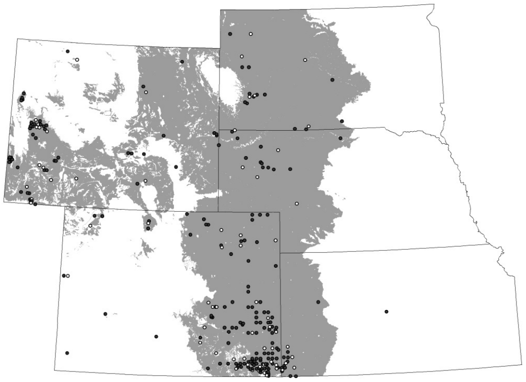
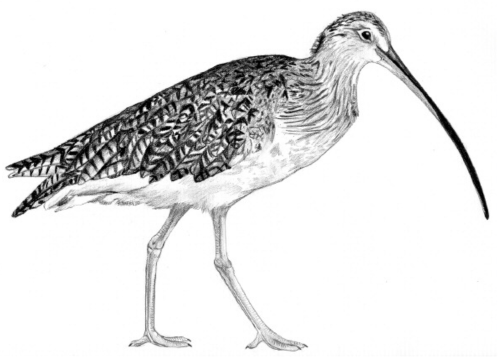
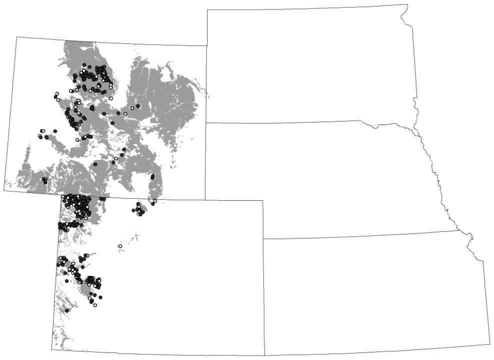
PREDICTIVE DISTRIBUTION MAPS FOR 54 SPECIES OF MANAGEMENT CONCERN IN THE ROCKY MOUNTAIN REGION OF THE USDA FOREST SERVICE







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This report is accompanied by multiple data files, images, and species-specific appendices on compact disc.

BACKGROUND

This report details the production of predictive distribution models and maps for 54 species of management concern that occur in the Rocky Mountain Region (Region 2) of the USDA Forest Service. It follows a similar report, completed 30 May 2003, that outlines the development of predictive distribution models and maps for an additional 15 species:

> *Beauvais, G.P., R. Thurston, and D. Keinath. 2003. Predictive range maps for 15 species of management concern in the Rocky Mountain Region of the USDA Forest Service. Report prepared for the U.S. Geological Survey-National Gap Analysis Program by the Wyoming Natural Diversity Database-University of Wyoming, Laramie, Wyoming, USA.*

Readers are encouraged to consult the 2003 report to more fully understand the context of this report. Also, readers are encouraged to consult Beauvais et al. (2004) for a complete discussion of the underlying concepts, procedures, and application of predictive distribution maps in general.

A significant terminological difference between this report and the 2003 report is more precise use of the terms "range", "distribution", and "habitat". As used here:

> *RANGE - The total areal extent occupied by a given taxon. "Range" considers only* geographic space*, and* known (or strongly suspected) occupation*. It is typically mapped across coarse geographic scales (e.g., continental, regional) using rather subjective methods. Most range maps are simple polygons that encompass the outermost points of known occurrence of a taxon and do not indicate fine-scale variations in occupation.*
>
> *DISTRIBUTION - The environments suitable for occupation by a given taxon. "Distribution" considers* multi-dimensional environments*, and* suitability for occupation*. It can be mapped at any geographic scale, and is often mapped via spatial extrapolations of inductive models that relate points of known occurrence to environmental gradients. Distribution maps depict within-range variation in occupation rather than simply the outer limits of occupied area.*
>
> *HABITAT - Environments with the combination of resources and conditions that promote occupancy, survival, and reproduction by an element (after Morrison et al. 1992). "Habitat" considers* multidimensional environments, *and* survival/ reproduction*. Habitat mapping often takes the form of indicating habitat quality; that is, categorizing portions of a taxon's distribution by the likelihood of supporting positive rates of survival and reproduction.*

The above definitions place the three biogeographic concepts in logical relationship to one another; habitat is a subset of distribution, and distribution is a subset of range.

INTRODUCTION

Species' distributions have traditionally been depicted in 1 of 2 ways: (1) all known locations where the target taxon has been observed are shown as point features, usually over a background map of the study area (e.g., Maj and Garton 1994, Hammerson 1999); or (2) areas known or suspected to be occupied are shown as broad, all-encompassing polygons, again usually over a background map (i.e., range maps; e.g., Wilson and Ruff 1999, Knopf 1996). Commonly, these 2 techniques are used in tandem to show both points of known occurrence and range polygons (e.g., Hall 1981, Clark and Stromberg 1987).

