion of bulrush/cattail/spikerush vegetation within 1-km radius
PACTIVEPAS	5. Proportion of active pasture within 1-km radius
PBROOM	6. Proportion of broom vegetation within 1-km radius
IJI	7. Interspersion / juxtaposition of general habitat types within 1-km radius
WETLANDSIZE	8. Mean patch size of wetland vegetation alliances (combined) within 1-km radius
WETLANDCOHES	9. Patch cohesion of wetland vegetation alliances (combined) within 1-km radius
TDENS1K	10. Trail density within 1-km radius
STREAMDIST	11. Inverse-distance weighted stream proximity
VEGCLASS	12. Local vegetation class (general habitat type at point)

Dark-eyed Junco

Dependent variable	Independent variables
PCONIFER	1. Proportion of conifer vegetation alliances (combined) within 1-km radius
PBISHOPPIN	2. Proportion of bishop pine vegetation within 1-km radius
PREDWOOD	3. Proportion of coast redwood vegetation within 1-km radius
PDOUGFIR	4. Proportion of douglas-fir vegetation within 1-km radius
PHARDWOOD	5. Proportion of hardwood vegetation alliances (combined) within 1-km radius
PMYCYPRESS	6. Proportion of Monterey cypress vegetation within 1-km radius
IJI	7. Interspersion / juxtaposition of general habitat types within 1-km radius
TDENS1K	8. Trail density within 1-km radius
SLOPE_MEAN	9. Mean slope within 1-km radius
ELEV_MEAN	10. Mean elevation within 1-km radius
SOUTHASPEC	11. South aspect (difference from 180º) at point
WESTASPECT	12. West aspect (difference from 270º) at point
VEGCLASS	13. Local vegetation class (general habitat type at point)

Golden-crowned Kinglet

Variable name	Description
PCONIFER	1. Proportion of conifer vegetation alliances (combined) within 1-km radius
PREDWOOD	2. Proportion of coast redwood vegetation within 1-km radius
PDOUGFIR	3. Proportion of douglas-fir vegetation within 1-km radius
PMYCYPRESS	4. Proportion of Monterey cypress vegetation within 1-km radius
IJI	5. Interspersion / juxtaposition of general habitat types within 1-km radius
TDENS1K	6. Trail density within 1-km radius
SLOPE_MEAN	7. Mean slope within 1-km radius
ELEV_MEAN	8. Mean elevation within 1-km radius
VEGCLASS	9. Local vegetation class (general habitat type at point)

Nuttall's White-crowned Sparrow

Variable name	Description
PGRASS	1. Proportion of grassland vegetation alliances (combined) within 1-km radius
PSCRUB	2. Proportion of scrub vegetation alliances (combined) within 1-km radius
PCOYOTEBRU	3. Proportion of coyote brush vegetation within 1-km radius
PSAGEBRUS	4. Proportion of California sagebrush vegetation within 1-km radius
PPOISONOAK	5. Proportion of poison oak vegetation within 1-km radius
PYBLUPINE	6. Proportion of yellow bush lupine vegetation within 1-km radius
PACTIVEPAS	7. Proportion of active pasture within 1-km radius
PBROOM	8. Proportion of broom vegetation within 1-km radius
IJI	9. Interspersion / juxtaposition of general habitat types within 1-km radius
TDENS1K	10. Trail density within 1-km radius
VEGCLASS	11. Local vegetation class (general habitat type at point)

Savannah Sparrow

Dependent variable	Independent variables
PGRASS	1. Proportion of grassland vegetation alliances (combined) within 1-km radius
PNNATANNGR	2. Proportion of non-native annual grassland vegetation within 1-km radius
PNATANNGR	3. Proportion of partly-native annual grassland vegetation within 1-km radius
PNNATPERGR	4. Proportion of introduced perennial grassland vegetation within 1-km radius
PACTIVEPAS	5. Proportion of active pasture within 1-km radius
PGRASSSIZE	6. Mean patch size of grassland vegetation alliances (combined) within 1-km radius
PGRASSCOHES	7. Patch cohesion of grassland vegetation alliances (combined) within 1-km radius
TDENS1K	8. Trail density within 1-km radius
SLOPE_MEAN	9. Mean slope within 1-km radius
VEGCLASS	10. Local vegetation class (general habitat type at point)

