EVALUATING HABITAT SELECTION WITH RADIO-TELEMETRY TRIANGULATION ERROR

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Abstract: Radio-telemetry triangulation errors result in the mislocation of animals and misclassification of habitat use. We present analytical methods that provide improved estimates of habitat use when misclassification probabilities can be determined. When misclassification probabilities cannot be determined, we use random subsamples from the error distribution of an estimated animal location to improve habitat use estimates. We conducted Monte Carlo simulations to evaluate the effects of this subsampling method, triangulation error, number of animal locations, habitat availability, and habitat complexity on bias and variation in habitat use estimates. Results for the subsampling method are illustrated using habitat selection by redhead ducks (*Aythya americana*). We recommend the subsampling method with a minimum of 50 random points to reduce problems associated with habitat misclassification.

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Use of radiotelemetry to study space and habitat use patterns of animals is standard practice in wildlife research and management. Triangulation is the most common technique used to estimate (Springer 1979) an animal's location. However, most investigators have treated radio-telemetry bearings, and subsequent locations, as exact and have failed to account for inaccuracies when estimating habitat use patterns.

Quality of the locations estimated by triangulation and precision of the associated bearings have been discussed previously. Hupp and Ratti (1983) and Saltz and Alkon (1985) considered the problem of radiotelemetry errors from mobile receivers. White (1985) considered optimal placement of fixed receivers, and Lee et al. (1985) addressed methods to assess accuracy of such a system. Most recently, White and Garrott (1986) performed a simulation experiment to show that location errors may have substantial effects on the power of multinomial procedures (Neu et al. 1974, Marcum and Loftsgaarden 1980) for evaluating habitat selection.
Measurement error, the difference between an estimated and "true" value, can have a substantial effect on the variability of statistical estimators (Koch 1973). Ignoring measurement error (or other non-sampling errors) may result in serious underestimation of total variability (Iachan 1983). Intrinsic biases in measurement also may produce unsuspected biases in statistical estimates (Cochran 1968, Koch 1973). In the survey-sample literature, these measurement errors also have been referred to as response errors (Koch 1969, 1973; Iachan 1983; Platek and Gray 1983).

Two types of errors occur when habitat use is misclassified as a result of radiotelemetry error. False negative errors occur when the true location of an animal is in habitat type \( h \), but the estimated location is in another habitat type (not \( h \)). False negatives result in underestimates of the true proportion of use that occurs in habitat \( h \). Alternatively, the estimated location may be in habitat type \( h \), but the true location is in another habitat type. These false positive errors result in an overestimate of the true proportion of use for habitat \( h \). It is possible, but unlikely (Cochran 1968, Quade et al. 1980), that false positive and false negative errors will balance and produce unbiased estimates of habitat use. Pace (1988) conducted computer simulations that showed balance did not occur under several realistic habitat distribution patterns. Herein, we describe new statistical procedures to estimate habitat use when misclassification occurs, illustrate these methods with data collected on redhead ducks, and use computer simulations to evaluate factors affecting misclassification rates.

Computer software used to determine duck locations, produce habitat raster maps, and assign habitat types to duckling locations from raster maps was developed by J. R. Cary, G. A. Bartelt, D. M. Heisey, D. L. Thomas, D. J. Twedt, and G. C. White provided many helpful suggestions and comments.

METHODS

Estimation of Measurement Error and Habitat Use

The standard method for determining the proportion of animal use (\( \bar{p} \)) for a single, pre-selected habitat type is based on the binomial distribution. Using this method

\[
\bar{p} = \frac{\sum_{i=1}^{n} y_i}{n}
\]

where

\[
n = \text{the number of locations}
\]

for an animal

and

\[
y_i = 1 \text{ if the } k\text{th estimated location is within the habitat; zero otherwise.}
\]

Then

\[
\text{var}(\bar{p}) = \frac{\bar{p}(1 - \bar{p})}{n}
\]

and this quantity is typically used in determining if use and availability are statistically different (e.g., Neu et al. 1974, Byers et al. 1984). However, both \( \bar{p} \) and \( \text{var}(\bar{p}) \) may be biased when habitat use is misclassified due to radiotelemetry error.