Although these 2 basic techniques can be effective at suggesting species distribution at coarse (e.g., global, continental) geographic scales, they typically fail to adequately predict presence and absence at finer (e.g., regional, state) scales. Point maps typically underpredict occupied area and overpredict unoccupied area; range maps usually do the opposite. Thus point maps and range maps can be seen as endpoints on a spectrum, with the ideal predictive distribution map sitting somewhere between the 2 extremes. It would draw on the information conveyed by the points of known occurrence without being overly restricted to those points, and would extrapolate that information across the landscape more realistically than does an all-encompassing range polygon.

The clear answer to creating more informative distribution maps is to first build a model of environmental selection appropriate to the geographic scale of the study area, then map that model across the study area using complete and consistent spatial layers of the predictor variables. Although such modeling has been a long-standing staple of wildlife science, only recently has computing power, spatial statistics, and (perhaps most importantly) geographic information system technology advanced to the point where models can be accurately mapped with realistic inputs of time, money, and expertise.

Over the past decade these technological breakthroughs have lead to a rapid increase in large-scale distribution mapping efforts, with the USGS Gap Analysis Program serving as one of the best examples. Gap Analysis teams in each state defined distribution models (either qualitative or statistical) for each of a series of native vertebrates, mapped those models across their respective states, then used map overlays to analyze patterns in biodiversity (e.g., Merrill et al. 1996). Collectively, the distribution maps produced by Gap Analysis efforts probably represent the most accurate depictions to-date of the distributions of terrestrial vertebrates in western North America. However, differences in modeling techniques, mapping protocols, and resolutions of environmental data have resulted in substantial state-to-state differences in Gap Analysis distribution maps. These differences are most problematic when attempting to combine the vertebrate distribution maps from different states to analyze patterns across larger regions.

The Rocky Mountain Region (Region 2) of the USDA Forest Service (hereafter "USFS R2") desires to use Gap Analysis distribution models and maps to inform resource management in general, and the revision of its Sensitive Species List in particular (Blankenship et al. 2001). This requires reformulation of the state-specific Gap Analysis models to eliminate differences and produce more consistent predictions of vertebrate distributions across the 5 states (Wyoming, South Dakota, Nebraska, Colorado, Kansas) encompassing USFS R2 management units.

This project produced predictive distribution models and maps for 43 vertebrates and 11 plants that occupy USFS R2 (Table 1), using as much information as possible from the Gap Analyses performed in each state and with the intent of showing the current (as opposed to historical) distribution of each target taxon. Because land cover is a primary driver of the distribution of most vertebrates, and because Gap Analysis mapped land cover differently in each state of USFS R2, this project necessarily depended on a re-mapping of landcover across the region in a consistent fashion. This initial work was performed by NatureServe (2003), following the ecological systems concept (Menard and Lauver 2000).

METHODS

For most of the target species we used a 3-part procedure to produce a final predictive distribution map. First, for each species we used points of known occurrence and a region-wide set of climatic variables to model and map a biophysical envelope that efficiently encompassed distributional extent in USFS R2. Second, we identified the ecological systems (NatureServe 2003) that corresponded to the land cover types identified by each state Gap Analysis team as being associated with each taxon. Finally, to produce final distribution maps, we intersected the biophysical envelope with its associated ecological systems for each target taxon.

Steps 2 and 3 were modified for species known to be associated with riparian environments. For riparian plants, whose distribution is typically better defined by the presence of open water and wetted soils than by dominant vegetation, we did not identify a set of suitable ecological systems with which to intersect the biophysical envelope. Rather, we produced a layer of buffered hydrological features to approximate the extent of riparian environments, and intersected that layer with each taxon's biophysical envelope to produce a final distribution map. For each riparian vertebrate we intersected the biophysical envelope with suitable ecological systems, as described above, but we also added in any buffered hydrologic features not already encompassed by the selected ecological systems. This was equivalent to adding an "unclassified riparian" ecological system to the region-wide ecological systems map, and then including this type in the list of suitable systems for each riparian vertebrate (Merrill et al. 1996).

In general our modeling approach is probably best described as producing 2 individual models for each species, then overlaying the 2 models and identifying their intersection as the best estimate of actual distribution. The first model is inductive; that is, a statistical model of climatic limits as defined by points of known occurrence. The second is a deductive or "expert systems" model of ecological systems (and/ or riparian environments) suitable for occupation by the target species. The intersection of the 2 models is assumed to be a better estimate of the distribution of the target species than is either model on its own (see Beauvais et al 2004).

The procedures and data manipulations necessary for modeling are discussed generally below; further details are given in the species-specific appendices that accompany this report.

Collection and manipulation of occurrence data

Occurrence data for each target taxon were collected from a variety of sources (Table 2). These data required several filtering steps to produce a subset that could be used to estimate a relatively unbiased biophysical envelope for each species (Beauvais et al. 2004). Filtering was done using the ArcInfo and ArcView (Environmental Systems Research Institute, Redlands, California) geographic information systems.

General filtering rules, applied to the majority of target species, are outlined below. For some species, however, it was necessary to relax the filtering rules in order to maintain a reasonable number and distribution of points of known occurrence for accurate biophysical modeling. In other words, applying strict filtering rules would have resulted in such a low number of points, or such a biased spatial patterning of points, that the resulting model would likely have been less accurate than a model based on a larger set of lower-quality points. Exceptions to the below filtering rules are outlined in the species-specific appendices that accompany this report.

