

***PREDICTIVE RANGE MAPS FOR 5 SPECIES OF
MANAGEMENT CONCERN IN SOUTHWESTERN
WYOMING***



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INTRODUCTION

Natural resource managers in western North America are increasingly challenged to integrate the conservation of wildlife and native plants with the development of energy resources. Such integration requires, in part, accurate estimates of the geographic distribution of rare species. Traditionally, species' distributions have been depicted as point-maps showing locations where target taxa have been documented in the past (e.g., Maj and Garton 1994, Hammerson 1999), or as broad polygons of occurrence covering large portions of the study area (e.g., Wilson and Ruff 1999, Knopf 1996). These 2 techniques have been used in tandem, showing points of known occurrence overlain on broad occurrence polygons (e.g., Hall 1981, Clark and Stromberg 1987).

Although these basic range-mapping techniques are effective at depicting species' distributions at coarse geographic (e.g., global, continental) scales, they typically fail to adequately predict areas of presence and absence at finer (e.g., regional, state) scales. Whereas point-maps usually underpredict occupied range and overpredict unoccupied range, broad polygon-maps usually do the opposite. In this context, point-maps and broad polygon-maps define a continuum. The ideal predictive range map is positioned somewhere between these 2 extremes; it should be grounded in the basic information conveyed by points of known occurrence without being overly restricted to those points, and it should extrapolate that information across the target landscape in a more appropriate manner than a simple and all-encompassing polygon.

This ideal can be approached via a 2-step process: first construct a statistical model of the environmental conditions at points of known occurrence, then express that model in map form across the study area. Statistical habitat modeling has long been a staple of wildlife science; however, only with recent advances in computing power and geographic information system technology have biologists had the capability to map such models over real landscapes with realistic inputs of time and expertise. Efforts such as the USGS Gap Analysis Program (e.g., Merrill et al. 1996) have taken advantage of these new capabilities and have laid a solid foundation for the production and distribution of predictive range maps.

The Wyoming Natural Diversity Database (WYNDD; University of Wyoming) has begun a program of researching and producing predictive range maps for rare species within the state of Wyoming and surrounding region, with the goal of informing natural resource management. Beauvais et al. (2003) exemplifies these efforts, and forms the basis for this report (see also Beauvais et al. 2001, Keinath 2001, Thurston and Fertig 2002a and b, Fertig et al. 2003a and b, Beauvais 2003, Beauvais and Smith 2003).

The objective of this project was to produce predictive range maps for 3 terrestrial vertebrates and 2 plants (Table 1) that occupy lands administered by the USDI Bureau of Land Management in southwestern Wyoming. These maps are intended to inform managers of the potential distribution of these rare species and thus contribute to more effective and reasonable strategies of integrating wildlife

conservation with natural resource extraction and development. As discussed under “Results and Discussion” these maps are not intended, nor are they appropriately used, as substitutes for field survey or the sole bases for management decisions. Rather, they should be used as spatially-explicit hypotheses on the distribution of the target taxa based on to-date knowledge of occurrence in the region.

METHODS

Collection and manipulation of occurrence data

Points of known occurrence data for each of the 5 target taxa were downloaded from the central species occurrence database at WYNDD. These data then required “filtering” to produce a subset that could estimate a relatively unbiased statistical model of preferred environmental conditions for each taxon. Filtering was done using the ArcInfo and ArcView (Environmental Systems Research Institute, Redlands, California) geographic information systems.

Negative record filter: For some species the WYNDD database contains negative records (i.e., records of survey efforts that failed to document the target taxon) as well as points of documented occurrence. Because the modeling algorithm used for this project requires only positive records (i.e., records of confirmed observation of the target taxon) all datasets were screened to remove negative records.

Identity filter: Different taxa partition available resources by selecting for different biophysical environments. Predictive range mapping is essentially a spatially-explicit quantification of the biophysical environments chosen by a given taxon, as represented by a cluster of positive records. Including positive records for other taxa in the modeling dataset will degrade the habitat selection “signal” of the target taxon. Therefore, we removed observation records that may have involved non-target taxa from the occurrence dataset for each target taxon. This involved removing records with “unknown”, “questionable”, or similar entries in a species-identification field in the WYNDD database.