Cochran (1968) discussed the consequences of binomial and multinomial measurement error (misclassification) on statistical estimation of proportions. We modified his approach to derive analytical estimators of the multinomial proportions of habitat use when the probability of misclassification can be estimated for each telemetry location (Appendix). An unbiased estimator for the proportion of use in a given habitat is:

\[
\hat{p}_i = \frac{\sum_{i=1}^{n} \hat{y}_i}{n},
\]

where \( \hat{y}_i \) is the estimated probability that an animal's true location is in a particular habitat. If no errors occur in any of the locations for an animal, then \( \hat{p}_i \) is the usual multinomial estimator (\( \hat{p} \)). If the habitat is relatively homogeneous, true habitat use also may be known, even though some error may occur in location.

The variance of \( \hat{p}_i \) may be estimated (Appendix) by:

\[
\text{var}(\hat{p}_i) = \frac{\hat{p}_i(1 - \hat{p}_i)}{n} + \sum_{i=1}^{n} \frac{\text{var}(\hat{y}_i)}{n^2}.
\]

Thus, the \( \text{var}(\hat{p}_i) \) is comprised of a sampling variance and a misclassification variance. If no misclassification occurs, then \( \text{var}(\hat{p}_i) = \text{var}(\hat{p}) \), which is the usual multinomial variance estimate. The relative precisions of \( \hat{p}_i \) and \( \hat{p} \) will depend upon the magnitude of the misclassification variance and the value of \( \hat{p}_i \) or \( \hat{p} \) because the sampling variance for a proportion ranges from a minimum at \( \hat{p} = 0 \) and 1 to a maximum at \( \hat{p} = 0.5 \).
Table 1. Calculation of habitat use from 5 locations of redhead duck No. T07 at Horicon Marsh, Wisconsin, 1985.

| Date/time of location | Habitat type
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>EM1F Typha*</td>
</tr>
<tr>
<td></td>
<td>m̄_k</td>
</tr>
<tr>
<td></td>
<td>1 10 50</td>
</tr>
<tr>
<td>16 Jul 0717</td>
<td>2 12</td>
</tr>
<tr>
<td>17 Jul 1121</td>
<td>1 13</td>
</tr>
<tr>
<td>18 Jul 0712</td>
<td>1</td>
</tr>
<tr>
<td>19 Jul 1128</td>
<td>1 8</td>
</tr>
<tr>
<td>22 Jul 1939</td>
<td>5 36</td>
</tr>
</tbody>
</table>

Sum random points

<table>
<thead>
<tr>
<th>p̂_k</th>
<th>0 3 26</th>
<th>2 20 107</th>
<th>3 27 117</th>
</tr>
</thead>
<tbody>
<tr>
<td>var(p̂_k)</td>
<td>0.0 0.060 0.100</td>
<td>0.4 0.400 0.430</td>
<td>0.6 0.540 0.470</td>
</tr>
<tr>
<td>var[∑ ŝ_k]</td>
<td>0.0 0.025 0.008</td>
<td>0.0 0.084 0.013</td>
<td>0.0 0.095 0.014</td>
</tr>
<tr>
<td>var(p̂)</td>
<td>0.0 0.012 0.018</td>
<td>0.048 0.051 0.050</td>
<td>0.048 0.053 0.050</td>
</tr>
</tbody>
</table>

*a Habitat type from Cowardin et al. (1979).

*b Random points were generated for 3 levels of subsampling (m̄ = 1, 10, 50) by adding random errors to each bearing and recalculating the maximum likelihood estimator developed by Lenth (1981).

*c See text for example calculation of p̂_k, ∑ var(∑ ŝ_k), and var(p̂).

