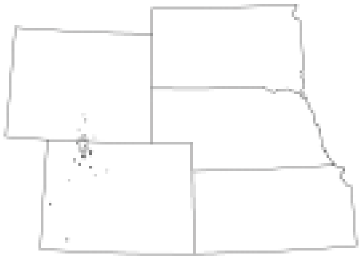
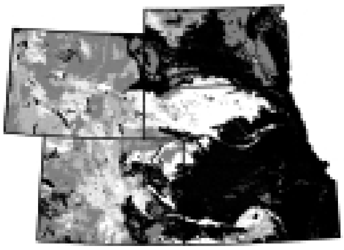
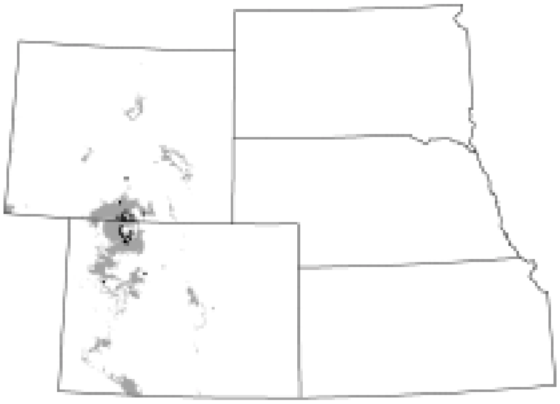
PREDICTIVE RANGE MAPS FOR 15 SPECIES OF MANAGEMENT CONCERN IN THE ROCKY MOUNTAIN REGION OF THE USDA FOREST SERVICE







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

INTRODUCTION

Distributions of vertebrate species 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 focus area (e.g., Maj and Garton 1994, Hammerson 1999); or (2) areas known to be occupied (and often also areas suspected to be occupied) are shown as broad, all-encompassing polygons, again usually over a background map (e.g., Wilson and Ruff 1999, Knopf 1996). Commonly, these 2 techniques are used in tandem to show both points of known occurrence and encompassing polygons (e.g., Hall 1981, Clark and Stromberg 1987).

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

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

Over the past decade these technological breakthroughs have lead to a rapid increase in large-scale range mapping efforts for vertebrates, with the USGS Gap Analysis Program serving as one of the best examples. Gap Analysis teams in each state defined habitat models, either qualitative or statistical, for a series of native vertebrates, mapped those models across their respective states, then used map overlays to analyze patterns of biodiversity (e.g., Merrill et al. 1996). Collectively, the range 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 range maps. These differences are most problematic when attempting to combine the vertebrate range 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 habitat models and range 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.

The objective of this project was to produce predictive range maps for 15 terrestrial vertebrates that occupy USFS R2 (Table 1), using as much information as possible from the Gap Analysis 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

In general we used a 2-part procedure to produce a predictive range map for each of the 15 target species. First, for each species we defined a biophysical envelope that efficiently encompassed the majority of points of known occurrence in USFS R2. We then identified the ecological systems (NatureServe 2003) that corresponded to the land cover types identified by each state Gap Analysis team as being associated with that particular vertebrate taxon. The final range map for each species was the intersection of that species' biophysical envelope with its associated ecological systems. This process and necessary data manipulations are discussed generally below; further details for each species are given in the species-specific appendices that accompany this report.

Collection and manipulation of occurrence data

Occurrence data for each of the 15 target taxa 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. Filtering was done using the ArcInfo and ArcView (Environmental Systems Research Institute, Redlands, California) geographic information systems. For some species it was necessary to relax the general filtering rules in order to maintain reasonable sample sizes for biophysical modeling; these exceptions 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 biophysical environments. A predictive range map is a spatially-explicit extrapolation of the biophysical environments chosen by a given taxon, as represented by a cluster of known locations of that taxon. Inclusion of locations of other taxa in the modeling dataset will degrade the habitat 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 range map is a spatially-explicit extrapolation of the biophysical environments chosen by a given taxon, as represented by a cluster of known locations of that taxon. Precisely-mapped locations will represent a taxon's habitat choices more accurately than 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 range maps produced here are intended to estimate the current distribution of the target taxa. The distribution of some taxa has 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, as bases for predictive range maps 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 removal of observation records made prior to 1970. It also usually involved removal of observation records where the date of observation was not given in the contributed dataset.

Spatial filter: Ideally, predictive range 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 range 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 range 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.

