
Wildlife Monitoring Across Multiple Spatial Scales Using Grid-Based Sampling

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Abstract.—Recently, noninvasive genetic sampling has become the most effective way to reliably sample occurrence of many species. In addition, genetic data provide a rich data source enabling the monitoring of population status. The combination of genetically based animal data collected at known spatial coordinates with vegetation, topography, and other available covariates enables development of habitat relationships and evaluation of population attributes, such as connectivity. Colocating animal occurrence sampling on an extensive vegetation plot grid, such as the forest inventory and analysis grid, provides opportunities to develop statistical models and monitor animal populations.

Introduction

The forest inventory and analysis (FIA) plot network provides a strong framework for assessing changes in forest resources over time and, with some constraints due to plot spacing and resource rarity, across space (Frayer and Furnival 1999). Linking FIA data to other co-occurring resources at FIA plot locations provides both direct monitoring of the state of these resources and the development of relationships between these resources and FIA data (Zielinski *et al.* 2006). Here we discuss opportunities associated with collecting animal occurrence data on grids where vegetation data are simultaneously collected. In many cases, noninvasive genetic sampling (e.g., DNA from hair or feces) provides an efficient and information-rich method to survey species.

Historically, direct monitoring of wildlife populations has been considered difficult and expensive, and wildlife population dynamics have largely been inferred through opinion-based habitat relationships. These include systems such as the California Habitat Relationships Database (CDFG 2000)

and specific Habitat Suitability Index (USFWS 1981) models that have been developed for many species. The accuracy of these models is unknown and probably low (Block *et al.* 1994); habitat relationships models generally evaluate habitat at a single spatial scale, involve relatively few variables, and weighting factors are based on guesses rather than on estimates that are statistically derived. In many cases, model quality is not formally testable because habitat rankings (e.g., high, medium, or low) have no precise definitions.

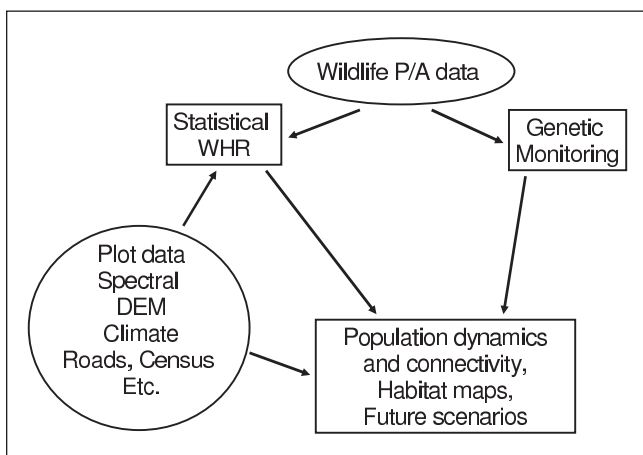
Recently, however, determining animal occurrence or abundance has become much easier due to the rapid evolution of genetic technologies. Rather than needing to trap or photograph an organism to determine presence, many organisms can be identified using evidence such as hair, scats, or feathers. These “noninvasive” genetic samples contain diagnostic DNA for identifying individuals, populations, and species (Morin *et al.* 2001, Taberlet *et al.* 1996). Snowshoe hares (*Lepus americanus*), for example, produce 400 to 500 pellets per day (Hodges 1999). Thus, if snowshoe hares are on a site, pellets (and through DNA confirmation that the pellets were produced by snowshoe hares) can be collected with high reliability and little effort. Because noninvasive sampling facilitates collection of representative samples, rare and elusive organisms such as Canada lynx (*Lynx canadensis*) can now be monitored (McDaniel *et al.* 2000).

An organism’s DNA contains a rich source of data. Identifying an organism to species using DNA is inexpensive, reliable, and unambiguous (McKelvey *et al.* 2006, Mills *et al.* 2000). Species identification, however, represents only a small portion of the information that can be gleaned through genetic analyses. The size of the organism’s population, genealogical relationships to other organisms identified in the area, movement between habitat islands, and many other population attributes can be inferred through analysis of genetic patterns (Luikart and England 1999, Schwartz *et al.* 2007). Many of these genetic analyses require relatively small samples on individuals (e.g., 20 to 40), obviating the need to sample a large proportion of the population to develop strong statistical inferences.