Swainson's Thrush

Variable name	Description
PRIPARIAN	1. Proportion of riparian vegetation alliances (combined) within 1-km radius
PREDALDER	2. Proportion of red alder vegetation within 1-km radius
PALLWILLOW	3. Proportion of willow vegetation within 1-km radius
PCONIFER	4. Proportion of conifer vegetation alliances (combined) within 1-km radius
PBISHOPPIN	5. Proportion of bishop pine vegetation within 1-km radius
PHARDWOOD	6. Proportion of hardwood vegetation alliances (combined) within 1-km radius
PSCRUB	7. Proportion of scrub vegetation alliances (combined) within 1-km radius
PEUCALYPU	8. Proportion of eucalyptus vegetation within 1-km radius
SIDI	9. Vegetation alliance diversity (modified Simpson index) within 1-km radius
IJI	10. Interspersion / juxtaposition of general habitat types within 1-km radius
TDENS1K	11. Trail density within 1-km radius
SOUTHASPEC	12. South aspect (difference from 180º) at point
VEGCLASS	13. Local vegetation class (general habitat type at point)

Warbling Vireo

Variable name	Description
PRIPARIAN	1. Proportion of riparian vegetation alliances (combined) within 1-km radius
PREDALDER	2. Proportion of red alder vegetation within 1-km radius
PALLWILLOW	3. Proportion of willow vegetation within 1-km radius
PCALIFBAY	4. Proportion of California bay laurel vegetation within 1-km radius
PWETLAND	5. Proportion of wetland vegetation alliances (combined) within 1-km radius
PEUCALYPTU	6. Proportion of eucalyptus vegetation within 1-km radius
RIPARIANCOHES	7. Patch cohesion of riparian vegetation alliances (combined) within 1-km radius
RIPARIANSIZE	8. Mean patch size of riparian vegetation alliances (combined) within 1-km radius
TDENS1K	9. Trail density within 1-km radius
STREAMDIST	10. Inverse-distance weighted stream proximity
VEGCLASS	11. Local vegetation class (general habitat type at point)

Wilson's Warbler

Variable name	Description
PRIPARIAN	1. Proportion of riparian vegetation alliances (combined) within 1-km radius
PREDALDER	2. Proportion of red alder vegetation within 1-km radius
PALLWILLOW	3. Proportion of willow vegetation within 1-km radius
PCONIFER	4. Proportion of conifer vegetation alliances (combined) within 1-km radius
PBISHOPPIN	5. Proportion of bishop pine vegetation within 1-km radius
PHARDWOOD	6. Proportion of hardwood vegetation alliances (combined) within 1-km radius
SIDI	7. Vegetation alliance diversity (modified Simpson index) within 1-km radius
TDENS1K	8. Trail density within 1-km radius
STREAMDIST	9. Inverse-distance weighted stream proximity
VEGCLASS	10. Local vegetation class (general habitat type at point)