Procedure for Estimating Habitat Use

In our illustration of the procedure, each telemetry location for an animal was estimated by triangulation using directional bearings from ≥2 known locations. We calculated a confidence interval for the estimated location (White and Garrett 1990) by maximum likelihood procedures (Lenth 1981) using the standard deviation of the directional bearings (Lee et al. 1985, White and Garrett 1990). A subsample of random points for each telemetry location was generated from this confidence interval by adding normally distributed (μ = 0, σ = bearing standard deviation) errors to each directional bearing (White and Garrett 1986). We used the resulting bearings to estimate the position of each random point by repeating the maximum likelihood procedure. The habitat type also was determined for each random point. We repeated this subsampling procedure until the desired number of random points was obtained. The subsample produced a distribution of points that approximates the error distribution for each estimated animal location. Typically, this distribution was concentrated near the mean location and resembled a bivariate normal distribution.

We calculated the proportion of habitat types used (p̂) and precision (var(p̂)) for the subsampling method from a sample data set of 5 redhead duck locations (Kenow 1989) using subsamples of m̄ = 1, 10, and 50 random points for each location (Table 1). Values for p̂ and var(p̂) were determined separately for each habitat type and subsampling category. We divided the number of random points in each habitat type by the total number of random points for the 5 locations to estimate p̂ (e.g., for EM1F Typha, m̄ = 10, p̂ = 3/50 = 0.06). We calculated misclassification variance

\[
\text{Var}(\hat{p}) = \left( \sum_{i=1}^{5} \text{Var}(\hat{s}_i) \right)
\]

by using the binomial variance of \(\hat{s}_i\) for each location. For example, on 16 July, 2 of the 10 random points (m̄ = 10) were located in EM1F Typha habitat (Table 1). For this day and habitat type, the \(\text{Var}(\hat{s}_i) = \text{Var}(\hat{s}_i)|1 - \hat{s}_i|/m̄ = (2/10)(1 - 2/10)/10 = 0.016\)

and for all 5 locations \(\sum \text{Var}(\hat{s}_i) = 0.025\). Because m̄ = 10 for each of the 5 locations, the misclassification variance component (eq. [2]) was calculated simply by

\[
\text{Var}(\hat{p}) = \frac{\left( \sum_{i=1}^{5} \text{Var}(\hat{s}_i)|1 - \hat{s}_i| \right)}{n^2m̄ = 0.25/25 = 0.001}
\]

We added this misclassification variance to sampling variance (eq. [2], p̂(1 - p̂)/n = 0.060.94/5 = 0.011) to produce a final estimated variance for EM1F Typha for m̄ = 10 of 0.012.

Comparison of Methods

We compared the subsample and standard methods of estimating habitat use for redhead ducks captured and fitted with radio transmit-
ters at Horicon Marsh, Wisconsin (Kenow 1989). Birds were located daily from mobile tracking vehicles. Duck locations were determined later from the solution of telemetry bearings using the maximum likelihood estimator of Lenth (1981). The terrain of the study area was flat and transmitted signals generally were not obstructed by trees. We classified habitat types within the study area from aerial photographs and from ground truthing using the classification system of Cowardin et al. (1979). A computerized raster map of the study area was produced identifying the habitat type within each 0.05-ha raster cell. We assigned habitat type to estimated duck locations by comparing the location to the raster map.

For the standard method, we assumed that animal locations were measured without error, and no habitat misclassification occurred. Thus, habitat use and precision were measured by using the usual multinomial estimates (Neu et al. 1974). For the subsampling method, we measured habitat use and precision by sampling $m_a = 100$ random points for each animal location. This method was identical to that subsequently used to generate subsamples for the Monte Carlo simulations (see below). We estimated the classification probability for each habitat type ($\pi_i$) as the proportion of random points occurring in the habitat type of interest. Equations (1) and (2) then were used to calculate the estimated habitat use ($\hat{p}$) and precision. Our calculations for equation (2) assumed that $\pi_i$ is the estimated probability from a binomial distribution (Appendix).