Duplicate record filter: For most species there were a substantial number of duplicate records in the initial occurrence dataset. For example, datasets contributed by state Natural Heritage Programs commonly contained records of specimens that were also contained in datasets contributed by museums. All datasets were carefully screened to remove all duplicate records.

Negative record filter: Contributed datasets for some species contained a number of negative records (i.e., records of survey efforts that failed to document the target taxon). Because our modeling technique was based solely on positive records (i.e., records of confirmed observation of the target taxon) all datasets were carefully screened to remove negative records.

Identity filter: Basic ecological principles dictate that different species will partition available resources by positioning themselves preferentially in different environments. A predictive distribution map is a spatially-explicit extrapolation of the environments chosen by a given taxon, as represented by a sample of known locations of that taxon. Inclusion of locations of other taxa in the modeling dataset will degrade the environmental selection "signal" of the target taxon, and therefore should be avoided. Following this reasoning we removed observation records that may have involved non-target taxa from the occurrence dataset for each target taxon. This typically involved removing records with "unknown", "questionable", "unlikely", or similar entries in a species-identification field in the contributed datasets.

Mapping precision filter: Field observations are rarely mappable to exact locations; i.e., there is some degree of spatial error inherent in assigning map coordinates to observational data. As stated previously, a predictive distribution map is a spatially-explicit extrapolation of the environments chosen by a given taxon, as represented by a sample of known locations of that taxon. Precisely-mapped locations will represent a taxon's environmental choices more accurately than will coarsely-mapped locations. Therefore, we minimized the use of coarsely-mapped locations as much as possible in defining the biophysical envelope for each target taxon. Mapping precision was estimated, at least qualitatively, for all observations in our occurrence datasets, either by the contributing data source or by ourselves using text descriptions in the records. Removal of coarsely-mapped locations typically involved removing observation records with "unmappable" precisions, and also those records with mapping precisions of ca. ±5 miles or greater (e.g., "G" precision points from state Natural Heritage Program datasets).

Date-of-observation filter: The predictive distribution maps produced here are intended to estimate the current distribution of the target taxa. The distributions of some taxa have changed dramatically over the past several decades as a result of population declines, habitat alterations, and climatic shifts. Therefore, older observation records may reflect a taxon's response to past conditions that no longer exist. Although models of such data may inform discussions of historic distribution, they may not be appropriate (and indeed may be misleading) input for predictive models of current distribution. Therefore, we minimized the use of older observations as much as possible in defining the biophysical envelope for each target taxon. In most cases this involved removing observation records made prior to 1970; it also often involved removing records with unspecified dates-of-observation in the contributed datasets.

Spatial filter: Ideally, predictive distribution maps are based on points of known occurrence from throughout the entire range of the target taxon in the study area. Furthermore, to best reflect areas of known presence and likely absence, such points should result from even application of sampling effort throughout that range. These conditions are rarely if ever met and, as is the case with this project, almost all predictive distribution maps are based on opportunistically-collected occurrence data that include an unknown degree of sampling bias; i.e., some areas within the study area are sampled much more intensively than others, with most of the study area receiving little or no sampling for the target taxon. If not accounted for, the clustering of points in heavily-sampled environments will bias the resulting distribution map towards those environments. To minimize this bias, we eliminated points of known occurrence such that no 2 points were within a certain distance of each other in the occurrence dataset for each target species. The separation distance differed by taxon, and roughly reflected the relative mobility of each taxon (see the species-specific appendices that accompany this report). Note that in many cases multiple records were mapped at the exact same point, and our removal procedure reduced such multi-records to a single record per point location. Also, prior to removing points from a cluster, our removal procedure evaluated the mapping precision of each record to ensure that records with the finest mapping precisions were preferentially retained, and those with the coarsest mapping precisions were preferentially removed.

Separating model data from evaluation data: For most target species we used only 75% of the post-filtering occurrence data to model the biophysical envelope, and reserved the remaining 25% as an independent dataset with which to evaluate the predictive accuracy of the biophysical envelope and the final distribution model. Selection of this “evaluation dataset” was done in a stratified-random fashion, with strata defined geographically. The cluster of post-filtering points was overlain with a grid in which each cell approximated about 10% of the cluster’s areal extent. Then 25% of all points within each grid cell was selected out and reserved to the evaluation set. If there were <40 occurrence points total in the post-filtering dataset we did not select an evaluation dataset, but rather used all 40 points in the modeling procedure and did not perform formal model evaluation.

Collection and manipulation of biophysical variables

There are so many climatic variables available in digital form that modelers are required to select a small subset with which to proceed. The major challenge is selecting a subset that is both efficient in number and also effective at modeling the distribution of several different taxa. We met this challenge by using a combination of principal components analysis (PCA) and reasoned selection to select a subset of climatic variables with which to define a biophysical envelope that best encompassed the post-filtering occurrence data for each target taxon.