Appendix 4. R code used to develop generalized additive models. For additional information on the R statistical package, see http://www.r-project.org/.

```
library(RODBC)
library(grasp)
options(scipen=10)
prns.data<-
odbcConnectAccess("Z:/Terrestrial/programs_and_projects/coastal_parks/DistributionModel/CoastalNP
SPC/ggnra_prns_pcdata.mdb")
setwd("Z:/Terrestrial/programs_and_projects/coastal_parks/DistributionModel/GRASP")
responsevars<-sqlFetch(prns.data,"ResponseVarsGroup")
predictorvars<-sqlFetch(prns.data,"PredictorVars")
predictorvarslu<-sqlFetch(prns.data,"PredictorVarsLU")
response<-as.data.frame(responsevars)
predictors<-as.data.frame(predictorvars)
as.factor(predictors$VEGCLASS)
lu<-as.data.frame(predictorvarslu)
as.factor(lu$VEGCLASS)
grasp.in(Ymat = response,Xmat = predictors, Xpred = predictors, Xlut = lu)

attach(response)
sr.y=c("SR")
simpson.y=c("Simpson")
shannon.y=c("Shannon")
detach(response)

attach(predictorvars)
sr.x=c("VEGCLASS", "NumVisits", "PWETLAND", "PRIPARIAN", "PEUCALYPTU", "SIDI", "IJI", "TDENS1K",
"ELEV_MEAN", "SLOPE_MEAN")
simpson.x=c("VEGCLASS", "NumVisits","PWETLAND", "PRIPARIAN", "PEUCALYPTU", "SIDI", "IJI",
"TDENS1K", "ELEV_MEAN", "SLOPE_MEAN")
shannon.x=c("VEGCLASS", "NumVisits", "PWETLAND", "PRIPARIAN", "PEUCALYPTU", "SIDI", "IJI",
"TDENS1K", "ELEV_MEAN", "SLOPE_MEAN")

grasp(selected.responses = sr.y, selected.predictors = sr.x, gr.fam = "gaussian", stepwise.models
= T, test = "AIC", df1 = 0, df2 = 3, make.summary = T, path =
"Z:/Terrestrial/programs_and_projects/coastal_parks/DistributionModel/GRASP", save.outputs = T,
save.PNG = T, plotpar = c(4,4), contributions = T, plot.contributions = T, plot.histograms = T,
plot.respvspred = T, plot.models = T, lookup.tables = T, cvgroups = 4, validate.models = T,
StdError = T, model.anova = T, weights = T,  corlim = 50, plot.correlation = T, use.correlation =
T)

grasp(selected.responses = simpson.y, selected.predictors = simpson.x, gr.fam = "gaussian",
stepwise.models = T, test = "AIC", df1 = 0, df2 = 3, make.summary = T, path =
"Z:/Terrestrial/programs_and_projects/coastal_parks/DistributionModel/GRASP", save.outputs = T,
save.PNG = T, contributions = T, plot.contributions = T, plot.respvspred = T, plot.models = T,
lookup.tables = T, StdError = T, model.anova = T, corlim = 50, plot.correlation = T,
use.correlation = T)

grasp(selected.responses = shannon.y, selected.predictors = shannon.x, gr.fam = "gaussian",
stepwise.models = T, test = "AIC", df1 = 0, df2 = 3, make.summary = T, path =
"Z:/Terrestrial/programs_and_projects/coastal_parks/DistributionModel/GRASP", save.outputs = T,
save.PNG = T, plotpar = c(4,4), contributions = T, plot.contributions = T, plot.histograms = T,
plot.respvspred = T, plot.models = T, lookup.tables = T, cvgroups = 4, validate.models = T,
StdError = T, model.anova = T, corlim = 50, plot.correlation = T, use.correlation = T)

sink("Z:/Terrestrial/programs_and_projects/coastal_parks/DistributionModel/GRASP/alonecontrib.txt
")
alone <- write.table(ALONE.CONTRIB, quote = F)
sink(alone)
sink("Z:/Terrestrial/programs_and_projects/coastal_parks/DistributionModel/GRASP/dropcontrib.txt"
)
drop <- write.table(DROP.CONTRIB, quote = F)
sink(drop)