**Monte Carlo Simulation**

We used Monte Carlo methods to simulate triangulation errors and evaluate habitat misclassification on a computer. Three towers were assumed on a unit square in the triangular configuration recommended by White (1985:Table 1). The area within the unit square was divided into a $10 \times 10$ or $20 \times 20$ checkerboard of grid squares. Uniform random (0,1) numbers were generated to assign 1 of 5 habitat types to each grid square according to 2 different distributions of habitat types. Habitat Mix 1 represented an equal distribution (20%) of 5 available habitat types. Habitat Mix 2 incorporated 2 common (40 and 30%), 1 intermediate (20%), and 2 rare (5%) components of habitat availability. We used uniform random numbers to generate coordinates of the animal’s true location (25, 50, or 100 locations) and determined the habitat type for each location. Then, we added normally distributed ($\mu = 0; \sigma = 1, 2, 3, 4$) random errors to each of the bearings intersecting the animal’s true location and the 3 towers. These simulated bearings were repeatedly generated to obtain subsamples of 1, 10, 30, or 50 random points/true location (Lenth 1981, White and Garrett 1986), and the habitat type for each random point was determined. We recorded the number of random points in each habitat type for each simulation (animal). Each combination of parameters was replicated 30 times, producing 5,760 simulations.

We used these simulation experiments to evaluate the effects of bias and mean square error (MSE) for the standard ($\hat{p}$) and subsampling ($\hat{p}^*$) methods when animals use the available habitat at random. MSE can be decomposed into 3 components (Koch 1969:859):

$$\text{MSE} = \text{bias}^2 + \sigma_i^2 + \sigma_m^2$$

(3)

where $\sigma_i^2$ represents the usual sampling variance and $\sigma_m^2$ represents the misclassification variance. Thus, the relative magnitude of bias$^2$ and $\sigma_m^2$ determine the reliability for estimated habitat use. When bias$^2$ represents an important component of MSE, habitat use estimators that reduce bias$^2$ and therefore MSE would be preferred over alternative estimators (Mendenhall et al. 1981:294–295). We summarized each simulation by the proportion of random points occurring in each of the 5 habitat types. Measures of bias and bias$^2$ ($n = 28,800$) were calculated for each simulation and habitat type. We calculated bias for each habitat type as the proportion of random points in each type minus the proportion of true locations.

We conducted separate 5-way ANOVAs of all factors (habitat complexity, triangulation error, no. of animal locations, no. of random points, and habitat type), and all possible interactions for each habitat mix and response variable (bias and bias$^2$). Several interactions were significant ($P \leq 0.05$) for each ANOVA. However, these interactions were not evaluated because their $F$-statistics were substantially smaller than those for the significant main effects. We determined the relative importance of each significant factor from its index of association with the response variable (Kirk 1982:387–388).

**RESULTS**

**Comparison of Methods**

Estimated habitat use by redhead ducks (Table 2) illustrated that $\hat{p}$ and $\hat{p}^*$ may differ for
Table 2. Habitat availability and estimated use by the standard ($\hat{\rho}$) and subsampling ($\bar{\rho}$) methods for redhead ducks at Horicon Marsh, Wisconsin, 1983 and 1985.