Mapping precision filter: Field observations are rarely mappable to exact locations, so some degree of spatial error in the reported coordinates of observations is expected. As stated above, predictive range mapping is a spatially-explicit quantification of the biophysical environments chosen by a given taxon, as represented by a cluster of positive records. Because coarsely-mapped records can misrepresent a taxon’s habitat choices, we minimized the use of coarsely-mapped locations as much as possible in predictive range mapping. Mapping precision was estimated, at least qualitatively, for all observations in our occurrence datasets, either by the original data contributor or by WYNDD technicians interpreting text descriptions in original observation records. Removal of coarsely-mapped locations typically involved

removing observation records with “unmappable” precisions, and also those records with mapping precisions of ≥ 5 miles.

Date-of-observation filter: The predictive range maps produced here are intended to estimate the current distribution of the target taxa. Because the distributions of some taxa have changed dramatically over the past several decades, older observation records can reflect a taxon’s response to past conditions that no longer exist and thus are not appropriate to use in predictive mapping of current distribution. We therefore minimized the use of older observations as much as possible in this project. In most cases this involved excluding 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 positive records that are well-distributed across the entire range of the target taxon in the study area, and that result from an even application of sampling effort throughout that range. However, these conditions are rarely met, and almost all predictive range maps are based on opportunistically-collected occurrence data. In other words, some portions of the study area have been sampled more intensively than others, and commonly much of the study area has received no sampling effort for the target taxon. Unless this is accounted for in the modeling process, the clustering of positive records in intensely-sampled environments will overly-bias the final range map towards those environments. To address this concern, for each taxon we eliminated positive records such that no 2 records were within a certain distance of each other. The separation distance differed by taxon, reflected the relative mobility of each taxon, and ranged between 1500 - 4000m. In some cases multiple records were mapped at exactly the same point, and our spatial filter procedure reduced such multi-records to a single record per point. Also, prior to removing points from a cluster, our procedure evaluated the mapping precision of each record to ensure that those with the finest mapping precisions (i.e., the best information on environmental conditions selected by that taxon) were preferentially retained, and those with the coarsest mapping precisions were removed.

Model vs. validation data set separation: For each taxon we used only 75% of the post-filtering occurrence data to produce the predictive range map, and reserved the remaining 25% as an independent dataset with which to evaluate that range map. Selection of the 25% 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 positive records within each grid cell was selected and placed in the validation set.

Collection and manipulation of biophysical variables

We selected a variety of biophysical predictor variables (Table 2) with which to produce the predictive range map for each target taxon. A basic set of 7 variables was applied to all taxa, including 4 climatic variables. Additional variables were included for some taxa if, based on knowledge of taxon habitat use and life history, we suspected they were important in limiting distribution.

There are so many variables that can describe the climate of an area that it is difficult to select a concise set that adequately explains major gradients. To select such a set for this project we employed principal components analysis. By entering 30 separate climatic variables into a principal components analysis we established that the first 4 principal components explained 98.1% of the variation in the full variable set. The 4 climatic variables ultimately selected as predictors (mean temperature of the driest quarter, mean number of frost days per year, mean annual precipitation, coefficient of variation of monthly precipitation) had the highest loadings (0.74 - 0.80) on each of the first four components.

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 analyses were performed at 60m resolution, and necessary spatial manipulations were performed within the ArcInfo and ArcView geographic information systems.

Producing predictive range maps

We used the DOMAIN modeling procedure (Carpenter et al. 1993) to quantify the environmental conditions that most efficiently encompassed the positive records for each target taxon in Wyoming. Although research comparing range-mapping algorithms is ongoing, preliminary comparisons suggest that DOMAIN generally produces more accurate maps than other commonly used techniques such as BIOCLIM, GARP, and BIOMAPPER (L. Master and P. Hernandez, NatureServe [Arlington, Virginia], personal communication).

Details on the DOMAIN procedure are in Carpenter et al. (1993). Briefly, for each target taxon 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 positive record (or an average of a set of most similar positive records) for that taxon. This measurement is known as the Gower similarity metric, and each point in the study area is attributed with its particular metric value. For all taxa addressed in this project we calculated the Gower metric between each point in the study area and the average of the most similar 5% of positive records. Averaging in this manner dampened the effect of “outlier” positive records, and by using a percentage rule we were able to roughly standardize the degree of dampening across all taxa.