sink("Z:/Terrestrial/programs_and_projects/coastal_parks/DistributionModel/GRASP/modelcontrib.txt
")
model <- write.table(MODEL.CONTRIB, quote = F)
sink(model)
```

```
attach(response)
oak.y=c("Oakmean")
grass.y=c("Grassmean")
riparian.y=c("Ripmean")
conifer.y=c("Conifmean")
scrub.y=c("Scrubmean")
detach(response)

attach(predictorvars)
riparian.x=c("VEGCLASS", "NumVisits", "PRIPARIAN", "PREDALDER", "PALLWILLOW", "PEUCALYPTU",
"SIDI", "IJI", "RIPARIANCOHES", "RIPARIANSIZE", "STREAMDENS", "TDENS1K")
oak.x=c("VEGCLASS", "NumVisits", "PRIPARIAN", "PGRASS", "PEUCALYPTU", "SIDI", "IJI", "TDENS1K",
"PCALIFBAY",  "PCLIVEOAK", "PTANOAK", "SOUTHASPEC", "WESTASPECT", "ELEV_CV")
scrub.x=c("VEGCLASS", "NumVisits", "PSCRUB", "PCOYOTEBRU", "PCSAGEBRUS", "PPOISONOAK",
"PSALMONBER", "PBROOM", "IJI", "TDENS1K", "SCRUBSIZE", "SLOPE_MEAN", "SOUTHASPEC")
grass.x=c("VEGCLASS", "NumVisits", "PGRASS", "PRUSH", "PNNATANNGR", "PACTIVEPAS", "IJI",
"SLOPE_MEAN", "GRASSCOHES", "GRASSSIZE", "TDENS1K")
conifer.x=c("VEGCLASS", "NumVisits", "PCONIFER", "PHARDWOOD", "PREDWOOD", "PDOUGFIR",
"CONIFERSIZE", "SLOPE_MEAN", "ELEV_MEAN", "IJI", "TDENS1K")


grasp(selected.responses = riparian.y, selected.predictors = riparian.x, gr.fam = "gaussian",
stepwise.models = T, test = "AIC", df1 = 0, df2 = 3, make.summary = T, path =
"Z:/Terrestrial/programs_and_projects/coastal_parks/DistributionModel/GRASP", save.outputs = T,
save.PNG = T, plotpar = c(4,4), contributions = T, plot.contributions = T, plot.histograms = T,
plot.respvspred = T, plot.models = T, lookup.tables = T, cvgroups = 4, validate.models = T,
StdError = T, model.anova = T, weights = T,  corlim = 50, plot.correlation = T, use.correlation =
T)

grasp(selected.responses = oak.y, selected.predictors = oak.x, gr.fam = "gaussian",
stepwise.models = T, test = "AIC", df1 = 0, df2 = 3, make.summary = T, path =
"Z:/Terrestrial/programs_and_projects/coastal_parks/DistributionModel/GRASP", save.outputs = T,
save.PNG = T, plotpar = c(4,4), contributions = T, plot.contributions = T, plot.histograms = T,
plot.respvspred = T, plot.models = T, lookup.tables = T, cvgroups = 4, validate.models = T,
StdError = T, model.anova = T, weights = T,  corlim = 50, plot.correlation = T, use.correlation =
T)

grasp(selected.responses = scrub.y, selected.predictors = scrub.x, gr.fam = "gaussian",
stepwise.models = T, test = "AIC", df1 = 0, df2 = 3, make.summary = T, path =
"Z:/Terrestrial/programs_and_projects/coastal_parks/DistributionModel/GRASP", save.outputs = T,
save.PNG = T, plotpar = c(4,4), contributions = T, plot.contributions = T, plot.histograms = T,
plot.respvspred = T, plot.models = T, lookup.tables = T, cvgroups = 4, validate.models = T,
StdError = T, model.anova = T, weights = T,  corlim = 50, plot.correlation = T, use.correlation =
T)

grasp(selected.responses = grass.y, selected.predictors = grass.x, gr.fam = "gaussian",
stepwise.models = T, test = "AIC", df1 = 0, df2 = 3, make.summary = T, path =
"Z:/Terrestrial/programs_and_projects/coastal_parks/DistributionModel/GRASP", save.outputs = T,
save.PNG = T, plotpar = c(4,4), contributions = T, plot.contributions = T, plot.histograms = T,
plot.respvspred = T, plot.models = T, lookup.tables = T, cvgroups = 4, validate.models = T,