In addition to the direct monitoring of wildlife populations based on genetic measures, new statistical approaches (Cushman and McGarigal 2002, 2004) enable development of habitat associations between animal occurrence or abundance with vegetation data from multiple scales, thereby increasing both the utility of habitat understandings and statistical power. Together, these new developments enable cost-effective wildlife monitoring and the generation of robust statistical wildlife habitat relationships (WHR) models.

Importantly, the monitoring of wildlife populations and the development of statistical WHR models can be analyzed using the same data, and we view these activities as complementary parts of a generalized approach to evaluating multiple wildlife species across extensive landscapes (fig 1). Genetic samples can be used to directly track population status, but, lacking links to vegetation, genetic monitoring contains little information about the effects of management on populations. Multiscale WHR, being population surrogates, are intrinsically weaker than direct monitoring for the purpose of tracking populations but enable quantification of direct relationships between organisms and the landscapes they inhabit. The combination of these two approaches enables higher level analyses such as estimation of the habitat quality and population status in future landscapes and evaluation of landscape connectivity. Therefore, we begin with discussions of genetic monitoring and multiscale WHR

Figure 1.—A diagram showing the relationships between animal occurrence data, vegetation, topography, and anthropogenic data, and monitoring products. The same data set serves multiple, mutually reinforcing purposes.



and follow with an evaluation of landscape connectivity using vegetation, topography, and genetic relationships derived from grid-based black bear (*Ursus americanus*) data.

Genetic Monitoring

Genetic monitoring can evaluate important population characteristics such as population size or connectivity. In many cases, information on the historical status of a population can be gleaned by recovering DNA from archived material (e.g., museum skins, fish scales, or trophy collections) or by inference from patterns of genetic variation in a single contemporary population sample (e.g., deficit of rare alleles [Luikart *et al.* 1998]). This process enables “retrospective monitoring” to assess historical conditions (Poulsen *et al.* 2006).

One type of genetic monitoring (called Category I genetic monitoring in Schwartz *et al.* [2007]) uses noninvasive genetic sampling to count individuals. Multiple samples can be analyzed in a capture-mark-recapture (CMR) framework (Otis *et al.* 1978) to provide population estimates. A second type evaluates changes in population status through changes in genetic diversity using metrics such as expected heterozygosity (H_e) or allelic diversity (A). Both of these metrics, which can be readily measured, theoretically decline over time inversely with population size. H_e , for example, declines at a rate inversely proportional to two times the effective population size (N_e ; a genetic measure of population size) and thus can be used to track population status. In a retrospective study on brown trout (*Salmo trutta*), H_e and A were examined in Denmark between 1944 and 1997; older samples were from scale collections found in museums (Østergaard *et al.* 2003). The analysis concluded that the population was stable over this time period, but maintenance of genetic diversity was dependent on gene flow between small local populations (Østergaard *et al.* 2003).

Several methods exist that convert changes in H_e or temporal changes in allele frequencies into N_e , thus enabling direct tests for changes in effective population size. In another retrospective study, N_e was estimated for brown bears in Yellowstone National Park using samples from the 1910s, 1960s, and 1990s

(Miller and Waits 2003). N_e estimates were ~85 for both time periods (1910–1960s and 1960s–1990s), again suggesting a stable, effective population size but a relatively small effective size.

Population estimates based on CMR yield immediate results whereas detecting a reduction in N_e requires a lag time (e.g., one generation) to allow changes in H_e or allele frequencies to occur (Schwartz *et al.* 1999). Thus, where an immediate estimate of population size is needed, calculating N_e has historically been viewed as a less desirable approach. However, new methods requiring only one sample for each N_e estimate are emerging (England *et al.* 2006, Waples 2006). Although their precision and reliability have not yet been thoroughly quantified, the ability to estimate N_e based on a single sample would greatly expand the utility of N_e as a monitoring tool (Schwartz *et al.* 2007).

