Biometrics Unit and Surveys

North Metro Area Office
5463 - C West Broadway
Forest Lake, Minnesota 55025
(651) 296-5200

QUANTIFYING THE EFFECT OF HABITAT AVAILABILITY ON SPECIES DISTRIBUTIONS[1]

Geert Aarts[2,3], **John Fieberg**, Sophie Brasseur[2], and Jason Matthiopoulos[4]

SUMMARY

1. If animals moved randomly in space, the use of different habitats would be proportional to their availability. Hence, deviations from proportionality between use and availability are considered the tell-tale sign of preference. This principle forms the basis for most habitat selection and species distribution models fitted to use-availability or count data (e.g. MaxEnt and Resource Selection Functions).

2. Yet, once an essential habitat type is sufficiently abundant to meet an individual's needs, increased availability of this habitat type may lead to a decrease in the use/availability ratio. Accordingly, habitat selection functions may estimate negative coefficients when habitats are superabundant, incorrectly suggesting an apparent avoidance. Furthermore, not accounting for the effects of availability on habitat use may lead to poor predictions, particularly when applied to habitats that differ considerably from those for which data have been collected.

3. Using simulations, we show that habitat use varies non-linearly with habitat availability, even when individuals follow simple movement rules to acquire food and avoid risk. The results show that the impact of availability strongly depends on the type of habitat (e.g. whether it is essential or substitutable) and how it interacts with the distribution and availability of other habitats.

4. We demonstrate the utility of a variety of existing and new methods that enable the influence of habitat availability to be explicitly estimated. Models that allow for non-linear effects (using b-spline smoothers) and interactions between environmental covariates defining habitats and measures of their availability were best able to capture simulated patterns of habitat use across a range of environments.

5. An appealing aspect of some of the methods we discuss is that the relative influence of availability is not defined a priori, but directly estimated by the model. This feature is likely to improve model prediction, hint at the mechanism of habitat selection, and may signpost habitats that are critical for the organism's fitness.

[1]Abstract from paper accepted for publication in *Journal of Applied Ecology*.
[2] IMARES Wageningen UR, PO Box 167, 1790AD, Den Burg, The Netherlands;
[3]Department of Aquatic Ecology and Water quality Management, Wageningen UR, PO Box 47, 6700AA, Wageningen, the Netherlands;
[4] Institute of Biodiversity, Animal Health and Comparative Medicine, College of Medicine, Veterinary & Life Sciences, University of Glasgow, Graham Kerr Building, Glasgow G12 8QQ, UK

ESTIMATING POPULATION ABUNDANCE USING SIGHTABILITY MODELS: R SIGHTABILITYMODEL PACKAGE[1]

John R. Fieberg

ABSTRACT

Sightability models are binary logistic-regression models used to estimate and adjust for visibility bias in wildlife-population surveys (Steinhorst and Samuel 1989). Estimation proceeds in 2 stages: (1) Sightability trials are conducted with marked individuals, and logistic regression is used to estimate the probability of detection as a function of available covariates (e.g., visual obstruction, group size). (2) The fitted model is used to adjust counts (from future surveys) for animals that were not observed. A modified Horvitz-Thompson estimator is used to estimate abundance: counts of observed animal groups are divided by their inclusion probabilities (determined by plot-level sampling probabilities and the detection probabilities estimated from stage 1). We provide a brief historical account of the approach, clarifying and documenting suggested modifications to the variance estimators originally proposed by Steinhorst and Samuel (1989). We then introduce a new R package, SightabilityModel, for estimating abundance using this technique. Lastly, we illustrate the software with a series of examples using data collected from moose (*Alces alces*) in northeastern Minnesota and mountain goats (*Oreamnos americanus*) in Washington State.

[1] Abstract from published paper: Fieberg, J. 2012. Estimating population abundance using sightability models: R SightabilityModel package. *Journal of Statistical Software* 51:1-20.

ABUNDANCE ESTIMATION WITH SIGHTABILITY DATA: A BAYESIAN DATA AUGMENTATION APPROACH[1]

J. Fieberg, M. Alexander[2], S. Tse[2], and K. St. Clair[2]

SUMMARY

1. Steinhorst & Samuel (1989) showed how logistic-regression models, fit to detection data collected from radiocollared animals, can be used to estimate and adjust for visibility bias in wildlife-population surveys. Population abundance is estimated using a modified Horvitz-Thompson (mHT) estimator in which counts of observed animal groups are divided by their estimated inclusion probabilities (determined by plot-level sampling probabilities and detection probabilities estimated from radiocollared individuals). The sampling distribution of the mHT estimator is typically right skewed, and statistical inference relies on asymptotic theory that may not be appropriate with small samples.

2. We develop an alternative, Bayesian model-based approach which we apply to data collected from moose (*Alces alces*) in Minnesota. We model detection probabilities as a function of visual obstruction (VO), informed by data from 124 sightability trials involving radiocollared moose. These sightability data, along with counts of moose from a stratified random sample of aerial plots, are used to estimate moose abundance in 2006 and 2007 and the log rate of change between the two years.

3. Unlike traditional design-based estimators, model-based estimators require assumptions regarding stratum-specific distributions of the detection covariates, the number of animal groups per plot, and the number of animals per animal group. We demonstrate numerical and graphical methods for assessing the validity of these assumptions and compare two different models for the distribution of the number of animal groups per plot, a beta-binomial model and a logistic-t model.