StdError = T, model.anova = T, weights = T,  corlim = 50, plot.correlation = T, use.correlation =
T)

grasp(selected.responses = conifer.y, selected.predictors = conifer.x, gr.fam = "gaussian",
stepwise.models = T, test = "AIC", df1 = 0, df2 = 3, make.summary = T, path =
"Z:/Terrestrial/programs_and_projects/coastal_parks/DistributionModel/GRASP", save.outputs = T,
save.PNG = T, plotpar = c(4,4), contributions = T, plot.contributions = T, plot.histograms = T,
plot.respvspred = T, plot.models = T, lookup.tables = T, cvgroups = 4, validate.models = T,
StdError = T, model.anova = T, weights = T,  corlim = 50, plot.correlation = T, use.correlation =
T)

sink("Z:/Terrestrial/programs_and_projects/coastal_parks/DistributionModel/GRASP/alonecontrib.txt
")
alone <- write.table(ALONE.CONTRIB, quote = F)
sink(alone)
sink("Z:/Terrestrial/programs_and_projects/coastal_parks/DistributionModel/GRASP/dropcontrib.txt"
)
drop <- write.table(DROP.CONTRIB, quote = F)
sink(drop)
sink("Z:/Terrestrial/programs_and_projects/coastal_parks/DistributionModel/GRASP/modelcontrib.txt
")
```

```
model <- write.table(MODEL.CONTRIB, quote = F)
sink(model)

responsevars<-sqlFetch(prns.data,"ResponseVars")
predictorvars<-sqlFetch(prns.data,"PredictorVars")
predictorvarslu<-sqlFetch(prns.data,"PredictorVarsLU")
response<-as.data.frame(responsevars)
predictors<-as.data.frame(predictorvars)
as.factor(predictors$VEGCLASS)
lu<-as.data.frame(predictorvarslu)
as.factor(lu$VEGCLASS)
grasp.in(Ymat = response,Xmat = predictors, Xpred = predictors, Xlut = lu)

attach(response)
coye.y=c("COYE")
wavi.y=c("WAVI")
brcr.y=c("BRCR")
bewr.y=c("BEWR")
wiwa.y=c("WIWA")
nwcs.y=c("NWCS")
swth.y=c("SWTH")
gcki.y=c("GCKI")
orju.y=c("ORJU")
savs.y=c("SAVS")
detach(response)

attach(predictorvars)
coye.x=c("VEGCLASS", "NumVisits", "PGRASS", "PRIPARIAN", "PWETLAND", "PBROOM", "PACTIVEPAS",
"PBULRUSH", "IJI", "TDENS1K", "STREAMDIST", "WETLANDCOHES", "WETLANDSIZE")
wavi.x=c("VEGCLASS", "NumVisits", "PRIPARIAN", "PWETLAND", "PREDALDER", "PALLWILLOW",
"PEUCALYPTU", "PCALIFBAY", "RIPARIANCOHES", "RIPARIANSIZE", "STREAMDIST")
brcr.x=c("VEGCLASS", "NumVisits", "PCONIFER", "PBISHOPPIN", "PREDWOOD", "PDOUGFIR", "PMYCYPRESS",
"PEUCALYPTU", "IJI", "CONIFERCOHES", "CONIFERSIZE", "TDENS1K")
bewr.x=c("VEGCLASS", "NumVisits", "PSCRUB", "PHARDWOOD", "PCOFFEEBER", "PCOYOTEBRU",
"PCSAGEBRUS", "PPOISONOAK", "PBROOM", "SIDI", "ELEV_CV", "IJI", "TDENS1K")
swth.x=c("VEGCLASS", "NumVisits", "PRIPARIAN", "PHARDWOOD", "PCONIFER", "PSCRUB", "PREDALDER",
"PALLWILLOW", "PBISHOPPIN", "PEUCALYPTU", "SIDI", "IJI", "TDENS1K", "SOUTHASPEC")
gcki.x=c("VEGCLASS", "NumVisits", "PCONIFER", "PREDWOOD", "PDOUGFIR", "PMYCYPRESS", "IJI",
"TDENS1K", "SLOPE_MEAN", "ELEV_MEAN")
wiwa.x=c("VEGCLASS", "NumVisits", "PRIPARIAN", "PCONIFER", "PHARDWOOD", "PREDALDER",
"PALLWILLOW", "PBISHOPPIN", "SIDI", "TDENS1K", "STREAMDIST")
nwcs.x=c("VEGCLASS", "NumVisits", "PGRASS", "PSCRUB", "PCOYOTEBRU", "PCSAGEBRUS", "PYBLUPINE",
"PPOISONOAK", "PACTIVEPAS", "PBROOM", "IJI", "TDENS1K")
orju.x=c("VEGCLASS", "NumVisits", "PCONIFER", "PHARDWOOD", "PBISHOPPIN", "PREDWOOD", "PDOUGFIR",
"PMYCYPRESS", "SIDI", "IJI", "CONIFERCOHES", "CONIFERSIZE", "TDENS1K", "SLOPE_MEAN", "ELEV_MEAN",