We first downloaded spatial layers of each of 54 different climatic variables available from the DAYMET U.S. Data Center (http://www.daymet.org/) and clipped all layers to our 5-state study area (Table 3). Some of these layers were then processed with the procedure developed by R. Hijmans (rhijmans@uclink.berkeley.edu; see also Nix 1986), resulting in a final set of 30 layers of biologically-relevant climatic variables, including 11 temperature variables, 9 precipitation variables, 5 humidity variables, and 5 radiation variables (Table 4).

In order for analyses to proceed it was necessary to spatially manipulate some of the variable grid layers so that component cells would match each other in size and position. All variable layers were resampled to form grid cells of 1km x 1km. Spatial manipulations were performed within the ArcInfo and ArcView (Environmental Systems Research Institute, Redlands, California) geographic information systems.

We then performed a PCA of the variables in each of the 4 classes (temperature, precipitation, humidity, radiation) separately, and used the output matrix to help guide selection of the variables in each class that explained most of the variation in the study area. For each class we selected the variables that loaded the highest on each of the first 3 principal components. For each of the temperature and precipitation classes we selected 3 additional variables that were relatively uncorrelated with the first 3 selected variables and that had some potential to constrain vertebrate distributions in the study area (Table 4).

To this initial set of 18 variables we added mean annual number of frost days and interannual variation in number of frost days for a preliminary set of 20 variables, which was subjected to a second PCA. For the final variable set we selected the 3 variables that loaded the highest on each of the first 3 principal components from this second PCA, and added elevation and mean annual number of frost days to form the final set of 5 predictor variables (Table 5).

This basic set of 5 variables was used to model the biophysical envelope for all target taxa. Additional variables were included for a few taxa when there was reason to suspect that such variables were important in limiting distribution (see the species-specific appendices that accompany this report).

Biophysical envelope modeling

We used the DOMAIN modeling procedure (Carpenter et al. 1993) to model the biophysical envelope that efficiently encompassed the points of known occurrence of each target species in the study area. Preliminary comparisons with other biophysical modeling programs (e.g., BIOCLIM, GARP, BIOMAPPER) have indicated that DOMAIN is generally the most accurate technique when dealing with large geographic areas, as is the case in this project (L. Master and P. Hernandez, personal communication).

Briefly, for each target species DOMAIN plots all points in the study area in the multivariate space defined by the biophysical predictor variables, then measures the multivariate distance between each point and the most similar point (or an average of a set of most similar points) of known occurrence for that species. Each point in the study area is attributed with this measurement, known as the Gower similarity metric. For all species in this project we specified calculation of the Gower metric as the environmental distance between each point in the study area and the average of the environmental values of the most similar 5% of the points of known occurrence. Averaging in this manner dampened the effect of outliers in the occurrence datasets; by using a percentage rule we were able to roughly equalize the degree of this dampening across all species.

The raw output from the DOMAIN procedure was a complete grid coverage (1km resolution) of the study area, with each grid cell attributed with its Gower metric. It was therefore necessary to select a threshold value of the metric for each species such that values above the threshold indicated suitable biophysical conditions (i.e., within the biophysical envelope for that species), and values below the threshold indicated unsuitable biophysical conditions (i.e., outside of the biophysical envelope for that species). For each species we selected the threshold such that 95% of the points of known occurrence were included in the biophysical envelope. The 5% of the points that were excluded had the lowest similarity metrics of all the points of known occurrence for a given species. Again, as with the averaging rule outlined above, this percentage rule allowed us to define the biophysical envelope consistently across all species.

It is important to reiterate that, for most target taxa, DOMAIN modeling used only 75% of the total number of post filtering occurrence points, with the remaining 25% reserved for later model evaluation.

Clipping the biophysical envelope

Upland taxa: clipped by suitable ecological systems. For each upland taxon we produced the final predictive distribution map by intersecting the biophysical envelope with the ecological systems (NatureServe 2003) that encompassed the land cover types chosen by each state Gap Analysis team as suitable for occupation by that taxon. For each taxon we first cross-walked the identified Gap Analysis land cover types to their respective ecological systems. Then, because of inherent differences between Gap Analysis land cover types and ecological systems, we reviewed the list of resulting ecological systems in the context of the taxon's environmental selection and biogeography to determine whether some systems should be dropped, and others added. This resulted in relatively few modifications which, along with the rationale behind them, are outlined in the species-specific appendices that accompany this report. The intersection of the biophysical envelope with suitable ecological systems produced the final predictive distribution map for each species.

Riparian plants: clipped by buffered hydrologic features. For each riparian plant we produced the final predictive distribution map by intersecting the biophysical envelope with a layer of buffered hydrologic features. This layer was created by buffering all hydrologic features within the National Hydrography Dataset (http://nhd.usgs.gov/) by 50 meters.

Riparian vertebrates: clipped by suitable ecological systems and buffered hydrologic features. For each riparian-associated vertebrate we produced the final predictive distribution map by intersecting the biophysical envelope grid with a grid of all suitable ecological systems plus additional buffered hydrologic features.