Model vs. validation data set separation: For each species we used only 75% of the post-filtering occurrence data to estimate the biophysical envelope, and reserved the remaining 25% as an independent dataset with which to evaluate the envelope and the intersection of the envelope with the associated ecological systems. Selection of this "validation 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 validation set.

Collection and manipulation of biophysical variables

We selected a variety of predictor variables (Table 3) with which to define a biophysical envelope that best encompassed the post-filtering occurrence data for each species. A basic set of 5 variables was applied to all taxa; more specific variables were included for some taxa if there was reason to suspect such variables were important in limiting distribution (see the species-specific appendices that accompany this report). 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.

Biophysical envelope modeling

We used the DOMAIN modeling procedure (Carpenter et al. 1993) to identify the biophysical envelope that efficiently encompassed the known distribution of each 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 output from DOMAIN as used in this project 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.

Clipping the biophysical envelope by ecological systems

To produce the final predictive range map for each species we intersected the biophysical envelope with the ecological systems (NatureServe 2003) that encompassed the land cover types chosen by each state Gap Analysis team to represent the distribution of that species. For each species 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 species' habitat 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 grid and the modified ecological systems grid produced the final predictive range map for each species.

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TABLES

Table 1. Fifteen species for which predictive range maps were produced.

CLASS	SPECIES	COMMON NAME	STATE(S) OF KNOWN OCCURRENCE IN R2
Amphibian	*Rana pipiens*	Northern leopard frog	SD, WY, NE, CO, KS
Amphibian	*Bufo boreas*	Boreal toad	WY, CO
Reptile	*Liochlorophis vernalis*	Smooth green snake	SD, WY, NE, CO
Mammal	*Corynorhinus townsendii*	Townsend's big-eared bat	SD, WY, NE, CO, KS
Mammal	*Sciurus aberti*	Abert's squirrel	CO
Mammal	*Microtus richardsoni*	Water vole	WY
Mammal	*Lontra canadensis*	Northern river otter	SD, WY, NE, CO, KS
Mammal	*Vulpes velox*	Swift fox	SD, WY, NE, CO, KS
Bird	*Tympanuchus phasianellus columbianus*	Columbian sharp-tailed grouse	WY, CO
Bird	*Charadrius montanus*	Mountain plover	SD, WY, NE, CO, KS
Bird	*Coccyzus americanus*	Yellow-billed cuckoo	SD, WY, NE, CO, KS
Bird	*Cypseloides niger*	Black swift	CO
Bird	*Calcarius ornatus*	Chestnut-collared longspur	SD, WY, NE, CO
Bird	*Calcarius mccownii*	McCown's longspur	SD, WY. NE, CO
Bird	*Spizella breweri*	Brewer's sparrow	SD, WY, NE, CO, KS

Table 2. Sources of species occurrence data.

SOUTH DAKOTA

South Dakota Natural Heritage Program (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)

Tim Wooley (Wyoming Game and Fish Department; Savery, 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)

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

Dr. Merav Ben-David (University of Wyoming; Laramie, Wyoming)

Scott Ellinwood (University of Northern Colorado [1978]; Greeley, Colorado)

Table 3. Predictor variables used to define biophysical envelopes for each target taxon.

VARIABLE	**DATA SOURCE**
Elevation [a]	Derived from 90m digital elevation model
Mean annual precipitation [a]	DAYMET climate dataset (http://www.daymet.org/)
Mean number of frost days per year [a]	DAYMET climate dataset (http://www.daymet.org/)
Average minimum January temperature [a]	DAYMET climate dataset (http://www.daymet.org/)
Average maximum July temperature [a]	DAYMET climate dataset (http://www.daymet.org/)
Inter-annual variation in frost days [b]	DAYMET climate dataset (http://www.daymet.org/)
Local relief [c]	Local variation in elevation; derived from 90m digital elevation model using a neighborhood of 500m radius
Minimum depth to bedrock [d]	STATSGO substrate coverage
Percent sand composition in soil [e]	STATSGO substrate coverage

[a] Used for all target taxa

[b] Used only for *Bufo boreas*

[c] Used only for *Corynorhinus townsendii, Vulpes velox, Charadrius montanus, Cypseloides niger, Calcarius ornatus,* and *Calcarius mccownii*

[d] Used only for *Corynorhinus townsendii* and *Cypseloides niger*

[e] Used only for *Vulpes velox*