"SOUTHASPEC", "WESTASPECT")
savs.x=c("VEGCLASS", "NumVisits", "PNNATANNGR", "PNATANNGRA", "PNNATPERGR", "PACTIVEPAS",
"GRASSCOHES", "GRASSSIZE", "PGRASS", "TDENS1K", "SLOPE_MEAN")

grasp(selected.responses = coye.y, selected.predictors = coye.x, gr.fam = "binomial",
stepwise.models = T, test = "AIC", df1 = 0, df2 = 3, make.summary = T, path =
"Z:/Terrestrial/programs_and_projects/coastal_parks/DistributionModel/GRASP", save.outputs = T,
save.PNG = T, plotpar = c(4,4), contributions = T, plot.contributions = T, plot.histograms = T,
plot.respvspred = T, plot.distry = T, plot.models = T, lookup.tables = T, cvgroups = 4,
validate.models = T, StdError = T, model.anova = T, weights = T,  corlim = 50, plot.correlation =
T, use.correlation = T)

grasp(selected.responses = wavi.y, selected.predictors = wavi.x, gr.fam = "binomial",
stepwise.models = T, test = "AIC", df1 = 0, df2 = 3, make.summary = T, path =
"Z:/Terrestrial/programs_and_projects/coastal_parks/DistributionModel/GRASP", save.outputs = T,
save.PNG = T, plotpar = c(4,4), contributions = T, plot.contributions = T, plot.histograms = T,
plot.respvspred = T, plot.distry = T, plot.models = T, lookup.tables = T, cvgroups = 4,
validate.models = T, StdError = T, model.anova = T, weights = T,  corlim = 50, plot.correlation =
T, use.correlation = T)

grasp(selected.responses = brcr.y, selected.predictors = brcr.x, gr.fam = "binomial",
stepwise.models = T, test = "AIC", df1 = 0, df2 = 3, make.summary = T, path =
"Z:/Terrestrial/programs_and_projects/coastal_parks/DistributionModel/GRASP", save.outputs = T,
save.PNG = T, plotpar = c(4,4), contributions = T, plot.contributions = T, plot.histograms = T,
plot.respvspred = T, plot.distry = T, plot.models = T, lookup.tables = T, cvgroups = 4,
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validate.models = T, StdError = T, model.anova = T, weights = T,  corlim = 50, plot.correlation =
T, use.correlation = T)

grasp(selected.responses = bewr.y, selected.predictors = bewr.x, gr.fam = "binomial",
stepwise.models = T, test = "AIC", df1 = 0, df2 = 3, make.summary = T, path =
"Z:/Terrestrial/programs_and_projects/coastal_parks/DistributionModel/GRASP", save.outputs = T,
save.PNG = T, plotpar = c(4,4), contributions = T, plot.contributions = T, plot.histograms = T,
plot.respvspred = T, plot.distry = T, plot.models = T, lookup.tables = T, cvgroups = 4,
validate.models = T, StdError = T, model.anova = T, weights = T,  corlim = 50, plot.correlation =
T, use.correlation = T)

grasp(selected.responses = swth.y, selected.predictors = swth.x, gr.fam = "binomial",
stepwise.models = T, test = "AIC", df1 = 0, df2 = 3, make.summary = T, path =
"Z:/Terrestrial/programs_and_projects/coastal_parks/DistributionModel/GRASP", save.outputs = T,
save.PNG = T, plotpar = c(4,4), contributions = T, plot.contributions = T, plot.histograms = T,
plot.respvspred = T, plot.distry = T, plot.models = T, lookup.tables = T, cvgroups = 4,
validate.models = T, StdError = T, model.anova = T, weights = T,  corlim = 50, plot.correlation =
T, use.correlation = T)

grasp(selected.responses = gcki.y, selected.predictors = gcki.x, gr.fam = "binomial",
