

## KANSAS GAP ANALYSIS: THE IMPORTANCE OF VALIDATING DISTRIBUTIONAL MODELS BEFORE USING THEM

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**ABSTRACT**—Maps of vertebrate distributions resulting from the Kansas Gap Analysis were compared with maps based on ecological-niche modeling of primary point-occurrence information. The latter maps were considerably more predictive of independent sets of test data than were the Gap maps, further supporting the idea that the method of Gap wildlife-habitat modeling has little analytical power. In general, the Kansas Gap maps were untested and unchecked, thus being heterogeneous, unreliable, and of little use for further analyses.

**RESUMEN**—Se compararon los mapas de distribuciones de vertebrados que resultaron del programa de análisis de “Gap” del estado de Kansas con mapas que se derivaron de modelaje de nichos ecológicos de datos de información primaria de puntos de ocurrencia. Estos últimos resultaron con bastante más poder predictivo de juegos de datos de pruebas independientes que los mapas de Gap, apoyando aún más a la idea de que el método de modelaje de hábitat silvestre de Gap tiene poco poder analítico. En general los mapas que se produjeron en el proyecto de Gap en Kansas no fueron probados ni revisados, y finalmente fueron heterogéneos, no confiables, y de poco valor para análisis posteriores.

Gap analysis consists of the integration of information on geographic distributions of species with information on land use, land cover, and land tenure, with the aim of improving strategies for conservation of biodiversity and natural ecosystems. The Gap method now has been implemented for many states in the United States and has sparked extensive discussion and development of methodological approaches (Scott et al., 1993; Scott et al., 1996), including a recent symposium volume summarizing recent developments in the field of modeling geographic distributions of species (Scott et al., 2002).

Nevertheless, Gap methods remain largely untested and have evolved little in recent years. The Gap approach to derivation of distributional information for species remains founded largely on the “wildlife habitat modeling” approach, which is a non-analytical, non-quantitative attempt to create an understanding of ecological requirements of species based on the scientific literature (Morrison and Marcot, 1998). Recent results of an analysis comparing Gap models from the Maine Gap Analysis project (Krohn et al., 1998) with quantitative mod-

els developed using techniques of modeling ecological niches demonstrated that the ecological-niche models were considerably better able to predict details of geographic distributions of various bird species in Maine (Peterson and Kluza, 2003). Herein, I compare the distributional information produced as part of a Gap project with the results of models of ecological niches for the recently-completed Kansas Gap Analysis project (Cully et al., 2003).

**METHODS**—Maps of vertebrate distributions produced by the Kansas Gap Analysis project were drawn from the original final project report (Cully et al., 2003). The Gap models were based on a complex combination of known occurrences of species in a hexagonal network across the state, plus decision “rules” regarding where in that extent of occurrence the species actually is to be found. The GIS grids provided in the report CD were reprojected into geographic coordinates to permit direct comparisons with results from ecological-niche models.

Models of ecological niches were based on primary point-occurrence information (Peterson et al., 2002*c*), which for these analyses was drawn from the 1995 results of the Breeding Bird Survey (BBS; Breeding Bird Survey, 2001). Specifically, I extracted from the BBS data all survey routes within 150 km

TABLE 1—Summary of results of direct comparisons between Gap distributional summaries and ecological-niche models developed using GARP for 10 species of birds in Kansas. For each species, the percentage of test points correctly predicted by each method is given, as well as the total test sample size. The proportional areas predicted by each method are provided, as well as probability values associated with each prediction, based on binomial tests. The “% correct” columns summarize avoidance of omission error, and the proportion of area (“Prob. area”) columns summarize a dimension closely tied to commission error (Anderson et al., 2003).

