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Evaluating confidence intervals for habitat suitability models

Louis C. Bender, Gary J. Roloff, and Jonathan B. Haufler

Abstract   Implicit in the use of wildlife habitat models is the assumption that different habitat ratings reflect differences in habitat quality. Using a gray squirrel habitat suitability index (HSI) model, we compared 6 different habitats within the Huron–Manistee National Forest, Michigan. We assessed variation in the final HSI scores from variation around model input variables using Monte Carlo simulation (parametric bootstrapping) and nonparametric bootstrapping. In our demonstration, HSI scores as divergent as 0.38 and 0.81 did not differ statistically. Habitat modeling should account for variability in HSI scores, as well as indicators of animal response. Modeling attempts that ignore this variability are unlikely to determine whether faulty relationships are a product of the habitat model or result from habitat or animal variation.

Key words   bootstrapping, confidence intervals, habitat suitability index models, HSI, Monte Carlo simulation

Wildlife habitat models are used for resource planning, mitigation, and environmental impact assessments (Schamberger and Krohn 1982, Cole and Smith 1983, Morrison et al. 1992). One such modeling approach, the habitat evaluation procedures (HEP; U.S. Fish and Wildl. Serv. 1981), is used extensively by federal and state resource management agencies (Morrison et al. 1992). Integral to HEP are habitat suitability index (HSI) models. HSI models are best viewed as hypotheses of species–habitat relationships and are based on the premise that habitat suitability can be linked to habitat attributes by some functional relationship (Morrison et al. 1992). The relationship is depicted as an HSI score ranging from 0.00 to 1.00, representing "poor" to "good" habitat quality, respectively (U.S. Fish and Wildl. Serv. 1981).

Development and implementation of HSI models have been hindered by limited field validation (Cole and Smith 1983). Critics of HSI models argue that management decisions should not be based on untested models (Lancia et al. 1982, Cole and Smith 1983, Marcot et al. 1983). Using a variety of validation techniques, some researchers have found positive correlations between model predictions and measures of wildlife distributions and abundance (Lancia et al. 1982, Cole and Smith 1983, Cook and Irwin 1985, Verner et al. 1986, Brennan 1991), whereas others have found negative or no correlations (Seitz et al. 1982, Clark and Lewis 1983, Bart et al. 1984, Robel et al. 1993). A variety of explanations for these discrepancies have been offered, including inadequate or unrepresentative sampling (Cole and Smith 1983), model equations not representative of actual wildlife-habitat relationships (Farmer et al. 1982, Cole and Smith 1983, Warwick and Cale 1988, Van Horne and Wiens 1991), misinterpretation of results (Brower and Zar 1984), or application of models to inappropriate spatial scales (Wiens 1986).

Failure to account for variability in model parameters (habitat variables) is a common problem associated with validation and application of HSI models. Model parameters are often estimated from sample means based on field measurements of habitat attributes. These values are used as model inputs; however, the variance associated with such mean values is often ignored. This variance represents sampling error and the natural heterogeneity in the replicate unit (i.e., stand, study plot, etc.), both of which are important consider-

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ations in habitat assessments. As a result, many HSI scores do not include a statistical estimate of dispersion. Without some measure of dispersion, it is not possible to infer whether HSI scores actually differ. If statistical differences between HSI scores cannot be demonstrated, there is no justification for inferences in model validation and application where it is assumed different HSI scores reflect differences in habitat quality.

We demonstrate 2 simple techniques to account for the variance associated with habitat model inputs. Applying randomization procedures such as Monte Carlo simulation (Hope 1968) and bootstrapping (Efron and Tibshirani 1993), we use variation associated with individual model variables to produce confidence intervals around HSI scores. To demonstrate the importance of accounting for this variance, we compare confidence intervals generated for a gray squirrel (*Sciurus carolinensis*) HSI model (Allen 1987) for 6 cover types from the Huron–Manistee National Forest (HMNF), Michigan.