A few species required specialized modeling procedures; these are described in more detail in the species-specific appendices.

Model evaluation

We evaluated the accuracy of the biophysical envelope and final model for each species by calculating the percentage of all modeling points, and all validation points, that were correctly classified.

Species in the original target set that were not modeled

The project originally intended to model and map the distribution of 63 taxa (51 vertebrates, 12 plants). However, we did not produce final models for 9 of these taxa (8 vertebrates, 1 plant).

Lark bunting (*Calamospiza melanocorys*) - We were unable to acquire occurrence data that sufficiently sampled the known range of this species in the study area. In particular, there was very little occurrence data from the state of South Dakota, which clearly forms part of the core of this species' range. Proceeding with such a markedly biased dataset would have produced misleading models and maps.

American beaver (*Castor canadensis*) - Historically, this taxon occupied essentially all waters in the study area. It then experienced a steep and rather patchy decline in both distribution and abundance due to human-caused mortality and habitat modification. This was followed by a complex pattern of active restoration and translocation, natural population expansion, and continued local declines. These dynamics have produced a current distribution that is not well-predicted by environmental features. The distribution of *C. canadensis* is not amenable to the modeling approach used here - at the scale of this project it is driven much more by historical events and human management actions than by mapped conditions like elevation, climate, and vegetation.

Wild turkey (*Meleagris gallopavo*) - This is an intensely-managed taxon that has experienced quite a bit of human-mediated translocation, population augmentation, and extralimital introduction in the study area. Similar to the situation with *C. canadensis*, the current distribution of *M. gallopavo* is controlled more by past and current management actions rather than environmental conditions. It is assumed that state wildlife management agencies possess qualitative maps of *M. gallopavo* populations, intended to support management activities, that approximate actual distribution better than would a mapped model produced via the procedures used in this project.

Greater prairie chicken (*Tympanuchus cupido*) - Reasonable efforts at collecting occurrence data for this taxon resulted in only a very few reliable points. Furthermore, these points did not adequately represent the known range of the taxon in the study area, and most had very coarse mapping precisions. We elected not to model such poor data. Similar to the situation with *M. gallopavo*, it is assumed that state wildlife management agencies possess qualitative maps of *T. cupido*, intended to support management activities, that approximate actual distribution better than would a mapped model produced via the procedures used in this project.

Western bluebird (*Sialia mexicana*) - There was taxonomic confusion at several levels surrounding this taxon, which prevented the collection of adequate occurrence data. The USDA Forest Service originally requested a model for the western bluebird, but cross-referenced that common name to *S. currucoides* (mountain bluebird). This error was not discovered until mid-way through the data collection process. Furthermore, datasets acquired from 2 significant sources (the Wildlife Observation System of the Wyoming Game and Fish Department, and the North American Breeding Bird Survey) exhibited similar confusion: many occurrence records were referenced to mismatched common and Latin names. Resolving this data confusion would require substantial effort, and such effort was determined to be beyond the scope of this project.

Pine squirrel (*Tamiasciurus hudsonicus*) - This taxon occupies essentially all conifer-dominated landscapes in Wyoming, Colorado, and western South Dakota. It is so ubiquitous in these areas that mapped occurrence data is virtually impossible to acquire - essentially no one records such data. Furthermore, such data is unnecessary. The best predictive distribution map for this taxon could be produced by simply selecting all conifer-dominated ecological systems in the 3 mentioned geographic areas.

Trumpeter swan (*Cygnus buccinator*) - This taxon has a somewhat complex distribution in the study area, owing to dynamics similar to those affecting *C. canadensis*. Historically, *C. buccinator* bred throughout the region. A precipitous decline in the early 20th century, due primarily to human-caused mortality and habitat modification, was followed by a slow recovery brought about by active management as well as natural population expansion. Current breeding locations include protected waters in northwestern Wyoming, most of which remained occupied through much of the historic decline, and a few protected waters elsewhere that have received active management for *C. buccinator*. Thus, current distribution at the scale of this project is not well-predicted by environmental conditions like elevation, climate, and vegetation. It is assumed that state wildlife management agencies possess qualitative maps of *C. buccinator* breeding locations that approximate actual distribution better than would a mapped model produced via the procedures used in this project.

Bighorn sheep (*Ovis canadensis*) - Because of their rather high value to hunters and wildlife viewers, bighorn sheep are well-monitored in this region. This has at least 2 important consequences for this project: (1) field data for bighorn sheep typically refers to herds and significant population segments, rather than sightings of individual animals, and (2) state wildlife management agencies possess good maps of not only distribution but also of seasonal habitat quality, based on many years of observation and management experience. The former presents a problem to our modeling procedure, which requires as input mapped observations of individual animals; the latter suggests that our modeling and mapping procedures may not be necessary for this taxon. A future report will outline efforts to refine existing agency maps of seasonal habitat quality for *O. canadensis* via inductive modeling of the type used in this project.