Species	% correct		Test <i>n</i>	Prop. area		<i>P</i>	
	Gap	GARP		Gap	GARP	Gap	GARP
<i>Ammodramus savannarum</i>	43.3	90.0	30	0.399	0.822	0.28	0.08
<i>Chondestes grammacus</i>	36.8	89.5	19	0.434	0.776	0.63	0.05
<i>Geothlypis trichas</i>	50.0	77.8	18	0.368	0.458	0.08	0.001
<i>Myiarchus crinitus</i>	12.5	87.5	24	0.082	0.625	0.13	0.001
<i>Sayornis phoebe</i>	18.2	90.9	22	0.050	0.525	0.004	0.0000147
<i>Sialia sialis</i>	10.0	90.0	20	0.083	0.680	0.23	0.005
<i>Thryothorus ludovicianus</i>	20.0	73.3	15	0.078	0.406	0.02	0.002
<i>Troglodytes aedon</i>	12.0	76.0	25	0.072	0.596	0.10	0.03
<i>Tyrannus forficatus</i>	50.0	93.8	16	0.377	0.655	0.10	0.001
<i>Vireo gilvus</i>	10.0	65.0	20	0.082	0.618	0.22	0.30

of Kansas (geo-referenced to the starting point of the survey route, which introduces some level of error), and identified those species for which  $\geq 40$  occurrence points (i.e., detection on at least one stop of a particular route) were available. From the resulting pool of 52 species, I chose 10 at random for analysis: *Ammodramus savannarum*, *Chondestes grammacus*, *Geothlypis trichas*, *Myiarchus crinitus*, *Sayornis phoebe*, *Sialia sialis*, *Thryothorus ludovicianus*, *Troglodytes aedon*, *Tyrannus forficatus*, and *Vireo gilvus*.

To characterize environments, I used 17 GIS coverages that summarized aspects of the ecological landscape in Kansas (and surrounding 150 km). These coverages included elevation, slope, aspect, flow direction, flow accumulation, and tendency to pool water from the United States Geological Survey Hydro-1K dataset (United States Geological Survey, 2001), and remotely-sensed images including monthly composite normalized difference vegetation indices (NDVI) for 1995 based on data from the AVHRR sensor (University of Maryland, 2001). These coverages were selected because they offer a fine-grained view of the landscapes of Kansas and summarize diverse ecological dimensions. Although not all coverages might seem directly relevant to avian distributions, they nevertheless hold information that might be informative; the analytical procedures were sufficiently general as to permit discarding of uninformative layers of data.

Ecological-niche models were developed using the Genetic Algorithm for Rule-set Prediction (GARP) (Stockwell and Noble, 1992; Stockwell, 1999; Stockwell and Peters, 1999; Scachetti-Pereira, 2002), an evolutionary computing algorithm that has been extensively tested for predictions of geographical dis-

tributions of species (Peterson and Cohoon, 1999; Peterson, 2001; Peterson et al., 2002a; Stockwell and Peterson, 2002a, 2002b; Anderson et al., 2003; Peterson and Kluza, 2003; Peterson and Shaw, 2003; Stockwell and Peterson, 2003). In general, GARP focuses on modeling ecological niches (the conjunction of ecological conditions wherein a species can maintain populations without immigration; Grinnell, 1917). Specifically, GARP relates ecological characteristics of occurrence points to those of points sampled randomly from the rest of the study region, developing a series of decision rules that best summarize factors associated with presence.

Occurrence points are divided evenly into training (for building models; occurrence data from outside of Kansas, but within 150 km of the boundaries of the state) and testing (for evaluating models; occurrence data from within Kansas) data sets (Fig. 1). My GARP models, thus, were based on no information from within the state, whereas the Gap models were based on extensive information from within Kansas from the extent of occurrence information and the scientific literature. GARP works in an iterative process of rule selection, evaluation, testing, and incorporation or rejection: a method is chosen from a set of possibilities (e.g., logistic regression, bio-climatic rules) and applied to the training data to develop or evolve a rule. Predictive accuracy is evaluated based on the test data set. Rules evolve in ways that mimic DNA evolution, such as point mutations or deletions. Change in predictive accuracy between iterations is used to evaluate whether particular rules should be incorporated into the model; the algorithm runs 1,000 iterations or until convergence. To optimize model performance, I developed

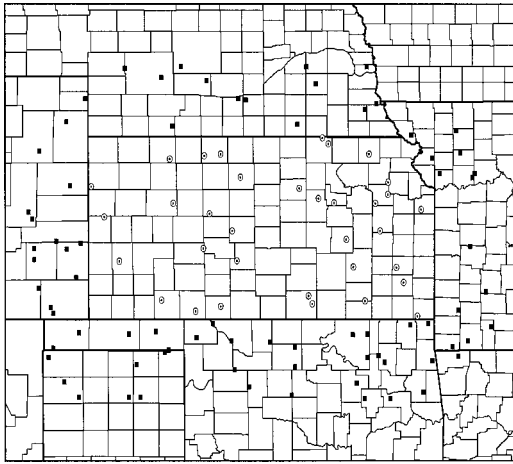


FIG. 1—Summary of data sets used to develop and test ecological-niche models. Black squares are from Breeding Bird Survey routes outside of Kansas, but within 150 km of its borders, used for model building; dotted circles are Breeding Bird Survey routes within Kansas used to test model quality.