<table>
<thead>
<tr>
<th>Habitat type*</th>
<th>Duck no./year</th>
<th>M43/1983b</th>
<th>M56/1983b</th>
<th>X77/1985b</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Avail.</td>
<td>$\hat{\rho}$</td>
<td>$\bar{\rho}$</td>
<td>Avail.</td>
</tr>
<tr>
<td>EM1F Typha</td>
<td>0.65</td>
<td>0.86d</td>
<td>0.75</td>
<td>0.45</td>
</tr>
<tr>
<td>EM2AC Typha</td>
<td>&lt;0.01</td>
<td>0.00</td>
<td>&lt;0.01</td>
<td>0.01</td>
</tr>
<tr>
<td>EM1/AB4F</td>
<td>0.30</td>
<td>0.06d</td>
<td>0.20</td>
<td>0.22</td>
</tr>
<tr>
<td>AB4F Lemma</td>
<td>0.01</td>
<td>0.24d</td>
<td>0.24d</td>
<td>0.01</td>
</tr>
<tr>
<td>AB3F Potamogeton</td>
<td>0.06</td>
<td>0.05</td>
<td>0.05</td>
<td>0.02</td>
</tr>
<tr>
<td>UB4GH open</td>
<td>0.01</td>
<td>0.00</td>
<td>0.00</td>
<td>0.15</td>
</tr>
<tr>
<td>EM2AC mixed</td>
<td>0.15</td>
<td>0.14</td>
<td>0.15</td>
<td>0.13</td>
</tr>
<tr>
<td>SS1CF Salix</td>
<td>0.01</td>
<td>0.00</td>
<td>0.00</td>
<td>0.01</td>
</tr>
</tbody>
</table>

*a Habitats types from Cowardin et al. (1979).

b Sample sizes M43 (n = 31); M56 (n = 25); X77 (n = 22).

c Estimated habitat use for the subsampling method ($\bar{\rho}$) calculated with $m_1 = 100$.

d Indicates a difference ($P \leq 0.05$) between use and availability.

some habitats. Assuming that $\rho^*$ is less biased than $\hat{\rho}$, then $\rho^*$ underestimated use in several instances and overestimated it in other situations. Although sample sizes were small, no apparent trends related to habitat type or magnitude of $\hat{\rho}$ were noted. Because the number of subsamples was large ($m_1 = 100$), misclassification variance (eq. (2)) had minimal impact on the precision of $\rho^*$.

Habitat availability for each duck was estimated as the proportion of each habitat type present (Table 2) within the minimum perimeter polygon home range of each duck. We used Bonferroni simultaneous confidence intervals to compare estimated proportions of habitat use $\rho^*$ and $\hat{\rho}$ with habitat availability (Neu et al. 1974, Byers et al. 1984). Habitat use estimates obtained from $\hat{\rho}$ indicated selection ($P \leq 0.05$) of habitat type EM1F Typha for duck M43, but no habitat selection was found for $\rho^*$ ($P > 0.05$). Habitat use estimates also were lower ($P \leq 0.05$) in type EM1/AB4F for ducks M43 and M56, when no differences ($P > 0.05$) were found for $\rho^*$. Habitat type AB3F Potamogeton was used less ($P \leq 0.05$) than its availability by duck X77 for use estimated by $\rho^*$, but not ($P > 0.05$) by $\hat{\rho}$.

Monte Carlo Simulations

We found no differences ($P \geq 0.27$) in bias for any of the main effects evaluated in the Monte Carlo experiment. This primarily reflects the random habitat distribution and use conditions of the simulation experiment in which values for bias were both positive and negative with a mean of zero. However, we found differences ($P \leq 0.0001$) for bias$^a$. These results indicated that the magnitude of values for bias (e.g., $|\text{bias}|$) and that reliability (MSE) of estimated habitat use were affected by factors in the simulation. The homogeneous mix of habitats (Fig. 1) provided similar results to the heterogeneous mix (Fig. 2).

Increasing the number of animal locations resulted in reductions ($P \leq 0.0001$) in bias$^a$ for both habitat mixes (Figs. 1 and 2). Bias$^a$ was reduced by approximately two-thirds when the number of locations was increased from 25 to 100. Reductions ($P \leq 0.0001$) in bias$^a$ also were obtained by subsampling when $>1$ random point was generated for each location.