Multiscale Wildlife Habitat Relationships

Multiscale gradient modeling is a multivariate, nonlinear regression approach that enables the researcher to predict habitat quality and abundance of organisms based on ecological factors from a range of spatial scales (Cushman and McGarigal 2002, 2003, 2004). Hierarchical gradient modeling maximizes predictive power by optimally incorporating the influence of driving variables across multiple spatial scales, enabling researchers to quantify the independent and interactive effects of multiple factors and scales simultaneously. This includes presence and abundance of species, which are generally related to habitat elements associated with multiple spatial scales as well. For instance, Zabel *et al.* (1995) found that the northern spotted owl (*Strix occidentalis*) habitat was linked to the presence of nest and roost trees (fine scale) and proximity to dense young forest, which contained abundant prey (mid scale). In addition, northern spotted owl range is limited to wet, coastal climates (broad scale). By optimizing the relationship between organisms and environmental structure across scales gradient, models can be used to quantitatively describe species-environment relationships, assess predictive accuracy, and predict and map current species distributions across geographical regions under alternative scenarios.

Gradient models are particularly powerful for WHR because of three important attributes. First, empirical statistical models are developed by optimizing the measured relationship between patterns of organism distribution and measured environmental variation. Importantly, subjective opinion and assumptions are avoided because inserting expert opinion into empirically derived species distribution models may reduce model performance and predictive success (Seoane *et al.* 2005). Second, the distribution and abundance of each modeled species is predicted directly on the basis of measured environmental variables. Thus, the result is not a subjective proxy relationship like most past wildlife habitat models. Third, such models can be directly validated, and their precision, predictive power and error rates are quantified through grid-based sampling.

Landscape Connectivity

Predicting population-level impacts of landscape change depends on identifying factors that influence population connectivity. Most putative movement corridors and barriers have not been based on empirical data, however, largely due to the fact that dispersals are relatively rare and difficult to document. Historically, animal movements were tracked using radio-telemetry. Transmitters were high frequency and had relatively short ranges, so if animals left an area, their signals would be lost. For example, most long-range movements for Canada lynx are associated with lynx that could not be relocated by their transmitters but which were, by chance, turned in by trappers (Aubry *et al.* 2000, Mech 1977). Beyond the difficulties in reliably recording dispersals, a further difficulty lay in separating consequential movements. To be meaningful to population structure, a migrant must affect the population into which it immigrates. Generally, this action would mean reproducing. Because a collared migrant, almost by definition, moved from a studied population to an unstudied one, however, its activities and interactions at the new location were entirely unknown.

Because consequential movements involve breeding, migrants that breed reveal their movement patterns by the genes they leave behind. While genetic similarity is expected to decline with distance, areas with greater similarity than expected (as

a result of more genes shared) represent movement corridors. Conversely, areas that are more divergent are associated with barriers. In theory, reliable inferences about population connectivity can be obtained by correlating genetic similarity of individuals across large landscapes with hypothetical movement-cost models.

As an example, Cushman *et al.* (2006) compared the patterns of genetic similarity among 146 individual black bears sampled across a 3,000-square-km study area in northern Idaho. Genetic similarity was correlated with 110 movement-cost hypotheses describing a range of potential relationships between movement cost and land cover, slope, elevation, roads, Euclidean distance, and a putative movement barrier (a large agricultural valley that bisected the study area). Movement resistance hypotheses were divided into seven organizational models enabling the influence of barriers, distance, and landscape features to be statistically separated. It was found that gene flow patterns, and therefore consequential dispersal movements, were facilitated by contiguous forest cover at middle elevations. Cushman *et al.* (2006) were then able to map these understandings and present a data-based corridor map for the study area.

Discussion

Animal occurrence data, when colocated on a vegetation plot grid can provide statistical links between vegetative condition and population status. When simple occurrence data are expanded through genetic analyses, measures of population size, fragmentation, and connectivity can also be linked to vegetation and other landscape features. The examples presented above serve to demonstrate the potential of these approaches. Although many of the current examples of genetic monitoring have occurred in fisheries, this is not because of any intrinsic sampling advantages associated with aquatic systems. Fish were easy to catch (and therefore easier to collect DNA samples) but hard to count; DNA methods were therefore rapidly implemented to monitor the status and nature of fish populations. With new noninvasive DNA methods, however, DNA from many terrestrial organisms can also be easily collected.

Genetic technologies are rapidly changing; in the future, genetic analyses will be more powerful and less costly. Given the rapid rate of change in genetic technologies, coupled with promising analytical developments such as those illustrated here, the next decade will likely see an explosion of both new analysis methods and on-the-ground applications. Those who are planning animal monitoring should incorporate these understandings to ensure that implementations are maximally cost effective.

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