



Accuracy or precision: Implications of sample design and methodology on abundance estimation



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ABSTRACT

Sampling by spatially replicated counts (point-count) is an increasingly popular method of estimating population size of organisms. Challenges exist when sampling by point-count method, and it is often impractical to sample entire area of interest and impossible to detect every individual present. Ecologists encounter logistical limitations that force them to sample either few large-sample units or many small sample-units, introducing biases to sample counts. We generated a computer environment and simulated sampling scenarios to test the role of number of samples, sample unit area, number of organisms, and distribution of organisms in the estimation of population sizes using *N*-mixture models. Many sample units of small area provided estimates that were consistently closer to true abundance than sample scenarios with few sample units of large area. However, sample scenarios with few sample units of large area provided more precise abundance estimates than abundance estimates derived from sample scenarios with many sample units of small area. It is important to consider accuracy and precision of abundance estimates during the sample design process with study goals and objectives fully recognized, although and with consequence, consideration of accuracy and precision of abundance estimates is often an afterthought that occurs during the data analysis process.

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1. Introduction

Estimation of population size by spatially replicated counts (point-count method) has been used for many large-scale animal-monitoring programs (e.g., North American Breeding Bird Survey, North American Amphibian Monitoring Program, and Christmas Bird Count; Royle, 2004). Such studies attempt to estimate abundance by counting organisms within a sample area on repeated visits to obtain an estimation of site-specific abundance (Otis et al., 1978; Williams et al., 2002). Multiple estimated site-specific abundances can be averaged and combined with covariate data to predict abundance across an area of interest (Royle, 2004). Covariate data also provide an understanding of the relation between

abundance and habitat use, which is a fundamental interest of many animal-population investigations (Royle, 2004).

A number of complications are associated with estimating population size from point-count data that arise from choices in how to survey a given area. In situations where it is impractical to sample the entire area in which study organisms inhabit, ecologists must decide how to conduct surveys at smaller scales that can provide reliable estimates to the larger area. In such situations, ecologists must make inferences about non-sampled portions of the area of interest from sampled portions of the area (Royle and Nichols, 2003). Furthermore, most survey methods do not detect all individuals present in the survey area. This problem is often minimized by the use of a detection estimator that quantifies the probability that an individual present in the survey area appears in a count statistic (Royle and Nichols, 2003). Lastly, many investigations of animal population size utilizing spatially replicated counts examine rare or elusive species that exhibit low detection probabilities (McDonald, 2004), and thus are characterized by zero-inflated data (Royle, 2004).

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Design of sampling scenarios (i.e., number of sampling units and area of each unit) for point-count population-estimate surveys can influence number of zero-counts encountered while conducting point-counts, and thus influence accuracy and precision of population estimates. Ecologists must carefully select sampling scenarios that will yield an acceptable level of accuracy and precision, while also bearing in mind the challenges faced when sampling organisms in the wild. Often, ideal sampling designs must be altered due to logistical constraints (e.g., monetary or time). Ecologists typically encounter limitations that force them to sample either few large-sample units or many small sample-units. Zeros in catch data are known to cause complications in statistical analysis (e.g., bias in estimate or overdispersion; Welsh et al., 1996), and thus an ecologist might increase sample unit area to reduce the chance of a zero catch. Likewise, more sample units yield greater statistical power (Cohen, 1977; Thompson, 2012). Thus, a trade-off likely exists between the number of zero-counts encountered and statistical power for ecologists devising survey design to measure population size. Does the trade-off between increasing size of the sample unit and decreasing number of sample units influence accuracy and precision of population estimates derived with point-count methodology?

Though the sampling scenario itself could potentially influence accuracy and precision of abundance estimates, density and distribution of animals within the population of interest could also be influential. Density of a population may affect the ability of an ecologist to detect individuals, and has been reported to affect accuracy and precision of population estimates from visual counts (Hegggenes et al., 1990; Rodgers et al., 1992; Pink et al., 2007). Detection probability may be low when sampling low-density populations (Rosenberg et al., 1995; Royle, 2004), due to infrequent encounters of scarce individuals (e.g., endangered species). Alternatively, saturation of sampling gear could produce misrepresentative count data in high-density populations. For example, catchability coefficient (i.e., proportion of individuals caught by each unit of effort) has been reported to vary inversely with abundance, and sampling gear was more effective at lower population density in Chinook salmon *Oncorhynchus tshawytscha* (Peterman and Steer, 1981).