Increasing the number of random points to 30 reduced the bias$^a$ to one-half that obtained for a single point. Number of random points was the second most important factor in the ANOVA for habitat Mix 1, where habitat type had equal availability and was therefore not a significant factor ($P \geq 0.26$). However, for habitat Mix 2, habitat type ($P \leq 0.01$) was the most important factor in the ANOVA, followed by the number of animal locations and the number of subsamples ($P \leq 0.01$). The proportion of available habitat affected ($P \leq 0.0001$) bias$^a$ in the heterogeneous habitat mix. Bias$^a$ was smaller for rare habitats than for common habitats (Fig. 2). However, the relative bias$^a$ (bias$^a$/available habitat) was higher for rare habitats. Increasing the habitat complexity (decreasing patch size) from a $10 \times 10$ to a $20 \times 20$ grid reduced ($P \leq 0.01$) bias$^a$ (Figs. 1 and 2). Telemetry error affected ($P \leq 0.02$) bias$^a$ in both habitat mixes but was the least important of the significant factors. Bias$^a$ appeared higher for the one-degree telemetry error in both habitat mixes. The reasons for the latter results are not completely
clear but probably are related to the interaction of telemetry error with other factors and the increased number of cells in the 20 × 20 simulations that provides a more precise estimate of available habitats.

**DISCUSSION**

The effects of radiotelemetry triangulation errors are seldom considered in the analysis of animal habitat selection. The ability to detect habitat selection depends on the size of habitat patches, relative telemetry error, and the number of animal locations (White and Garrott 1986). When habitat patches are large relative to telemetry error, misclassification will have little effect on estimated habitat use or selection unless animals occur near the edge of habitat patches. However, if habitat patches are small relative to telemetry error, then animals may appear to use the available habitat types randomly. The more biologically realistic situation probably occurs between these 2 extremes. In addition, animal preference for habitat types, habitat edges, and the spatial association of habitat types may influence both variability and misclassification in estimated habitat use patterns (Pace 1988, Nams 1989). Habitat preference or avoidance can be calculated using Bonferroni simultaneous confidence intervals for habitat use and availability (Neu et al. 1974, Byers et al. 1984). Using the standard method, these calculations are made for $\hat{p}$ by using $\text{var}(\hat{p}) = \hat{p}(1 - \hat{p})/n$. However, a confidence interval for the subsampling method ($\hat{p}^*$), must use the $\text{var}(\hat{p}^*)$ (eq. [2]) not the $\text{var}(\hat{p})$. In particular, the number of random points in the subsample ($m_*$) should not be used to replace $n$ in the calculation of $\text{var}(\hat{p})$.

The direction and magnitude of habitat misclassification may be difficult to predict. Misclassification rates for both preference and avoidance can be influenced by the true proportion of habitat type available, the size of habitat patches relative to telemetry error, the use of habitat edges, and other factors (Pace 1988, Nams 1989). Results from Quade et al. (1980) indicate that false positive errors are a more important source of bias for rare habitats, and false negative errors are more important for common habitats. Thus, preferred habitats may
Fig. 2. Average bias\(^2\) (× 1,000) ± 2 SE from Monte Carlo simulation with heterogeneous habitat mix with 30 replications (14,400 total) for each combination of independent factors.

be more susceptible to false negative errors that tend to reduce the estimated proportion of use. Habitats in which proportional use is significantly lower than availability may show an increase in apparent use caused by excessive false positive errors. In either situation, it may be more difficult to demonstrate habitat selection (preference or avoidance).

White and Garrott (1986) recommended computer simulations before collecting field data to determine the effects of triangulation error on statistical tests for habitat selection. They concluded that triangulation error reduces the statistical power to detect habitat selection. However, their simulation approach is likely to be impractical because proportions of habitats used by the animals must be known prior to simulations. In addition, their approach is probably unrealistic for most field projects because misclassification may depend upon the actual amounts and distributions of available habitat and the use of edge by animals. Presumably the need for a computer simulation was based on lack of appropriate analytical methods to estimate and account for habitat misclassification.