stepwise.models = T, test = "AIC", df1 = 0, df2 = 3, make.summary = T, path =
"Z:/Terrestrial/programs_and_projects/coastal_parks/DistributionModel/GRASP", save.outputs = T,
save.PNG = T, plotpar = c(4,4), contributions = T, plot.contributions = T, plot.histograms = T,
plot.respvspred = T, plot.distry = T, plot.models = T, lookup.tables = T, cvgroups = 4,
validate.models = T, StdError = T, model.anova = T, weights = T,  corlim = 50, plot.correlation =
T, use.correlation = T)

grasp(selected.responses = wiwa.y, selected.predictors = wiwa.x, gr.fam = "binomial",
stepwise.models = T, test = "AIC", df1 = 0, df2 = 3, make.summary = T, path =
"Z:/Terrestrial/programs_and_projects/coastal_parks/DistributionModel/GRASP", save.outputs = T,
save.PNG = T, plotpar = c(4,4), contributions = T, plot.contributions = T, plot.histograms = T,
plot.respvspred = T, plot.distry = T, plot.models = T, lookup.tables = T, cvgroups = 4,
validate.models = T, StdError = T, model.anova = T, weights = T,  corlim = 50, plot.correlation =
T, use.correlation = T)

grasp(selected.responses = nwcs.y, selected.predictors = nwcs.x, gr.fam = "binomial",
stepwise.models = T, test = "AIC", df1 = 0, df2 = 3, make.summary = T, path =
"Z:/Terrestrial/programs_and_projects/coastal_parks/DistributionModel/GRASP", save.outputs = T,
save.PNG = T, plotpar = c(4,4), contributions = T, plot.contributions = T, plot.histograms = T,
plot.respvspred = T, plot.distry = T, plot.models = T, lookup.tables = T, cvgroups = 4,
validate.models = T, StdError = T, model.anova = T, weights = T,  corlim = 50, plot.correlation =
T, use.correlation = T)

grasp(selected.responses = orju.y, selected.predictors = orju.x, gr.fam = "binomial",
stepwise.models = T, test = "AIC", df1 = 0, df2 = 3, make.summary = T, path =
"Z:/Terrestrial/programs_and_projects/coastal_parks/DistributionModel/GRASP", save.outputs = T,
save.PNG = T, plotpar = c(4,4), contributions = T, plot.contributions = T, plot.histograms = T,
plot.respvspred = T, plot.distry = T, plot.models = T, lookup.tables = T, cvgroups = 4,
validate.models = T, StdError = T, model.anova = T, weights = T,  corlim = 50, plot.correlation =
T, use.correlation = T)

grasp(selected.responses = savs.y, selected.predictors = savs.x, gr.fam = "binomial",
stepwise.models = T, test = "AIC", df1 = 0, df2 = 3, make.summary = T, path =
"Z:/Terrestrial/programs_and_projects/coastal_parks/DistributionModel/GRASP", save.outputs = T,
save.PNG = T, plotpar = c(4,4), contributions = T, plot.contributions = T, plot.histograms = T,
plot.respvspred = T, plot.distry = T, plot.models = T, lookup.tables = T, cvgroups = 4,
validate.models = T, StdError = T, model.anova = T, weights = T,  corlim = 50, plot.correlation =
T, use.correlation = T)

sink("Z:/Terrestrial/programs_and_projects/coastal_parks/DistributionModel/GRASP/alonecontrib.txt
")
alone <- write.table(ALONE.CONTRIB, quote = F)
sink(alone)
sink("Z:/Terrestrial/programs_and_projects/coastal_parks/DistributionModel/GRASP/dropcontrib.txt"
)
drop <- write.table(DROP.CONTRIB, quote = F)
sink(drop)
sink("Z:/Terrestrial/programs_and_projects/coastal_parks/DistributionModel/GRASP/modelcontrib.txt
")
model <- write.table(MODEL.CONTRIB, quote = F)
sink(model)
```