100 replicate models of ecological niches for each species. A “best subset” of these models was selected based on optimal error distributions for individual replicate models (Anderson et al., 2003): median area predicted across all replicate models was calculated; the 20 models with predicted areas closest to the median were identified; and the 10 models with most extreme predictions in terms of area predicted present (that is, the largest and smallest areas predicted to be present) were discarded. The geographic predictions of the remaining 10 models were summed to summarize potential geographic distributions. I reserved all BBS data from within Kansas for an independent test of model validity. Hence, all ecological-niche models presented herein are based on information from outside of the state only.

Model quality was evaluated via the independent testing data set aside prior to modeling; a chi-square test was used to compare observed success in predicting the distribution of test points with that expected under a random model. The proportional area predicted present provides an estimate of occurrence points correctly predicted, if the prediction was random with respect to the distribution of the test points.

**RESULTS**—Reviewing Gap models prior to choosing species for detailed analysis showed that these models were highly variable in quality; many species were predicted to occur only in tiny, scattered areas, whereas others were

predicted to occur broadly and continuously across large portions of the state. For instance, in one particularly striking comparison, the 2 species of *Sayornis* in Kansas contrasted in their Gap predictions. *Sayornis phoebe* was predicted only in widely scattered points across eastern Kansas, whereas *S. saya* was predicted to occur broadly and continuously across essentially all of western Kansas (Figs. 2 and 3). The 2 species are about equivalently abundant in their respective sectors of Kansas (Schukman, 1993), so the difference in the Gap maps likely results from careless selection of land-cover classes for prediction of presence in one or both species.

The 10 species chosen for detailed analysis showed clearly the contrast between Gap and GARP models in predictive ability. Although no Gap model could predict >50% of the independent test points, no GARP model predicted <65% of the same independent set of test points. GARP models were statistically significantly better than random models in 7 species ( $P < 0.05$ ), and marginally so in 2 more ( $0.05 < P < 0.10$ ), failing to achieve significance only in one species (*Vireo gilvus*). Gap models, on the other hand, were significantly better predictors than random models in only 2 species, and marginally so in 2 more ( $0.05 < P < 0.10$ ), failing to achieve significance in 6 species.

**DISCUSSION**—The initial purpose of this comparison was to continue the debate regarding methods of mapping distributions of species (Peterson et al., 2002c), in which the relative merits of existing Gap methods are compared with those of ecological-niche models based on primary point-occurrence information. This debate already has included one comparison, in which the Gap results for birds from Maine were compared quantitatively with GARP models (Peterson and Kluza, 2003).

Results of the Maine comparisons and those presented herein were similar, in that GARP models generally predicted larger areas present than did the Gap models, and in the better ability of GARP to avoid errors of omission. In the present case, however, the contrast was even clearer, with GARP models proving superior on overall measures of significance as well. The difference seems to be a result of uneven methods in the Kansas Gap program for establishing likely presence of a particular