Our simulations show that the average misclassification rate for habitat use caused by telemetry error is unbiased when animals use the available habitat at random (i.e., no selection). We found that variation in estimated habitat use (bias\(^2\)) associated with misclassification can be reduced by subsampling from the error distribution for each location and by increasing the number of locations. White and Garrott (1986) also recommend increased samples (telemetry locations) to increase the power of the statistical tests. Unfortunately, when animals select (or avoid) habitat types, an increase in sample size primarily reduces the minimum difference between use and availability that will produce a statistically significant result, but will not remove bias resulting from misclassification errors (Quade et al. 1980:504). While power may be increased, there is no guarantee that the biased results reflect true habitat selection. The preferred solution is to develop methods that minimize the potential bias. One approach is to ensure that habitat locations are observed without error. This solution will be difficult even in ideal conditions because of the disturbance caused by
closely monitoring some animals. Other approaches, which deserve further research, include validation studies which attempt to estimate the false positive (f) and false negative (F) error rates. Internal validation may be possible if the true habitat use can be determined for a random sample of animal locations. External validation employing randomly located radio transmitters to assess the effect of telemetry error on habitat estimation also may be feasible. Alternatively, the amount of bias can be decreased by subsampling from the error distribution for each telemetry location, and statistical tests can more adequately reflect variance associated with misclassification. However, the subsampling method may not provide completely unbiased results because the misclassification rate can only be estimated rather than be known exactly (Rogan and Gladen 1978).

RESEARCH IMPLICATIONS

Telemetry errors produced while sampling the locations of radio-marked animals can be attributed to equipment and a variety of time- and site-specific factors. In practice, these errors should be considered when estimating habitat use and analyzing habitat selection. Biases in the estimated proportions of habitat use may be substantial if the animal’s estimated locations do not provide reliable information on the actual habitat used. Use of the error distribution for each location, rather than a simple mean estimate, provides 1 approach for considering the inaccuracy of telemetry locations. However, this approach does not negate the importance of obtaining precise telemetry locations. Precise locations will be especially important when habitats have a patchy distribution in relation to the location error (Nams 1989). We recommend subsampling a minimum of 50 random points from the error distribution of each animal location to reduce variability associated with habitat misclassification. We suggest that animal locations that do not produce subsample estimates of the f > 0.50 for at least 1 habitat type are unreliable for use in selection studies. The subsampling method reduces the variation associated with telemetry error, and therefore provides an alternative procedure to increasing the number of animal locations (White and Garrott 1986) to improve the power of habitat selection analysis. The use of 50 random points for each location is approximately equivalent to increasing the number of telemetry locations for each animal from 25 to 50.

LITERATURE CITED


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APPENDIX

The standard multinomial probability estimate for proportional use of a particular habitat type is given by:

$$\hat{p} = \sum_{i=1}^{n} \frac{y_i}{n}$$

where $n =$ the number of telemetry locations for an individual animal and $y_i = 1$ if the $k$th location is in the habitat type of interest; zero otherwise. When the locations are an estimate of the animal's true position, $y_i$ will usually be measured with error. In this situation, $y_i$ is assessed for the habitat found at the animal's estimated location. Misclassification will occur when the estimated location is in a habitat type different from that actually used by the animal. Thus, the probability of correct classification may be defined as $\Pr(y_i = Y_i)$, where $Y_i = 1$ if the $k$th true location is in the habitat type of interest; zero otherwise.

Classification errors may be false negatives, or false positives. These misclassification rates are defined by:

$$\theta_i = \Pr(y_i = 0|Y_i = 1)$$
false negative

and

$$\phi_i = \Pr(y_i = 1|Y_i = 0)$$
false positive.

A multinomial probability estimator considering misclassification rates is given by Cochran (1968:643) and is equivalent to:

$$\hat{p} = \sum_{i=1}^{n} \left[ \frac{y_i(1 - \theta_i)}{n} + \frac{(1 - y_i)\phi_i}{n} \right]$$

$$= \hat{p}^*(1 - \theta) + (1 - \hat{p}^*)\phi,$$  (2)

where $\hat{p}^*$ is an unbiased estimate of probability and $\theta$ and $\phi$ are the average misclassification rates. When no misclassification occurs $\theta_i = \phi_i = 0$, equation (2) reduces to equation (1), and $\hat{p} = \hat{p}^*$. When $\theta$ and $\phi$ are sufficiently known to be considered constants, then Cochran (1968) indicates that

$$\text{var}(\hat{p}^*) = \frac{\hat{p}^*(1 - \hat{p}^*)}{n}.$$

the usual binomial variance estimator with parameters $n$ and $\hat{p}^*$.