Simple bog sedge (*Kobresia simpliciuscula*) - This taxon is known to occur in only one location in the study area, in the Clark's Fork Valley of northwestern Wyoming. The single point serves as the best distribution map at this time, and is an inadequate base on which to proceed with formal modeling. A predictive model could be produced by shifting the study area boundaries to encompass Montana and Idaho. Points of known occurrence in those states, plus the single point from Wyoming, would likely be enough data for modeling and would inform estimates of distribution in USFS R2.

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TABLES

Table 1. Fifty-four species of management concern in the Rocky Mountain Region (Region 2) of the USDA Forest Service, for which predictive distribution maps were produced.

TYPE	COMMON NAME	LATIN NAME
Vertebrate (amphibian)	Columbia spotted frog	*Rana luteiventris*
Vertebrate (amphibian)	Plains leopard frog	*Rana blairi*
Vertebrate (amphibian)	Wood frog	*Rana sylvatica*
Vertebrate (reptile)	Black Hills redbelly snake	*Storeria occipitomaculata pahasapae*
Vertebrate (reptile)	Massasauga	*Sistrurus catenatus*
Vertebrate (mammal)	Common hog-nosed skunk	*Conepatus leuconotus*
Vertebrate (mammal)	Fringed myotis	*Myotis thysanodes*
Vertebrate (mammal)	Kit fox	*Vulpes macrotis*
Vertebrate (mammal)	Pygmy shrew	*Microsorex hoyi*
Vertebrate (mammal)	Spotted bat	*Euderma maculatum*
Vertebrate (mammal)	Wyoming pocket gopher	*Thomomys clusius*
Vertebrate (mammal)	Gunnison's prairie dog	*Cynomys gunnisoni*
Vertebrate (mammal)	White-tailed prairie dog	*Cynomys leucurus*
Vertebrate (bird)	Chestnut-collared longspur	*Calcarius ornatus*
Vertebrate (bird)	Harlequin duck	*Histrionicus histrionicus*
Vertebrate (bird)	Long-billed curlew	*Numenius americanus*
Vertebrate (bird)	McCown's longspur	*Calcarius mccownii*
Vertebrate (bird)	Pinion jay	*Gymnorhinus cyanocephalus*
Vertebrate (bird)	Three-toed woodpecker	*Picoides tridactylus*
Vertebrate (bird)	White-tailed ptarmigan	*Lagopus leucurus*
Vertebrate (bird)	American bittern	*Botaurus lentiginosus*
Vertebrate (bird)	Black tern	*Chlidonias niger*
Vertebrate (bird)	Cassin's sparrow	*Aimophila cassinii*
Vertebrate (bird)	Grasshopper sparrow	*Ammodramus savannarum*
Vertebrate (bird)	Greater sage grouse	*Centrocercus urophasianus*
Vertebrate (bird)	Gunnison sage grouse	*Centrocercus minimus*
Vertebrate (bird)	Lesser prairie chicken	*Tympanuchus pallidicinctus*
Vertebrate (bird)	Lewis' woodpecker	*Melanerpes lewis*
Vertebrate (bird)	Lincoln's sparrow	*Melospiza lincolnii*
Vertebrate (bird)	Olive-sided flycatcher	*Contopus cooperi*
Vertebrate (bird)	Purple martin	*Progne subis*
Vertebrate (bird)	Pygmy nuthatch	*Sitta pygmaea*
Vertebrate (bird)	Sage sparrow	*Amphispiza bellii*
Vertebrate (bird)	Short-eared owl	*Asio flammeus*
Vertebrate (bird)	White-crowned sparrow	*Zonotrichia leucophrys*
Vertebrate (bird)	Wilson warbler	*Wilsonia pusilla*
Vertebrate (bird)	Blue grouse	*Dendragapus obscurus*
Vertebrate (bird)	Brown creeper	*Certhia americana*
Vertebrate (bird)	Ferruginous hawk	*Buteo regalis*
Vertebrate (bird)	Hairy woodpecker	*Picoides villosus*
Vertebrate (bird)	Loggerhead shrike	*Lanius ludovicianus*
Vertebrate (bird)	Northern harrier	*Circus cyaneus*
Vertebrate (bird)	Burrowing owl	*Athene cunicularia*
Plant	Barr's milkvetch	*Astragalus barrii*
Plant	Lesser bladderwort	*Utricularia minor*
Plant	Bristlystalked sedge	*Carex leptalea*
Plant	Chamisso's cottongrass	*Eriophorum chamissonis*
Plant	Dwarf raspberry	*Rubus arcticus ssp. acaulis*

(Table 1; continued)

Plant	Kotzebue’s grass of parnassus	*Parnassia kotzebuei*
Plant	Lesser panicled sedge	*Carex diandra*
Plant	Livid sedge	*Carex livida*
Plant	Sageleaf willow	*Salix candida*
Plant	Slender cottongrass	*Eriophorum gracile*
Plant	Yellow lady’s slipper	*Cypripedium parviflorum*

Table 2. Sources of species occurrence data used to model and map the distribution of 54 species of management concern in the Rocky Mountain Region (Region 2) of the USDA Forest Service.