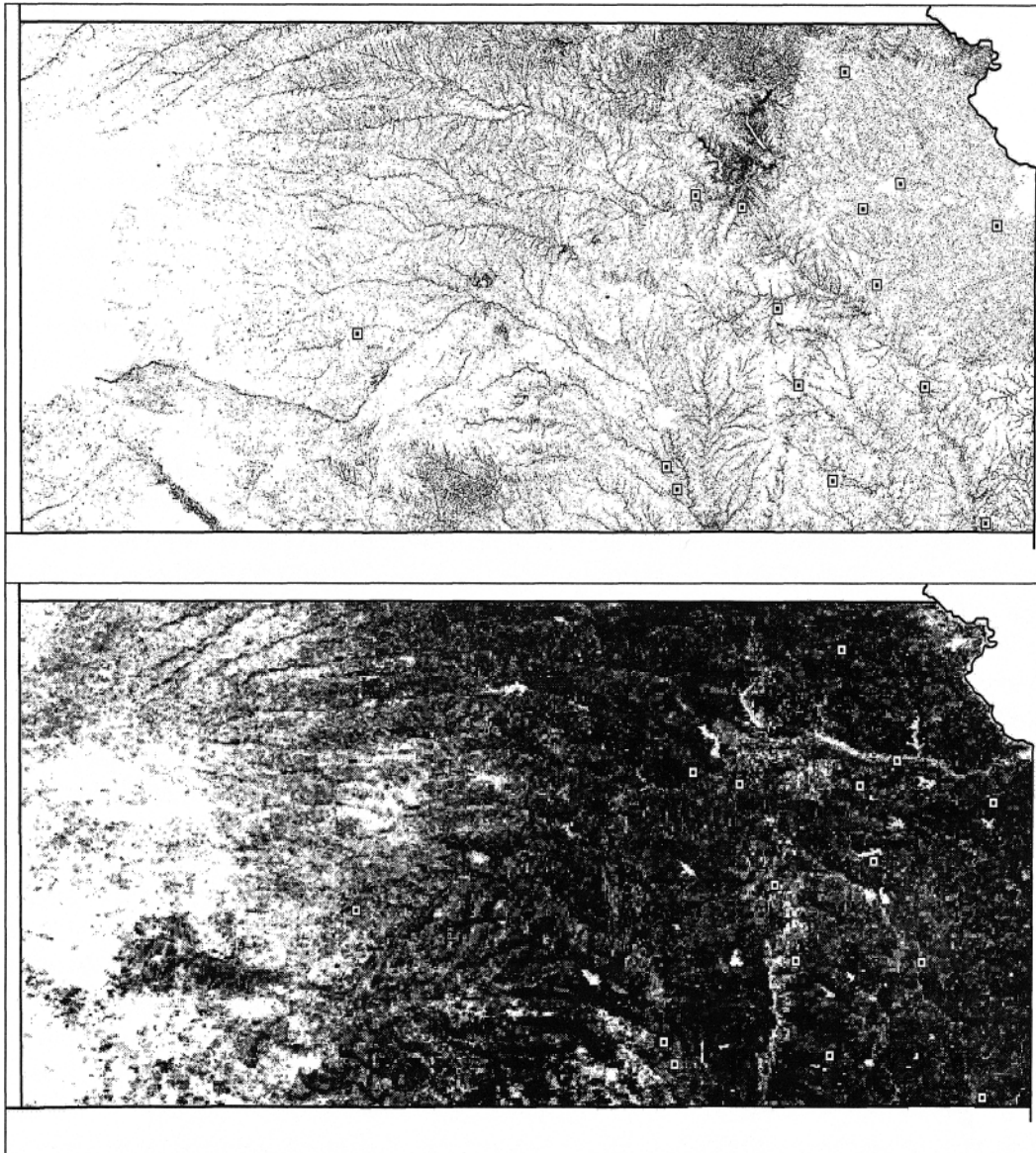


FIG. 2—Predicted distribution for *Sayornis phoebe* from Kansas Gap Analysis Program (top; areas predicted as present indicated in black) and from ecological-niche models developed in this study (bottom; greater model agreement in prediction of presence shown in darker shades of gray). Independent test presence points are shown as dotted squares.

species in a particular land use or land cover type, making for unstable predictions using the Gap method.

The problems with the Gap approach in Kansas, however, seem to run more deeply than in the previous Maine study. For example, although the method for the Gap report men-

tioned consultation of the BBS data, the Gap maps nevertheless failed to include most of the BBS occurrences. For instance, the map for *Bartramia longicauda* excluded almost all of the Flint Hills, which happens to be the global focus of its populations; other such examples include the comparisons of *Sayornis* mentioned