4. Estimates of the log-rate of change (95%CI) between 2006 and 2007 were -0.21 (-0.53, 0.12), -0.24 (- 0.64, 0.16), and -0.25 (-0.64, 0.15) for the beta-binomial model, logistic-t model, and mHT estimator, respectively. Plots of posterior-predictive distributions and goodness-of-fit measures both suggest the beta-binomial model provides a better fit to the data.

5. The Bayesian framework offers many inferential advantages, including the ability to incorporate prior information and perform exact inference with small samples. More importantly, the model-based approach provides additional flexibility when designing and analyzing multi-year surveys (e.g., rotational sampling designs could be used to focus sampling effort in important areas, and random effects could be used to share information across years).

---

[1] Abstract from paper accepted for publication in *Methods in Ecology and Evolution.*
[2] Department of Mathematics, Carleton College, Northfield, MN 55057, USA

USING TIME-OF-DETECTION TO EVALUATE DETECTABILITY ASSUMPTIONS IN TEMPORALLY REPLICATED AURAL COUNT INDICES: AN EXAMPLE WITH RING-NECKED PHEASANTS [1]

John H. Giudice, **Kurt J. Haroldson**, Alison Harwood[2,3], Brock R. McMillan[4]

ABSTRACT

The validity of treating counts as indices to abundance is based on the assumption that the expected detection probability, E(*p*), is constant over time or comparison groups or, more realistically, that variation in p is small relative to variation in population size that investigators seek to detect. Unfortunately, reliable estimates of E(*p*) and var(*p*) are lacking for most index methods. As a case study, we applied the time-of-detection method to temporally replicated (within season) aural counts of crowing male Ring-necked Pheasants (*Phasianus colchicus*) at 18 sites in southern Minnesota in 2007 to evaluate the detectability assumptions. More specifically, we used the time-of-detection method to estimate E(*p*) and var(*p*), and then used these estimates in a Monte Carlo simulation to evaluate bias-variance tradeoffs associated with adjusting count indices for imperfect detection. The estimated mean detection probability in our case study was 0.533 (SE = 0.030) and estimated spatial variation in E(*p*) was 0.081 (95% CI: 0.057–0.126). On average, both adjusted (for $\hat{p}$) and unadjusted counts of crowing males qualitatively described the simulated relationship between pheasant abundance and grassland abundance, but the bias-variance tradeoff was smaller for adjusted counts (MSE = 0.003 vs. 0.045, respectively). Our case study supports the general recommendation to use, whenever feasible, formal population-estimation procedures (e.g., mark-recapture, distance sampling, double sampling) to account for imperfect detection. However, we caution that interpreting estimates of absolute abundance can be complicated, even if formal estimation methods are used. For example, the time-of-detection method was useful for evaluating detectability assumptions in our case study and the method could be used to adjust aural count indices for imperfect detection. Conversely, using the time-of-detection method to estimate absolute abundances in our case study was problematic because the biological populations and sampling coverage could not be clearly delineated. These estimation and inference challenges may also be important in other avian surveys that involve mobile species (whose home ranges may overlap several sampling sites), temporally replicated counts, and inexact sampling coverage.

[1] Abstract from published paper: Giudice et al. 2013. Using time-of-detection to evaluate detectability assumptions in temporally replicated aural count indices: an example with Ring-necked pheasants. Journal of Field Ornithology.84(1):98-112.
[2] Department of Biological Sciences, Minnesota State University, Mankato, Minnesota 56001.
[3] Present address: WSB & Associates, 701 Xenia Ave S., Suite 300, Minneapolis, MN 55416.
[4] Department of Plant and Wildlife Sciences, Brigham Young University, Provo, Utah 84602.

A COMPARISON OF MODELS USING REMOVAL EFFORTS TO ESTIMATE ANIMAL ABUNDANCE [1]

Katherine St. Clair[2], **Eric Dunton**[3], and **John Giudice**

SUMMARY OF FINDINGS

This paper compares methods for modeling the probability of removal when variable amounts of removal effort are present. A hierarchical modeling framework can produce estimates of animal abundance and detection from replicated removal counts taken at different locations in a region of interest. A common method of specifying variation in detection probabilities across locations or replicates is with a logistic model that incorporates relevant detection covariates. As an alternative to this logistic model, we propose using a catch–effort (CE) model to account for heterogeneity in detection when a measure of removal effort is available for each removal count. This method models the probability of detection as a nonlinear function of removal effort and a removal probability parameter that can vary spatially. Simulation results demonstrate that the CE model can effectively estimate abundance and removal probabilities when average removal rates are large but both the CE and logistic models tend to produce biased estimates as average removal rates decrease.We also found that the CE model fits better than logistic models when estimating wild turkey abundance using harvest and hunter counts collected by the Minnesota Department of Natural Resources during the spring turkey hunting season.

[1] Abstract from published paper: St. Clair et al. 2013. A comparison of models using removal efforts to estimate animal abundance. Journal of Applied Statistics 40(3):527-545.

[2] Department of Mathematics, Carleton College, Northfield, Minnesota 55057.
[3] Present address: Shiawassee National Wildlife Refuge, U.S. Fish and Wildlife Service, Saginaw, Michigan 48601.