Study area and methods

Gray squirrel model

The gray squirrel model is forest stand-based and consists of 2 sub-models: (1) cover-reproduction and (2) winter food. Habitat parameters required to run the models include canopy closure, number and coverage of hard-mast-producing species, and size of overstory trees (Allen 1987; Table 1). Habitat parameters were sampled using a variety of plot and line intercept techniques as part of a habitat modeling study conducted on the HMNF (Roloff 1994).

Data collection

We selected 6 forest cover-types (Table 1) that represented a range of habitat conditions across the

HMNF. Cover types were defined by the U.S. Forest Service's Corporate Database Classification (U.S. For. Serv. 1988) and included: (1) pole-sized (12.7–27.9 cm dbh), well-stocked (>70% stand density), mixed lowland conifers (primarily northern white-cedar [*Thuja occidentalis*], and balsam fir [*Abies balsamea*]); (2) pole-sized, medium-stocked (40–69% stand density) red pine (*Pinus resinosa*); (3) pole-sized, medium-stocked jack pine (*P. banksiana*) and oak (*Quercus* spp.) mix; (4) pole-sized, well-stocked northern red oak (*Q. rubra*); (5) saw-sized (>27.9 cm dbh), well-stocked red pine; and (6) saw-sized, well-stocked big-tooth aspen (*Populus grandidentata*; Table 1). Mean HSI scores were calculated for the winter food and cover-reproduction sub-models for each cover-type by applying habitat variable means (Table 1) to the gray squirrel suitability index curves presented by Allen (1987).

Data analysis

We calculated approximate confidence intervals around the mean HSI scores for each sub-model in each cover-type using Monte Carlo (Hope 1968) and bootstrapping (Efron and Tibshirani 1993) approaches. For the Monte Carlo approach, the habitat variable (e.g., canopy coverage, dbh of overstory trees, coverage of hard-mast-producing species, and number of hard-mast-producing species) mean and standard deviation were used to generate random values fitting the observed frequency distribution. The data were normally distributed in our example ($P > 0.10$ for all habitat variables; Kolmogorov–Smirnov test; Siegel 1956). However, other frequency distributions could be generated as warranted. We designated N as the number of bootstrap- or Monte Carlo-generated values and generated N = 1,000 values for each variable to meet adequate testing requirements

Table 1. Descriptive statistics of 4 gray squirrel habitat model variables for 6 cover types in the Huron-Manistee National Forest, Michigan.

Cover type	*n*	Stock[a]	Mean (SE)[b]			
			HARDCOV	**HARDSPP**	**CANCOV**	**DBH**
Mixed lowland conifers	7	6	0.0 (0.0)	0.0 (0.0)	55.4 (10.5)	19.1 (2.6)
Red pine	6	5	0.0 (0.0)	0.5 (0.6)	44.4 (37.9)	17.3 (2.7)
Jack pine-oak mix	7	5	1.2 (2.5)	1.1 (0.7)	54.1 (26.5)	21.1 (3.2)
Northern red oak	13	6	30.6 (29.9)	1.5 (0.5)	85.2 (20.1)	23.2 (2.8)
Red pine	7	9	0.0 (0.0)	0.1 (0.4)	73.0 (12.4)	29.7 (6.5)
Big-tooth aspen	6	9	6.1 (15.0)	0.3 (0.5)	100.0 (0.0)	27.5 (2.7)

[a] U.S. Forest Service Corporate Database stocking/size codes where 5 and 6 = pole-sized (12.7–27.9 cm dbh), medium and well stocked, respectively; and 9 = saw-sized (>27.9 cm dbh), well stocked (U.S. Forest Service 1988).

[b] HARDCOV = proportion of total tree canopy that is hard mast producing trees ≥25 cm dbh; HARDSPP = number of hard mast tree species; CANCOV = percent canopy cover of trees; DBH = mean diameter at breast height of overstory trees (Allen 1987).

at the 90% level of N$\alpha \geq 5$ (Marriott 1979). Random values were iterated into the gray squirrel HSI equations to produce 1,000 estimates of the HSI scores. Approximate 90% confidence intervals were determined by eliminating the extreme 50 (i.e., 0.5Nα) values from both ends of the distributions of HSI scores.