Random distribution of individuals within a population is an assumption made when estimating population size by the point-count method (Royle, 2004). Random distribution rarely occurs in nature, and is probably only justified within a homogeneous landscape (Royle, 2004). Distribution of individuals can be influenced by habitat use and availability (Conroy et al., 2008). When a random sampling design is employed, biased estimates of population size are possible if used habitats are not sampled (Pink et al., 2007). Homogenous landscapes rarely occur in nature and therefore habitat heterogeneity likely influences distribution of individuals and likewise influences detection probability. Heterogeneous detection probabilities are known to occur when estimating population size (Royle and Nichols, 2003), and several models for both occupancy and abundance have been developed to account for heterogeneous detection probabilities (Dorazio and Royle, 2003; Royle and Nichols, 2003; Tyre et al., 2003; Royle et al., 2005). Variation of abundance among sample sites induces site-specific heterogeneous detection probabilities, and can be exploited to model population size assuming spatial distribution of individuals across survey sites follow a prior distribution (e.g., Poisson distribution; Royle and Nichols, 2003). A heterogeneous landscape with variable habitat likely induces heterogeneous detection of individuals and possibly influences accuracy and precision of population estimates derived from the point-count method.

The N -mixture model has been used to estimate population size from spatially replicated count data (Royle, 2004). The N -mixture model allows for spatial variation in detection and abundance to be calculated directly. The N -mixture is unbiased in parameter

estimation even when similar covariates are used in both the detection and abundance models (Kéry, 2008). The model integrates the binomial likelihood for observed counts over possible values of abundance for each sample point using a prior distribution on abundance (e.g., Poisson, negative binomial, or zero-inflated Poisson; Royle, 2004). The N -mixture model is defined as:

$$n_{it} \sim \text{Binomial}(N_i, p)$$

where n_{it} is the number of distinct individuals counted at location i in time t , N_i is the number of individuals available for sampling (i.e., the population size at location i), and p is the detection probability (Royle, 2004). The likelihood for N_i is then integrated over a prior distribution. The Poisson distribution is a commonly used model for the distribution of organisms. The Poisson mixture estimator is defined as:

$$f(N; \lambda) = \frac{e^{-\lambda} \lambda^N}{N!},$$

where N is the number of individuals available for sampling, and λ is mean of Poisson distribution such that N values follow a Poisson distribution with mean λ (Royle, 2004).

Our objective was to examine how different sampling scenarios, given interaction with environmental factors (i.e., true abundance of individuals and distribution of individuals), influences the accuracy and precision of population estimates derived from the point-count survey method. Accuracy and precision of abundance estimates are both desired for development of sound management practices. Therefore, the influence of sample design on accuracy and precision of population estimates derived from the point-count method must be understood to improve management decisions.

2. Methods

2.1. Modeling approach

We applied sampling scenarios to a computer modeled environment to evaluate the influence of sampling-unit size and number on accuracy and precision of point-count population estimates. A virtual environment consisting of a 10×10 matrix was created to assess the influence of sampling-unit size and the number of sample units on the accuracy and precision of population estimates derived from the point-count method. In our simulations, the total area sampled remained constant among the sample scenarios evaluated (i.e., a total of 24 cells sampled of the 100 available), but scenarios ranged from few samples of large area to many samples of small area.

In addition to the number and unit size of the samples, we also examined how true abundance (density) and distribution of individuals influenced accuracy and precision of population estimates. Individual treatments of true abundance and distribution of individuals were assessed simultaneously with sampling scenarios. All possible combinations of sample scenario, true abundance, and distribution of individuals were evaluated.

The number of individuals that could occur within any one cell was constrained only by true abundance. In order to vary whether an individual within a cell was sampled during any of the three sampling events, each individual within a cell was assigned a detection probability for each sampling event from a random uniform distribution between 0 and 1. Individuals were viewed as sampled if the assigned detection probability exceeded the assigned cell-specific detection probability, which introduced habitat-based heterogeneity to the virtual environment (probabilities were derived from a study of largemouth bass *Micropterus salmoides* detection in a small [12-ha] impoundment;

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