SOUTH DAKOTA

South Dakota Natural Heritage Program (South Dakota Department of Game, Fish, and Parks; Pierre, South Dakota)

South Dakota Department of Game, Fish, and Parks (Pierre, South Dakota)

South Dakota Gap Analysis Program (South Dakota State University; Brookings, South Dakota)

Dr. Brian Smith (Black Hills State University; Spearfish, South Dakota)

WYOMING

Wyoming Natural Diversity Database (University of Wyoming; Laramie, Wyoming)

Wyoming Gap Analysis Program (University of Wyoming; Laramie, Wyoming)

University of Wyoming Zoological Collection (University of Wyoming; Laramie, Wyoming)

Wildlife Observation System (Wyoming Game and Fish Department; Cheyenne, Wyoming)

USDI Bureau of Land Management - Worland Field Office (Worland, Wyoming)

USDI Bureau of Land Management - Casper Field Office (Casper, Wyoming)

Fremont County Weed and Pest Control District (Lander, Wyoming and Riverton, Wyoming)

NEBRASKA

Nebraska Natural Heritage Program (Nebraska Game and Parks Commission; Lincoln, Nebraska)

Nebraska Gap Analysis Program (University of Nebraska; Lincoln, Nebraska)

Nebraska State Museum (University of Nebraska; Lincoln, Nebraska)

COLORADO

Colorado Natural Heritage Program (Colorado State University; Ft. Collins, Colorado)

Colorado Gap Analysis Program (Colorado Division of Wildlife / Natural Resource Ecology Center; Ft. Collins, Colorado)

Colorado Breeding Bird Atlas (Colorado Wildlife Heritage Foundation; Denver, Colorado)

Colorado Division of Wildlife (Denver, Colorado)

KANSAS

Kansas Natural Heritage Program (University of Kansas; Lawrence, Kansas)

Kansas Gap Analysis Program (Kansas State University; Manhattan, Kansas)

MULTIPLE STATES

Denver Museum of Nature and Science (Denver, Colorado)

Field Museum (Chicago, Illinois)

Smithsonian Institution / National Museum of Natural History (Washington, DC)

(Table 2; continued)

Sternberg Museum of Natural History (Fort Hays State University; Hays, Kansas)

University of Colorado Museum of Natural History (Boulder, Colorado)

University of Kansas Museum of Natural History (Manhattan, Kansas)

Species Analyst Museum Specimen Database (University of Kansas - Natural History Museum and Biodiversity Research Center; Lawrence, Kansas)

Rocky Mountain Bird Observatory (Barr Lake State Park, Brighton, Colorado)

North American Breeding Bird Survey (USGS Patuxtent Research Center; Laurel, Maryland)

Hall, E.R. 1981. The mammals of North America. Second edition. John Wiley and Sons. New York, New York, USA.

Beauvais, G.P., R. Thurston, and D. Keinath. 2003. Predictive range maps for 15 species of management concern in the Rocky Mountain Region of the USDA Forest Service. Report prepared for the U.S. Geological Survey-National Gap Analysis Program by the Wyoming Natural Diversity Database-University of Wyoming, Laramie, Wyoming, USA.

Table 3. Climatic variables downloaded from the DAYMET U.S. Data Center and used to model and map the distribution of 54 species of management concern in the Rocky Mountain Region (Region 2) of the USDA Forest Service.

Annual number of frost days
Interannual variation in annual number of frost days
Daily average water vapor pressure (annual)
Daily average water vapor pressure (by month)
Total annual precipitation
Total precipitation (by month)
Daily total shortwave radiation (annual)
Daily total shortwave radiation (by month)
Daily minimum air temperature (annual)
Daily minimum air temperature (by month)

Table 4. Principal components analyses (PCA) of biologically-relevant climatic variables derived from the DAYMET dataset (see Table 3). A separate PCA was performed on the variables in each class: (a) temperature, (b) precipitation, (c) humidity, and (d) radiation. Results of only the first four principal components are shown. Variables in bold type were entered into a second PCA, along with mean annual number of frost days and interannual variation in number of frost days, to guide selection of a final variable set to use in predicting the distribution of 54 taxa of management concern in the Rocky Mountain Region (Region 2) of the USDA Forest Service.

(a) Temperature variables:

Principal component	1	2	3	4
Eigenvalues (val)	10,152	4,383	1,327	656
Prop. of var. explained	0.60	0.26	0.08	0.04
Cumulative prop.	0.60	0.86	0.93	0.97
VARIABLES				
Annual mean temp.	**0.30**	**0.22**	**-0.01**	**-0.17**
Mean diurnal temp. range	-0.03	0.04	0.28	0.29
Hottest month mean max. temp.	**0.31**	**0.17**	**-0.03**	**0.11**
Coldest month mean min. temp.	0.20	0.28	0.12	-0.44
Annual temp. range	0.11	-0.10	-0.15	0.56
Isothermality	**-0.17**	**0.18**	**0.82**	**0.22**
Standard dev. of monthly temp.	0.05	-0.06	-0.16	0.09
Wettest quarter mean temp.	**0.70**	**-0.01**	**0.12**	**0.36**
Driest quarter mean temp.	**-0.28**	**0.83**	**-0.31**	**0.30**
Warmest quarter mean temp.	**0.36**	**0.15**	**-0.17**	**-0.06**
Coldest quarter mean temp.	0.21	0.29	0.24	-0.30