Because the frequency distribution of habitat variables is not always known, or sample sizes are too small to infer the distribution, we also used nonparametric bootstrapping (Efron and Tibshirani 1993) to estimate confidence intervals. One thousand random subsamples of size *n* (i.e., the original sample size for each cover-type variable) with replacement were drawn from each habitat variable sample. Subsamples were used to calculate 1,000 iterations of the gray squirrel HSI model. Again, N = 1,000 was chosen to meet adequate sampling requirements (Efron and Tibshirani 1993). Approximate 90% confidence intervals were determined by eliminating the 0.5Nα extreme values from the final HSI distribution. Significant differences in HSI scores for both techniques were evaluated by comparing confidence intervals (i.e., if the comparative confidence intervals overlapped, no difference occurred). Sample programs for each technique are included in Appendices 1 and 2.

Results

Final HSI scores ranged from 0.38 to 0.81 and from 0.06 to 0.17 for cover-reproduction (Table 2) and winter food (Table 3) sub-models, respectively. Cover-reproduction HSI scores formed 2 overlapping significant groupings (0.38–0.81, excluding 0.76, and 0.51–0.81, including 0.76) based on overlapping 90% Monte Carlo confidence intervals (Table 2). Bootstrap 90% confidence intervals yielded 3 significant groupings of cover-reproduction HSI scores (0.38–0.51, 0.51 and 0.64, and 0.76–0.81; Table 2).

The highest HSI score for winter food was associated with the northern red oak cover type (Table 3). This score differed from all other cover types using 90% bootstrap confidence intervals (Table 3). No differences were present in winter food HSI scores based on non-overlapping 90% Monte Carlo confidence intervals (Table 3).

Bootstrap confidence intervals were always tighter than Monte Carlo intervals, resulting in different statistical interpretations (Tables 2,3). Mean HSI scores as different as 0.38 (mixed lowland conifer) and 0.81 (saw-sized red pine) did not differ based on Monte Carlo 90% confidence intervals (Table 2). Using 90% bootstrap intervals, mean HSI values as different as 0.51 (jack pine–oak mix) and 0.64 (northern red oak) did not differ (Table 2). Both methods demonstrated

Table 2. Mean habitat suitability index (HSI) model scores and 90% confidence intervals for the gray squirrel cover-reproduction submodel for 6 cover types in the Huron-Manistee National Forest, Michigan.

Cover type	Stock[a]	HSI	90% confidence interval[b,c]	
			Monte Carlo	Bootstrap
Mixed lowland conifer	6	0.38	0.00–0.59a	0.20–0.49a
Red pine	5	0.41	0.00–0.52a	0.25–0.49a
Jack pine-oak mix	5	0.51	0.00–0.70ab	0.29–0.61ab
Northern red oak	6	0.64	0.49–0.78ab	0.61–0.68b
Red pine	9	0.81	0.48–1.00ab	0.74–0.91c
Big-tooth aspen	9	0.76	0.63–0.86b	0.72–0.80c

[a] U.S. Forest Service Corporate Database stocking-size codes where 5 and 6 = pole-sized (12.7–27.9 cm dbh), medium and well stocked, respectively; and 9 = saw-sized (>27.9 cm dbh), well stocked (U.S. Forest Service 1988).
[b] Confidence intervals (90%) generated by Monte Carlo simulation and bootstrapping techniques, respectively.
[c] Confidence intervals and associated means sharing a letter within a column do not differ (*P* = 0.90).

overlapping confidence intervals and subsequent lack of statistical differences between mean HSI scores for the majority of the 6 cover types (Tables 2,3).

Discussion and implications

Implicit in HSI or similar habitat model validation attempts is the assumption that different HSI scores represent actual differences in habitat quality. Our gray squirrel example demonstrated that different HSI scores may not represent real differences. Habitat model validation attempts should account for variability in HSI scores, as well as indicators of animal response. Validation attempts that ignore this variability are likely to generate mixed results, without determining whether faulty relationships are a product of the HSI model or a result of habitat or animal variation. Validation attempts which relate statistically significant HSI groupings with statistically significant animal-indicator groupings may provide clearer insight into the ability of HSI models to accurately assess habitat quality.