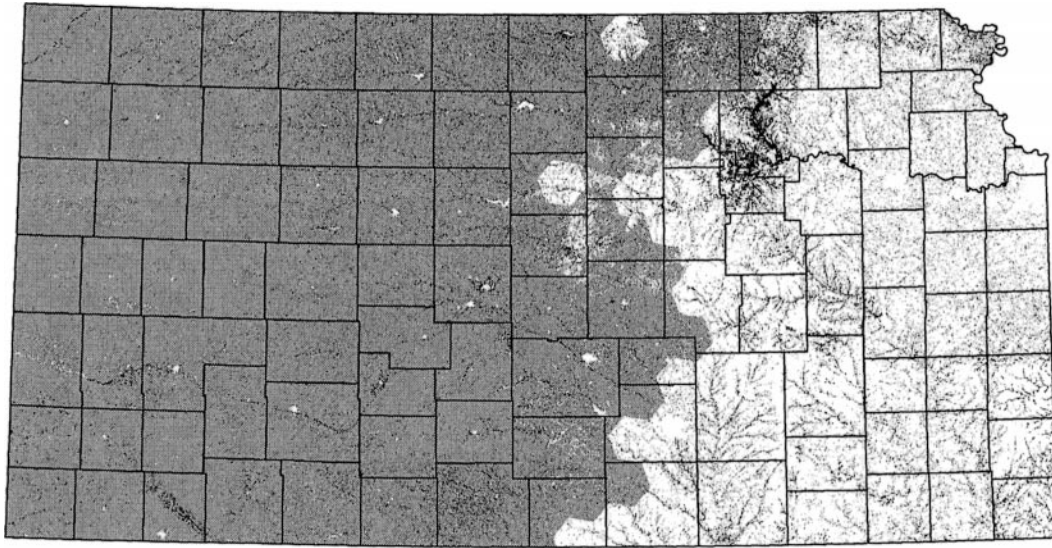


FIG. 3—Map of Kansas, with the Kansas Gap summaries of distributions of *Sayornis phoebe* (minuscule black areas) and *S. saya* (gray areas) overlaid.

above. Overall, the quality of the Gap distributional information is uneven.

The problem would seem to be a lack of inspection and validation of the Gap models after their creation. The final report (Cully et al., 2003) indicated a 3-step process of model creation: tallying of county records, conversion of county records into presences and absences in a network of hexagons covering the state, and reduction of the hexagons to the land use or land cover types known to be inhabited by the species. Although this procedure is rife with problems (Peterson and Kluza, 2003), several of which are apparent in the example used to illustrate the procedure in the final report, the manifestation of those problems in inferior maps would have been noted (and perhaps corrected) had some sort of validation or checking procedure been employed as part of the Kansas Gap method. The report stated (Cully et al., 2003:79), "Accuracy assessments for vertebrate distribution models have not been conducted at this time." Under this view, any arbitrary model (which might be, for example, a 20-km radius circle centered on Wichita) is just as valid as the maps presented in the report.

Some readers might suggest that some information is better than nothing at all, or that the Gap results might be useful at some level of

analysis, or that the results might be useful for poorly known taxa (such as some reptiles and amphibians). Although it is true that the Gap effort united an admirable amount of information in a single publication, the value of the information presented is unclear. For example, compare the Gap models for the 2 species of *Sayornis* (Fig. 3). Is *S. saya* really much more broadly distributed than *S. phoebe*? This sort of inconsistency would add noise to any analysis based on the Gap results, in particular for groups that are less well known than birds. Without a validation procedure as an integral part of the modeling process, distributional information such as that presented in the Kansas Gap report is useless.

The point of this paper was to be—before my appreciation of the unedited nature of the Gap distributional information—the benefits that would be brought to the Gap process by a shift to an ecological-niche modeling perspective, based explicitly on primary point-occurrence information. This approach not only produces models that are considerably more predictive, but also can include validation steps explicitly, which adds considerably to the reliability and utility of the result. Although the GARP models produced herein were based on no occurrence information from within Kansas, the Gap models explicitly incorporated the

data used to test these models in their development, and yet the GARP models were more predictive.

As a final point, Gap work began in Kansas in 1995 and the report (Cully et al., 2003) was published in 2003. The ecological-niche modeling approaches explored herein are not only more objective and quantitative, but are also considerably more efficient. Based on prior modeling efforts for hundreds to thousands of species (e.g., Peterson et al., 2002*b*), and given the broad availability of point-occurrence information for vertebrates in Kansas at <http://www.gbif.net>, <http://elib.cs.berkeley.edu/manis/>, and elsewhere (e.g., 19,000+ mammal records, 29,000+ bird records), Gap objectives could have been achieved better and with a fraction of the time and effort expended.

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