For typical habitat use studies $\theta$ and $\phi$ will not be known, but must be estimated. One approach is to conduct an internal validation study to determine the true habitat use for a sample of animal locations. This situation is complicated because the animal's true location often remains unknown and thus $\theta_i$ and $\phi_i$ cannot be determined. A second approach is to conduct an external validation using radio transmitters placed in the study area to estimate the false positive ($\phi$) and false negative ($\theta$) error rates. An alternative approach is to develop an estimator based on the probability that each estimated location is within the habitat type of interest. Using equation (2) and Bayes Theorem we developed a new equation that estimates the true proportion of use

$$\hat{p}^* = \sum_{i=1}^{n} \left[ \frac{y_i\Pr(Y_i = 1|y_i = 1)}{n} + \frac{(1 - y_i)\Pr(Y_i = 1|y_i = 0)}{n} \right].$$  (4)

For this approach we denoted $\pi_{i1} = \Pr(Y_i = 1|y_i = 1)$ for those estimated locations in the appropriate habitat type and similarly $\pi_{i0} = \Pr(Y_i = 1|y_i = 0)$ for those estimated locations in a different habitat type. This provides a simplified version of equation (4):

$$\hat{p}^* = \sum_{i=1}^{n} \left[ \frac{y_i\pi_{i1}}{n} + \frac{(1 - y_i)\pi_{i0}}{n} \right].$$

Because $\pi_{i1}$ and $\pi_{i0}$ generally will not be known, we estimated these quantities by subsampling from the error distribution for each telemetry location ($k$). We used a single estimator ($\hat{p}_{i}$) be-
cause each location is unique and belongs to the exclusive sets of either \( y_i = 1 \) or \( y_i = 0 \). Then equation (4) can be replaced by:

\[
p^* = \sum_{i=1}^{n} \left[ \frac{y_i \tilde{x}_i}{n} + \frac{(1 - y_i) \tilde{\pi}^*_i}{n} \right] = \sum_{i=1}^{n} \tilde{x}_i/n. \tag{5}
\]

This estimator may not be totally unbiased because the misclassification rates are estimated rather than known exactly (Rogan and Gladen 1978). However, our Monte Carlo simulations (see text) indicated that this estimator was both unbiased and reduced MSE.

The variance of eq. (5) may be determined using the conditional variance method (Feller 1966:164). Thus,

\[
\text{var}(p^*) = E_u \left[ \sum_{i=1}^{n} \left( \frac{y_i \tilde{x}_i}{n} + \frac{(1 - y_i) \tilde{\pi}^*_i}{n} \right) \right] + \sum_{i=1}^{n} \text{var}(\tilde{x}_i)
\]

where equation (3) is substituted for the first portion of equation (6) and by assuming that \( \text{cov}(\tilde{x}_i, \tilde{x}_j) = 0 \) for \( i \neq j \). When \( \tilde{x}_i \) is the estimated probability from a binomial distribution, equation (6) simplifies to

\[
\text{var}(p^*) = \frac{\hat{p}^*(1 - \hat{p}^*)}{n} + \sum_{i=1}^{n} \frac{\tilde{x}_i(1 - \tilde{x}_i)}{n^2 m_i} \tag{7}
\]

where \( m_i \) is the number of Bernoulli trials conducted to obtain \( \tilde{x}_i \). Equations (5) and (7) may be used to estimate habitat use when an animal's true location cannot be exactly determined and when the probability of the estimated location occurring in each habitat type is available.