In our example, even large differences in gray squirrel HSI scores (e.g. 0.38 vs. 0.81) were not significant. Further, the confidence intervals around the gray squirrel HSI scores showed considerable overlap throughout the range of cover-types for both submodels. Verification attempts using only the final HSI score may thus fail simply because the assumed differences in habitat quality (different HSI scores) do not exist. If the gray squirrel model correctly evalu-

Table 3. Mean habitat suitability index (HSI) model scores and 90% confidence intervals for the gray squirrel winter food sub-model for 6 cover types in the Huron-Manistee National Forest, Michigan.

Cover type	Stock[a]	HSI	90% confidence interval[b,c]	
			Monte Carlo	Bootstrap
Mixed lowland conifer	6	0.06	0.00–0.10a	0.02–0.10a
Red pine	5	0.09	0.00–0.10a	0.03–0.10a
Jack pine-oak mix	5	0.08	0.00–0.14a	0.03–0.14a
Northern red oak	6	0.17	0.08–0.39a	0.15–0.25b
Red pine	9	0.10	0.05–0.10a	0.09–0.10a
Big-tooth aspen	9	0.10	0.08–0.15a	0.08–0.12a

[a] U.S. Forest Service Corporate Database stocking-size codes where 5 and 6 = pole-sized (12.7–27.9 cm dbh), medium and well stocked, respectively; and 9 = saw-sized (>27.9 cm dbh), well stocked (U.S. Forest Service 1988).

[b] Confidence intervals (90%) generated by Monte Carlo simulation and bootstrapping techniques, respectively.

[c] Confidence intervals and associated means sharing a letter within a column do not differ ($P = 0.90$).

ates gray squirrel habitat suitability, then a valid indicator of gray squirrel habitat response and the HSI scores should correlate poorly, given the demonstrated overlap in HSI scores. Verification attempts could thus find the gray squirrel HSI invalid, simply by failing to consider the variation in the HSI scores.

Brennan (1991) attempted to determine the variability associated with HSI scores by treating each sampling plot as a replicate, and L. Bender (Wash. Dep. Fish and Wildl., unpub. data) modeled habitat in a regression format, calculating confidence intervals directly. The techniques we demonstrated are more versatile than others for several reasons: (1) not all habitat variables need to be collected from the same plot (e.g., sampling methods such as we employed can be used to characterize habitat attributes of a stand), (2) statistical significance comparisons are possible, the power of which can be increased simply by increasing the number of iterations, and (3) bootstrapping or Monte Carlo simulation allows calculation of confidence intervals for traditional HEP HSI models, not only those developed in a regression format. Either technique can be used to calculate confidence intervals for statistical comparisons; however, in our example the Monte Carlo confidence intervals were consistently larger than the bootstrap. This was due to small sample sizes, and subsequently, large standard deviations around the mean estimates in our data (Table 1).

Nonparametric bootstrapping is robust to low sample sizes and unknown data distributions; however, using only the range in data found in sampling may result in underestimation of the variability in habitat attributes. If minimum sample size is adequate to confidently determine data distribution (Freese [1978] or similar methods), then the Monte Carlo technique or parametric bootstrapping (Efron and Tibshirani 1993) may provide a better assessment of the overall variability in sampled habitat parameters and, subsequently, HSI scores.

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Appendix 1: computer program for confidence intervals