The DOMAIN output is a complete grid coverage (60m resolution) of the study area with each cell attributed with its Gower metric value. It was therefore necessary to select a threshold value of the metric for each taxon such that values above the threshold indicated suitable environmental conditions (i.e., within the predicted range of that taxon), and values below the threshold indicated unsuitable environmental conditions. For each taxon we selected the threshold such that 95% of the positive records in the modeling dataset were included as predicted range. The 5% of the positive records that were excluded had the lowest similarity metrics of all positive records for a given taxon. Similar to the averaging rule outlined above, this percentage rule allowed us to define predicted range in a standardized fashion for all target taxa.

Validating predictive range maps

We measured validation success of each of the maps as the percent of the independent positive records that were correctly classified as inside the predicted range for each taxon.

RESULTS AND DISCUSSION

Validation success for the 5 maps produced in this project ranged from 40% - 88%, with an average of 69% (Table 3). It is important to note the rather small sample size of positive records for the 2 maps with the lowest success rates (*Physaria condensata*, n= 5 validation points, success = 40%; *Phlox pungens*, n=4 validation points, success = 50%). Small sample sizes make precise estimates of map quality rather difficult to generate. All 5 predictive range maps were delivered to Advanced Resources International, Inc., on 17 December 2003 following vectorization of the original grid output.

As raised in the “Introduction”, these maps are not intended, nor are they appropriately used, as substitutes for field survey or the sole bases for management decisions. Rather, they should be used as spatially-explicit hypotheses on the distribution of the target taxa based on to-date knowledge of occurrence in the region. As with all models, these maps are approximations of the underlying phenomena (i.e., the true distribution of each taxon) rather than a direct mapping of that phenomena. Plant and animal distributions are dynamic in both space and time, necessitating careful interpretation and re-evaluation of range maps as new information becomes available.

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TABLES

Table 1. Five taxa for which predictive range maps were produced.

KINGDOM	GROUP	SPECIES	COMMON NAME
Animal	(Class) Amphibian	<i>Bufo boreas</i>	Boreal toad
Animal	(Class) Reptile	<i>Crotalus viridis concolor</i>	Midget-faded rattlesnake
Animal	(Class) Mammal	<i>Brachylagus idahoensis</i>	Pygmy rabbit
Plant	(Family) Mustard	<i>Physaria condensata</i>	Tufted twinpod
Plant	(Family) Phlox	<i>Phlox pungens</i>	Beaver rim phlox

Table 2. Predictor variables used to produce predictive range maps for target taxa.

VARIABLE	DATA SOURCE
Elevation ^a	90m digital elevation model
Topographic slope ^a	90m digital elevation model
Ecological system ^a	NatureServe (2003), following Menard and Lauver (2000)
Mean temperature of the driest quarter ^a	DAYMET climate dataset (http://www.daymet.org/)
Mean number of frost days per year ^a	DAYMET climate dataset (http://www.daymet.org/)
Mean annual precipitation ^a	DAYMET climate dataset (http://www.daymet.org/)
Coefficient of var. of monthly precipitation ^a	DAYMET climate dataset (http://www.daymet.org/)
Inter-annual variation in frost days ^b	DAYMET climate dataset (http://www.daymet.org/)
Distance to permanent water ^b	1:100K Wyoming hydrography (http://www.sdvc.uwyo.edu/)
Percent clay in substrate ^c	STATSGO substrate coverage
Percent sand in substrate ^c	STATSGO substrate coverage
Index of sagebrush coverage ^c	Modified from Merrill et al. (1996)
Local variation in elevation ^d	90m digital elevation model; 500m neighborhood radius
Distance to cliff ^d	90m digital elevation model
Bedrock geology ^e	Munn and Arneson (1998)

^a Used for all target taxa

^b Additional variables used for *Bufo boreas*

^c Additional variables used for *Brachylagus idahoensis*

^d Additional variables used for *Crotalus viridis concolor*

^e Additional variables used for *Physaria condensata* and *Phlox pungens*

Table 3. Validation success for 5 predictive range maps. Success was measured as the percent of independent points of known occurrence that were correctly classified as inside the predicted range for each taxon.

TARGET TAXON	NO. MODEL POINTS	NO. VALIDATION POINTS	SUCCESS
Boreal toad	103	34	85.3%
Midget-faded rattlesnake	15	5	80.0%
Pygmy rabbit	50	17	88.2%
Tufted twinpod	13	5	40.0%
Beaver rim phlox	12	4	50.0%