(b) Precipitation variables:

Principal component	1	2	3	4
Eigenvalues (val)	55859	19930	1674	157
Prop. of var. explained	0.72	0.26	0.02	0.01
Cumulative prop.	0.72	0.98	(1.0)	(1.0)
VARIABLES				
Annual mean precip.	**0.88**	**0.08**	**0.12**	**0.28**
Precip. of the wettest month	0.10	0.08	-0.01	0.07
Precip. of the driest month	0.03	-0.03	0.02	0.12
Annual precip. range	0.07	0.11	-0.03	-0.05
Precip. of the wettest quarter	**0.28**	**0.22**	**0.01**	**-0.34**
Precip. of the driest quarter	**0.12**	**-0.13**	**0.09**	**0.49**
Precip. of the warmest quarter	**0.23**	**0.32**	**-0.63**	**-0.40**
Precip. of the coldest quarter	**0.16**	**-0.22**	**0.65**	**-0.60**
CV of monthly precip.	**-0.19**	**0.87**	**0.40**	**0.14**

(Table 4, continued)

(c) Humidity variables:

Principal component	1	2	3	4
Eigenvalues (val)	22,934	4,354	520	85
Prop. of var. explained	0.82	0.16	0.02	0.01
Cumulative prop.	0.82	0.98	(1.0)	(1.0)
VARIABLES				
Annual mean relative humidity (RH)	**0.51**	**0.26**	**-0.38**	**0.74**
RH of the most humid month	**0.28**	**0.67**	**0.18**	**-0.33**
RH of the least humid month	**0.62**	**0.02**	**0.51**	**-0.16**
Annual RH range	-0.33	0.64	-0.33	-0.17
CV of monthly RH	-0.43	0.27	0.67	0.54

(d) Radiation variables:

Principal component	1	2	3	4
Eigenvalues (val)	62,848	24,427	105	24
Prop. of var. explained	0.72	0.28	0.01	0.01
Cumulative prop.	0.72	(1.0)	(1.0)	(1.0)
VARIABLES				
Annual total radiation	**0.27**	**0.48**	**0.84**	**-0.02**
Radiation of the lightest month	**0.71**	**0.20**	**-0.34**	**0.07**
Radiation of the darkest month	**0.06**	**0.67**	**-0.39**	**0.25**
Annual radiation range	0.64	-0.46	0.05	-0.19
CV of monthly radiation	0.07	-0.27	0.16	0.95

Table 5. Principal components analyses (PCA) of biologically-relevant climatic variables derived from the DAYMET dataset (see Table 3). Variables entered into this PCA were selected with the aid of 4 preliminary PCA s (see Table 4). Results of only the first five principal components are shown. Variables in bold type were selected, along with elevation, as the final set of variables for predicting the distribution of 54 taxa of management concern in the Rocky Mountain Region (Region 2) of the USDA Forest Service.

Principal component	1	2	3	4	5
Eigenvalues (val)	93,114	42,206	17,823	5,622	2,911
Prop. of var. explained	0.56	0.26	0.11	0.03	0.02
Cumulative prop.	0.56	0.82	0.93	0.96	0.98
VARIABLES					
Wettest quarter mean temp.	-0.07	-0.24	0.30	-0.23	0.14
Driest quarter mean temp.	0.03	0.21	0.06	-0.16	-0.75
Hottest month mean max. temp.	-0.02	-0.09	0.15	-0.20	-0.16
Isothermality	0.08	0.07	0.08	0.15	-0.04
Warmest quarter mean temp.	-0.05	-0.10	0.16	-0.21	-0.13
Annual mean temp.	-0.04	-0.06	0.18	-0.17	-0.12
Annual mean precip.	**-0.61**	**0.44**	**0.12**	**0.30**	**-0.10**
CV of monthly precip.	**-0.03**	**-0.59**	**0.10**	**0.66**	**-0.21**
Precip. of the coldest quarter	-0.06	0.24	-0.07	0.14	-0.27
Precip. of the wettest quarter	-0.23	0.03	0.06	0.22	-0.05
Precip. of the warmest quarter	-0.22	-0.07	0.17	0.09	0.21
Precip. of the driest quarter	-0.05	0.14	-0.01	-0.01	0.01
Relative humidity (RH) of least humid month	-0.28	0.13	-0.08	-0.04	0.31
RH of the most humid month	-0.14	0.01	-0.28	-0.18	0.11
Annual mean RH	-0.24	0.05	-0.13	-0.04	0.12
Radiation of the lightest month	0.52	0.37	-0.17	0.27	0.10
Annual total radiation	0.25	0.22	0.37	0.09	0.10
Radiation of the darkest month	**0.10**	**0.21**	**0.67**	**0.05**	**0.19**
Mean annual number of frost days	**0.06**	**0.08**	**-0.17**	**0.24**	**0.11**
Interannual variation in number of frost days	0.01	0.01	-0.01	0.02	-0.01