Computer program used to calculate Monte Carlo confidence intervals for the gray squirrel HSI model for the big-tooth aspen cover-type in the Huron–Manistee National Forest, Michigan. Variables X1–X4 are the habitat suitability input variables; X1 = HARDSPP (number of hard mast tree species), X2 = HARDCOV (proportion of total tree canopy that is hard-mast-producing trees ≥25 cm dbh), X3 = CANCOV (percent canopy cover of trees), and X4 = DBH (mean diameter at breast height of overstory trees). PC SAS (SAS Inst., Cary, N.C.) software was used for this program.

```
DATA A;
*Generating distributions for habitat variables;
 RETAIN SEED1 SEED2 SEED3 SEED4 1613218064;
 DO I = 1 TO 1000;
 X1 = 0.33 + 0.52 * RANNOR(SEED1);
 X2 = 6.13 + 15.02 * RANNOR(SEED2);
 X3 = 100 + 0 * RANNOR(SEED3);
 X4 = 27.53 + 2.72 * RANNOR(SEED4);
*Calculating SI for HARDSPP;
 IF X1 LT 0.5 THEN X10=0.1;
   IF X1 GE 0.5 LT 1.5 THEN X10=0.1;
   IF X1 GE 1.5 LT 2.5 THEN X10=0.2;
   IF X1 GE 2.5 LT 3.5 THEN X10=0.45;
   IF X1 GE 3.5 LT 4.5 THEN X10=0.8;
   IF X1 GE 4.5 THEN X10=1.0;
*Calculating SI for HARDCOV;
 IF X2 LT 0 THEN X20=0.1;
   IF X2 GE 0 LE 100 THEN X20 = 0.009 * X2 + 0.10;
   IF X2 GT 100 THEN X20=1.0;
*Calculating SI for CANCOV for Winter Food
sub-model;
 IF X3 LT 0 THEN X30=0.0;
   IF X3 GE 0 LE 40 THEN X30 = 0.025 * X3;
   IF X3 GT 40 LT 75 THEN X30=1.0;
   IF X3 GE 75 LE 100 THEN X30 = -0.004 * X3 + 1.2;
   IF X3 GT 100 THEN X30=0.8;
*Calculating SI for DBH;
 IF X4 LE 12.7 THEN X40=0.0;
   IF X4 GT 12.7 LT 38.1 THEN X40 = 0.039 * X4 -
0.49;
   IF X4 GE 38.1 THEN X40=1.0;
*Calculating SI for CANCOV for Cover-Reproduction sub-model;
 IF X3 LT 0 THEN X300=0.0;
   IF X3 GE 0 LE 40 THEN X300 = 0.025 * X3;
   IF X3 GT 40 THEN X300=1.0;
*Calculating HSI for Winter Food sub-model;
 X100 = (X10 * X20)**0.5 * X30;
*Calculating HSI for Cover-Reproduction sub-model;
 X200 = (X40 * X300)**0.5;
*Generating frequency distributions for HSI scores;
OUTPUT;
PROC FREQ;
 TABLES X100 X200;
RUN;
```

Appendix 2: computer program for bootstrap means

Computer program for generating bootstrap (subsamples with replacement) means from sampled

habitat variables. In this example, A = HARDSPP (number of hard mast tree species), B = HARDCOV (proportion of total tree canopy that is hard-mast-producing trees ≥25 cm dbh), C = CANCOV (percent canopy cover of trees), and D = DBH (mean diameter at breast height of overstory trees); sample sizes are n_a, n_b, n_c, and n_d, respectively. The export file can be read into SAS (SAS Inst., Inc., Cary, N.C.) as a replacement for the random value generation step in Appendix 1 (using the INFILE and INPUT statements, i.e. INFILE 'C:\HSI'; INPUT X1-X4;). Programming in this example uses the software RESAMPLING STATS (RESAMPLING STATS, Arlington, Va.).

```
'Program for generating bootstrap iterations.
'Enter sample plot data for variables A, B, C, D.
COPY (enter data) A
COPY (enter data) B
COPY (enter data) C
COPY (enter data) D
'Take subsamples with replacement of size n from
the entered data.
REPEAT 1000
  SAMPLE n_a A AA
  SAMPLE n_b B BB
  SAMPLE n_c C CC
  SAMPLE n_d D DD
'Calculate the mean of the subsamples.
  MEAN AA AAA
  MEAN BB BBB
  MEAN CC CCC
  MEAN DD DDD
'Store the subsamples means.
  SCORE AAA W
  SCORE BBB X
  SCORE CCC Y
  SCORE DDD Z
'Finish first trial. Go back and repeat N times.
END
'Write final output (N mean samples of variables
A-D) to an
'export ASCII file.
WRITE FILE "C:\HSI" W X Y Z
```